

PT (ESTs), useful in diagnostic, forensic, gene therapy or chromosome  
PT mapping procedures, or for designing expression vectors and secretion  
PT vectors.  
XX  
PS Disclosure; Fig 5; 163pp; English.  
XX  
CC The invention relates to purified nucleic acids, which comprise sequences  
CC selected from any of more than 50000 sequences not defined in the  
CC specification. The polynucleotide sequences are useful in making cDNA,  
CC polypeptides and promoter DNA, and in diagnostic, forensic, gene therapy  
CC or chromosome mapping procedures. The nucleic acid sequences are also  
CC useful for designing expression vectors and secretion vectors. This  
CC polynucleotide sequence represents a p15B4 promoter transcription binding  
CC site of the invention  
XX  
SQ Sequence 11 BP; 1 A; 7 C; 0 G; 3 T; 0 U; 0 Other;  
  
Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 9 TCGCCCTTCC 19  
Db 1 TCCACCTTCC 11  
  
RESULT 717  
ABK99454  
ID ABK99454 standard; DNA; 11 BP.  
XX  
AC ABK99454;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human CYP3A5 gene polymorphic reference DNA sequence #40.  
XX  
KW Human; CYP3A5; polymorphism; cancer; cardiovascular disease; diabetes;  
KW AIDS; African American; forensic marker; pharmacological; cytostatic;  
KW antidiabetic; anti-HIV; gene therapy; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200253775-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 21-DEC-2001; 2001WO-EP015290.  
XX  
PR 28-DEC-2000; 2000EP-00128627.  
PR 28-DEC-2000; 2000US-0258684P.  
PR 29-DEC-2000; 2000US-0258952P.  
PR 16-JAN-2001; 2001EP-00100172.  
PR 18-JAN-2001; 2001US-0262859P.  
PR 16-AUG-2001; 2001EP-00118884.  
PR 16-AUG-2001; 2001US-0312825P.  
XX  
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.  
XX  
PI Wojnowski L, Haberl M, Hustert E;  
XX  
DR WPI; 2002-583628/62.  
XX  
PT Novel CYP3A5 polynucleotide useful for diagnosis and treatment of cancer,  
PT cardiovascular diseases, diabetes and AIDS, and for identifying  
PT polymorphisms.  
XX  
PS Example 2; Page 51; 138pp; English.  
XX  
CC The present invention relates to a new CYP3A5 polynucleotide encoding a  
CC polypeptide, where the polynucleotide is capable of hybridising to a  
CC CYP3A5 gene. The invention is useful in an in vitro method for  
CC identifying a polymorphism. The invention is also useful for useful for  
CC diagnosing a disorder related to the presence of a molecular variant of a

CC CYP3A5 or susceptibility to such a disorder, where the disorder is  
CC cancer, or diseases including cardiovascular diseases, diabetes and AIDS.  
CC The invention can further be used for the preparation of a diagnostic  
CC composition for diagnosing a disease in a subject having a genome  
CC comprising a variant allele of the CYP3A5 gene, where the subject is an  
CC African American. The molecules of the invention are as forensic markers  
CC and in pharmacological studies. The present nucleic acid sequence  
CC represents a human CYP3A5 gene polymorphism reference DNA sequence, as  
CC described in the invention  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 CCTCATCGCCC 14  
Db 1 CATCATTGCCC 11  
  
RESULT 718  
ADG28157/c  
ID ADG28157 standard; DNA; 11 BP.  
XX  
AC ADG28157;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human Myo/V1 protein-related NFkappaB regulation site SegID161.  
XX  
KW cardiac-associated protein; Myo/V1 protein; MP; cardiant; vasotropic;  
KW immunosuppressive; vulnery; NFkappaB p50; NFkappaB p65;  
KW cardiovascular disease; cardiac hypertrophy; myocardial infarction;  
KW ischaemia; reperfusion injury; heart transplantation;  
KW anti-ageing treatment; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200245659-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 26-OCT-2001; 2001WO-US051272.  
XX  
PR 27-OCT-2000; 2000US-0243985P.  
XX  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX  
PI Sivasubramanian N, Knuefermann P, Mann DL;  
XX  
DR WPI; 2002-537532/57.  
XX  
PT Novel dominant negative mutant sequence or constitutively active mutant  
PT sequence of Myo/V1 polypeptide, useful for treating cardiovascular  
PT disorders and inhibiting formation of NFkappaB homodimers.  
XX  
PS Example 21; SEQ ID NO 161; 217pp; English.  
XX  
CC This invention relates to a novel dominant negative or constitutively  
CC active mutant sequence of the cardiac-associated Myo/V1 protein (MP). The  
CC invention may be useful for the development of compounds with a cardiant,  
CC vasotropic, immunosuppressive or vulnery activity through the  
CC inhibition of formation of NFkappaB p50 or NFkappaB p65 homodimers. The  
CC invention may be useful for the development of treatments for  
CC cardiovascular disease including cardiac hypertrophy, myocardial  
CC infarction, ischaemia/reperfusion injury and heart transplantation, in a  
CC mammal, for anti-ageing treatment, for inhibiting formation of NFkappaB  
CC p50 homodimers or NFkappaB p65 homodimers in a cell of a mammal and for  
CC reducing formation of NFkappaB p65 homodimers in a cell of a mammal.  
XX  
SQ Sequence 11 BP; 3 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCCCTTCCT 20  
Db 11 CGGCGCTTCCT 1

RESULT 719  
ADC66432  
ID ADC66432 standard; DNA; 11 BP.

AC ADC66432;  
XX  
KW 18-DEC-2003 (first entry)  
DT  
XX  
DE Signalling aptamer complex related oligonucleotide.  
XX  
KW signalling aptamer complex; detection; target binding domain;  
KW target complementary region; duplex structure; aptamer; ss.

OS Synthetic.  
XX  
PN WO2003062422-A1.  
XX  
PD 31-JUL-2003.  
XX  
PF 22-JAN-2003; 2003WO-CA000086.  
XX  
PR 22-JAN-2002; 2002US-0349340P.

XX (UYMC-) UNIV MCMASTER.

PI Li Y, Nutiu R;  
XX  
DR WPI; 2003-748010/70.

PT A signaling aptamer complex having a fluorophore and a quencher where  
PT fluorescent signal is quenched when the aptamer is not bound to a target  
PT molecule is useful to detect target molecules including nucleic acids and  
PT proteins in a sample.

XX Example 8; Fig 7A; 59pp; English.

CC The present invention describes a signalling aptamer complex (I) for  
CC detecting a target. (I) comprises a first oligonucleotide (ON1) having a  
CC target binding domain and at least a second oligonucleotide (ON2) having  
CC a sequence complementary to a region of ON1, where in the absence of  
CC target complementary regions of ON1 and ON2 form a duplex structure, and  
CC in the presence of target the duplex dissociates and a reporter signal is  
CC generated. The signaling aptamer complex (I) can be used to detect target  
CC molecules in a sample. Aptamers can bind to nucleic acid molecules,  
CC proteins, small organic compounds or entire organisms. Aptamers are  
CC easier and more cost-effective to make than other recognition molecules  
CC such as antibodies. The present sequence represents an oligonucleotide  
CC which is used in the exemplification of the present invention.

XX Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCTTAAGCA 25  
Db 1 CTTCTCCGCA 11

RESULT 720  
ADH77013  
ID ADH77013 standard; DNA; 11 BP.

XX

AC ADH77013;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE SOX18 wild type DNA sequencing fragment #2.  
XX  
KW Mouse; ds; SOX18; cell differentiation; vasculogenesis; angiogenesis;  
KW hair follicle development; MEF2C; atherosclerosis; cancer; restenosis;  
KW pulmonary disease; tissue injury; hair loss; tumorigenesis;  
KW subgroup F SOX; HMG domain; trans-activation domain;  
KW conserved C terminal domain; arterial wall; vascular smooth muscle;  
KW blood supply; cardiovascular disorder; ischaemic heart injury;  
KW neo-vascularisation; atherosclerotic plaque;  
KW double balloon intravascular catheter; gene transfer;  
KW fibroblast growth factor-1; FGF-1; platelet derived growth factor; PDGF;  
KW femoral artery; intimal hyperplasia; matrix deposition; gene therapy;  
KW cyostatic; antiarteriosclerotic; vasotropic.  
XX  
OS Mus sp.  
XX  
PN US2002142415-A1.  
XX  
PD 03-OCT-2002.  
XX  
PF 23-MAR-2001; 2001US-00814777.  
XX  
PR 24-MAR-2000; 2000AU-00006457.  
XX  
PA (KOOP/) KOOPMAN P A.  
PA (MUSC/) MUSCAT G E O.  
XX  
PI Koopman PA, Muscat GEO;  
XX  
DR WPI; 2003-155943/15.  
XX  
PT Novel SOX18 polypeptide useful for modulating cell differentiation,  
PT vasculogenesis, angiogenesis, hair follicle development, cell  
PT proliferation and tumorigenesis.

PS Disclosure; Fig 13A; 148pp; English.

XX The invention discloses an isolated SOX18 polypeptides, given in the  
CC specification, and biologically active fragments having at least 6 amino  
CC acids in length, or variants having at least 85% sequence identity. Also  
CC claimed are isolated polynucleotides encoding the polypeptides; isolated  
CC polynucleotides encoding polypeptides which modulates an activity  
CC selected from cell differentiation, vasculogenesis, angiogenesis, hair  
CC follicle development; detecting a specific polypeptide or polynucleotide  
CC sequence; detecting a SOX18 polypeptide, by contacting a test polypeptide  
CC with a MEF2C polypeptide in a biological sample; an antigen-binding  
CC molecule that is specifically immuno-interactive; detecting the activity  
CC selected from cell differentiation, vasculogenesis, angiogenesis and hair  
CC follicle development; a composition for treatment and/or prophylaxis of  
CC at least one condition selected from atherosclerosis, cancer, restenosis,  
CC pulmonary disease, tissue injury and hair loss, comprising a SOX18  
CC polypeptide and an agent that enhances the level and/or functional  
CC activity of the polypeptide, together with a carrier; a composition for  
CC treatment and/or prophylaxis of tumorigenesis, comprising an agent that  
CC reduces the level and/or functional activity of at least one subgroup F  
CC SOX polypeptide, together with a carrier and a composition comprising one  
CC or more agents that enhances the level and/or functional activity of at  
CC least two subgroup F SOX polypeptides. The biologically active fragment  
CC is at least 8 amino acids in length and comprises a SOX18 HMG domain,  
CC SOX18 trans-activation domain, SOX18 conserved C terminal domain, or a  
CC portion of the domain having at least 6 amino acids in length. Delivery  
CC of recombinant Sox18 into arterial walls had use in the stimulation of  
CC vascular smooth muscle cells to improve blood supply and flow in a  
CC several cardiovascular disorders including ischaemic heart injury and the  
CC neo-vascularisation of atherosclerotic plaques. This was achieved using a  
CC similar double balloon intravascular catheter mediated gene transfer  
CC approach of fibroblast growth factor (FGF)-1 and platelet derived growth  
CC factor (PDGF) into the femoral arteries resulted in induced intimal  
CC hyperplasia, angiogenesis and matrix deposition. The polynucleotides may



CC be used in gene therapy. The sequence presented is wild-type mouse SOX18  
CC fragment.  
XX  
SQ Sequence 11 BP; 0 A; 6 C; 3 G; 2 T; 0 U; 0 Other; 0; Gaps 0;

Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCCTTCCT 20  
Db 1 CGCCCCTGGCT 11

RESULT 721  
ADQ36146  
ID ADQ36146 standard; DNA; 11 BP.  
XX  
AC ADQ36146;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 963.  
XX  
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260931-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060931.  
XX  
PR 20-DEC-2002; 2002DE-01060931.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518857/50.  
XX  
PT In vitro identification of genes important for hair-bearing skin, useful  
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 4; SEQ ID NO 963; 250pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for hair-bearing skin in humans. The method  
CC comprises recovering, from hair-bearing skin, a first mixture of  
CC genetically expressed (transcribed and optionally translated) factors  
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar  
CC mixture from skin on which hair does not grow and subjecting both  
CC mixtures to serial analysis of gene expression (SAGE) to identify those  
CC genes for which expression is markedly different between the two types of  
CC skin. The invention also describes in vitro methods for determining  
CC homeostasis of human hair-bearing skin and for determining activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and  
CC a test kit comprising a solid support (flexible or rigid) with  
CC immobilised probes are also described for determining homeostasis. The  
CC hair-bearing skin is from the scalp and the other skin is from the face.  
CC The method allows identification of as many as possible of the genes  
CC important for hair-bearing skin, and therefore, of a very wide range of  
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent  
CC human DNA Tag fragments used to identify genes associated with hair-  
CC bearing skin.  
XX  
SQ Sequence 11 BP; 2 A; 8 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15  
Db 1 CTCAACCCCC 11

RESULT 722  
ADQ35222  
ID ADQ35222 standard; DNA; 11 BP.  
XX  
AC ADQ35222;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 39.  
XX  
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260931-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060931.  
XX  
PR 20-DEC-2002; 2002DE-01060931.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518857/50.  
XX  
PT In vitro identification of genes important for hair-bearing skin, useful  
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 9; SEQ ID NO 39; 250pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for hair-bearing skin in humans. The method  
CC comprises recovering, from hair-bearing skin, a first mixture of  
CC genetically expressed (transcribed and optionally translated) factors  
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar  
CC mixture from skin on which hair does not grow and subjecting both  
CC mixtures to serial analysis of gene expression (SAGE) to identify those  
CC genes for which expression is markedly different between the two types of  
CC skin. The invention also describes in vitro methods for determining  
CC homeostasis of human hair-bearing skin and for determining activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and  
CC a test kit comprising a solid support (flexible or rigid) with  
CC immobilised probes are also described for determining homeostasis. The  
CC hair-bearing skin is from the scalp and the other skin is from the face.  
CC The method allows identification of as many as possible of the genes  
CC important for hair-bearing skin, and therefore, of a very wide range of  
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent  
CC human DNA Tag fragments used to identify genes associated with hair-  
CC bearing skin.  
XX  
SQ Sequence 11 BP; 3 A; 7 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22

Db		
	1 CCCCCACCTAA	11
RESULT 723		
ADQ35034/c		
ID	ADQ35034	standard; DNA; 11 BP.
XX		
AC	ADQ35034;	
XX		
DT	23-SEP-2004	(first entry)
XX		
DE	Human facial skin-associated DNA fragment	SEQ ID NO 3124.
XX		
KW	facial skin; human; serial analysis of gene expression; SAGE;	
KW	homeostasis; biochip; cosmetic; pharmaceutical; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	DE10260928-A1.	
XX		
PD	08-JUL-2004.	
XX		
PF	20-DEC-2002; 2002DE-01060928.	
XX		
PR	20-DEC-2002; 2002DE-01060928.	
XX		
PA	(HENK ) HENKEL KGAA.	
XX		
PI	Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;	
PI	Conradt M, Hofmann K;	
XX		
DR	WPI; 2004-518855/50.	
XX		
PT	In vitro identification of genes important for facial skin, useful for	
PT	assessing homeostasis and in screening for pharmaceutical or cosmetic	
PT	agents, based on differential expression analysis.	
XX		
PS	Claim 4; SEQ ID NO 3124; 577pp; German.	
XX		
CC	This invention describes a novel in vitro method for identifying genes	
CC	that are significant for facial skin in humans. The method comprises	
CC	recovering, from facial skin, a first mixture of genetically expressed	
CC	(transcribed and optionally translated) factors (i.e. proteins, mRNA or	
CC	their fragments), recovering a second, similar mixture from some other	
CC	human tissue, preferably skin from a protected area, especially from the	
CC	breast and subjecting the mixtures to serial analysis of gene expression	
CC	(SAGE) to identify those genes for which expression is markedly different	
CC	between facial skin and the other tissue. The invention also describes an	
CC	in vitro method for determining homeostasis of human facial skin; a test	
CC	kit which comprises a solid support (flexible or rigid) on which are	
CC	immobilised probes that bind specifically to the factors of interest and	
CC	a biochip for determining homeostasis of human facial skin. The products	
CC	of the invention are also used in a method which determines activity of	
CC	cosmetic and pharmaceutical agents for use against disorders or	
CC	disturbances of the homeostasis of human skin and a screening method for	
CC	identifying cosmetic and pharmaceutical agents. The method allows	
CC	identification of as many as possible of the genes important for facial	
CC	skin and thus of a very wide range of potential therapeutic and cosmetic	
CC	agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to	
CC	identify the facial skin-associated genes described in the invention.	
XX		
SQ	Sequence 11 BP; 3 A; 2 C; 6 G; 0 T; 0 U; 0 Other;	
Query Match 30.0%; Score 7.8; DB 1; Length 11;		
Best Local Similarity 81.8%; Pred. No. 3.2e+02;		
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 6 TCATCGCCCT 16		
Db	11 TCTGGGCCCT 1	

RESULT 724		
ADQ34728		
ID	ADQ34728	standard; DNA; 11 BP.
XX		
AC	ADQ34728;	
XX		
DT	23-SEP-2004	(first entry)
XX		
DE	Human facial skin-associated DNA fragment	SEQ ID NO 2818.
XX		
KW	facial skin; human; serial analysis of gene expression; SAGE;	
KW	homeostasis; biochip; cosmetic; pharmaceutical; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	DE10260928-A1.	
XX		
PD	08-JUL-2004.	
XX		
PF	20-DEC-2002; 2002DE-01060928.	
XX		
PR	20-DEC-2002; 2002DE-01060928.	
XX		
PA	(HENK ) HENKEL KGAA.	
XX		
PI	Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;	
PI	Conradt M, Hofmann K;	
XX		
DR	WPI; 2004-518855/50.	
XX		
PT	In vitro identification of genes important for facial skin, useful for	
PT	assessing homeostasis and in screening for pharmaceutical or cosmetic	
PT	agents, based on differential expression analysis.	
XX		
PS	Claim 4; SEQ ID NO 2818; 577pp; German.	
XX		
CC	This invention describes a novel in vitro method for identifying genes	
CC	that are significant for facial skin in humans. The method comprises	
CC	recovering, from facial skin, a first mixture of genetically expressed	
CC	(transcribed and optionally translated) factors (i.e. proteins, mRNA or	
CC	their fragments), recovering a second, similar mixture from some other	
CC	human tissue, preferably skin from a protected area, especially from the	
CC	breast and subjecting the mixtures to serial analysis of gene expression	
CC	(SAGE) to identify those genes for which expression is markedly different	
CC	between facial skin and the other tissue. The invention also describes an	
CC	in vitro method for determining homeostasis of human facial skin; a test	
CC	kit which comprises a solid support (flexible or rigid) on which are	
CC	immobilised probes that bind specifically to the factors of interest and	
CC	a biochip for determining homeostasis of human facial skin. The products	
CC	of the invention are also used in a method which determines activity of	
CC	cosmetic and pharmaceutical agents for use against disorders or	
CC	disturbances of the homeostasis of human skin and a screening method for	
CC	identifying cosmetic and pharmaceutical agents. The method allows	
CC	identification of as many as possible of the genes important for facial	
CC	skin and thus of a very wide range of potential therapeutic and cosmetic	
CC	agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to	
CC	identify the facial skin-associated genes described in the invention.	
XX		
SQ	Sequence 11 BP; 0 A; 5 C; 2 G; 4 T; 0 U; 0 Other;	
Query Match 30.0%; Score 7.8; DB 1; Length 11;		
Best Local Similarity 81.8%; Pred. No. 3.2e+02;		
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY 10 CGCCCTTCTT 20		
Db	1 CGCCGCTTCTT 11	

RESULT 725		
ADQ32871		
ID	ADQ32871	standard; DNA; 11 BP.
XX		

AC ADQ32871;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 961.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 961; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
XX identify the facial skin-associated genes described in the invention.  
SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 CCTCATCGCCC 14  
Db ||||| |||  
1 CCTCATTTCCC 11  
  
RESULT 726  
ADQ33165/C  
ID ADQ33165 standard; DNA; 11 BP.  
XX  
AC ADQ33165;  
XX  
DT 23-SEP-2004 (first entry)  
XX

DE Human facial skin-associated DNA fragment SEQ ID NO 1255.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 5; SEQ ID NO 1255; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
XX identify the facial skin-associated genes described in the invention.  
SQ Sequence 11 BP; 3 A; 0 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 12 CCCCTTCCTAA 22  
Db ||||| |||  
11 CCCCTTCCTAA 1  
  
RESULT 727  
ADQ33777/C  
ID ADQ33777 standard; DNA; 11 BP.  
XX  
AC ADQ33777;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 1867.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.

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XX OS Homo sapiens.
XX PN DE10260928-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX DR WPI; 2004-518855/50.
XX PT In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX PS Claim 5; SEQ ID NO 1867; 577pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match          30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCGCCCTTC 19
Db 11 TCGACCTGCC 1

RESULT 728
ADY89233/c
ID ADY89233 standard; RNA; 11 BP.
XX AC ADY89233;
XX DT 16-JUN-2005 (first entry)
XX DE VEGF siRNA SEQ ID NO 2269.
XX ss; siRNA; short interfering RNA; RNA interference; gene silencing; VEGF;
KW pharmaceutical; cancer; neoplasm; Cytostatic.
XX OS Synthetic.
XX PN WO2005028649-A1.
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XX 31-MAR-2005.
XX 16-SEP-2004; 2004WO-US030488.
XX 16-SEP-2003; 2003US-00664767.
XX 16-SEP-2003; 2003US-00665255.
XX 23-SEP-2003; 2003US-00670011.
XX 23-OCT-2003; 2003US-00693059.
XX 24-NOV-2003; 2003US-00720448.
XX 03-DEC-2003; 2003US-00727780.
XX 14-JAN-2004; 2004US-00757803.
XX 26-JAN-2004; 2004US-00764957.
XX 10-FEB-2004; 2004US-0543480P.
XX 13-FEB-2004; 2004US-00780447.
XX 16-APR-2004; 2004US-00826966.
XX 23-APR-2004; 2004US-00831620.
XX 30-APR-2004; 2004US-00013456.
XX 11-MAY-2004; 2004US-00844076.
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX PI Jadhav V, Kossen K, Zinnen S, Vaish N, Mcswiggen J;
XX WPI; 2005-254128/26.
XX DR New multifunctional siNA molecule that directs cleavage of the first and
XX PT second VEGF or VEGFR target sequences via RNA interference, useful in
XX PT preparing a composition for treating cell proliferative disorders e.g.
XX PT cancers.
XX PS Disclosure; SEQ ID NO 2269; 396pp; English.
XX CC The invention relates to a multifunctional siNA molecule comprising a
XX CC structure having Formula MF-III and which directs cleavage of the first
XX CC and second VEGF or VEGFR target sequences via RNA interference. The
XX CC multifunctional siNA molecule is useful in preparing a pharmaceutical
XX CC composition for treating cell proliferative disorders, e.g. cancer. The
XX CC present sequence represents a VEGF siRNA.
XX SQ Sequence 11 BP; 5 A; 0 C; 6 G; 0 T; 0 U; 0 Other;

Query Match          30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
Db 11 CTCCTCTTCCT 1

RESULT 729
AEA14699/c
ID AEA14699 standard; DNA; 11 BP.
XX AC AEA14699;
XX DT 14-JUL-2005 (first entry)
XX DE Immunostimulatory oligonucleotide ~ SEQ ID 14.
XX KW immune stimulation; viral infection; virucide; bacterial infection;
KW antibacterial; fungal infection; fungicide; parasitic infection;
KW antiparasitic; allergy; antiallergic; asthma; antiasthmatic; cancer;
KW cytostatic; ss.
XX OS Unidentified.
XX PN WO2005042018-A2.
XX PD 12-MAY-2005.
XX PF 29-OCT-2004; 2004WO-US036240.
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XX 30-OCT-2003; 2003US-0516193P.  
PR (COLE-) COLEY PHARM GMBH.  
XX (COLE-) COLEY PHARM GROUP INC.  
PA  
PA  
XX  
PI Uhlmann E, Vollmer J, Krieg AM, Noll BO;  
XX WPI; 2005-333611/34.  
DR  
XX  
XX  
PT New composition comprising an immunostimulatory nucleic acid molecule  
PT useful for manufacturing a medicament for the treatment of an infection  
PT (e.g. viral or bacterial), allergic condition (e.g. allergic asthma) or  
PT cancer.  
XX  
PS Claim 29; SEQ ID NO 14; 113pp; English.  
XX  
CC The invention comprises a composition that contains an immunostimulatory  
CC nucleic acid. The immunostimulatory nucleic acid of the invention is  
CC useful for manufacturing a medicament for the treatment of an infection  
CC (e.g. viral, bacterial, fungal or parasitical), an allergic condition  
CC (e.g. allergic asthma), or cancer. The present DNA sequence represents an  
CC immunostimulatory oligonucleotide of the invention.  
XX  
SQ Sequence 11 BP; 2 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 30.0%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 3.2e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 3 ACCTCATCGCC 13  
Db 11 ACCTCCTCGAC 1

Search completed: May 9, 2006, 16:57:18  
Job time : 1 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:59:40 ; Search time 0.001 Seconds  
(Without alignments)  
203.528 Million cell updates/sec

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Sequence: 1 ccacctcatcgccctcctaagcat 26

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 309 seqs, 3914 residues

Total number of hits satisfying chosen parameters: 618

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 309 summaries

Database : pubmaindb4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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C 122	9.4	36.2	12	1	US-10-257-017B-377399	Sequence 377399,
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C 124	9.4	36.2	12	1	US-11-078-601-53	Sequence 53, Appl
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C 158	9.4	36.2	13	1	US-10-257-017B-117648	Sequence 117648,
C 159	9.4	36.2	13	1	US-10-257-017B-126495	Sequence 126495,
C 160	9.4	36.2	13	1	US-10-257-017B-126496	Sequence 126496,
C 161	9.4	36.2	13	1	US-10-257-017B-131503	Sequence 131503,
C 162	9.4	36.2	13	1	US-10-257-017B-131504	Sequence 131504,
C 163	9.4	36.2	13	1	US-10-257-017B-131881	Sequence 131881,
C 164	9.4	36.2	13	1	US-10-257-017B-131882	Sequence 131882,
C 165	9.4	36.2	13	1	US-10-257-017B-131885	Sequence 131885,
C 166	9.4	36.2	13	1	US-10-257-017B-131886	Sequence 131886,
C 167	9.4	36.2	13	1	US-10-257-017B-149605	Sequence 149605,
C 168	9.4	36.2	13	1	US-10-257-017B-149606	Sequence 149606,
C 169	9.4	36.2	13	1	US-10-257-017B-154545	Sequence 154545,
C 170	9.4	36.2	13	1	US-10-257-017B-154546	Sequence 154546,
C 171	9.4	36.2	13	1	US-10-257-017B-160177	Sequence 160177,
C 172	9.4	36.2	13	1	US-10-257-017B-160178	Sequence 160178,
C 173	9.4	36.2	13	1	US-10-257-017B-160495	Sequence 160495,
C 174	9.4	36.2	13	1	US-10-257-017B-160496	Sequence 160496,
C 175	9.4	36.2	13	1	US-10-257-017B-167797	Sequence 167797,
C 176	9.4	36.2	13	1	US-10-257-017B-167798	Sequence 167798,
C 177	9.4	36.2	13	1	US-10-257-017B-169489	Sequence 169489,
C 178	9.4	36.2	13	1	US-10-257-017B-169490	Sequence 169490,
C 179	9.4	36.2	13	1	US-10-257-017B-171151	Sequence 171151,

:

,



253	8.8	33.8	12	1	US-10-257-017B-295712	Sequence 295712,
254	8.8	33.8	12	1	US-10-257-017B-298724	Sequence 298724,
C 255	8.8	33.8	12	1	US-10-257-017B-299865	Sequence 299865,
C 256	8.8	33.8	12	1	US-10-257-017B-300302	Sequence 300302,
C 257	8.8	33.8	12	1	US-10-257-017B-302104	Sequence 302104,
C 258	8.8	33.8	12	1	US-10-257-017B-303551	Sequence 303551,
259	8.8	33.8	12	1	US-10-257-017B-304348	Sequence 304348,
260	8.8	33.8	12	1	US-10-257-017B-306913	Sequence 306913,
C 261	8.8	33.8	12	1	US-10-257-017B-313065	Sequence 313065,
C 262	8.8	33.8	12	1	US-10-257-017B-313798	Sequence 313798,
263	8.8	33.8	12	1	US-10-257-017B-314753	Sequence 314753,
264	8.8	33.8	12	1	US-10-257-017B-314756	Sequence 314756,
265	8.8	33.8	12	1	US-10-257-017B-314759	Sequence 314759,
266	8.8	33.8	12	1	US-10-257-017B-314762	Sequence 314762,
C 267	8.8	33.8	12	1	US-10-257-017B-315110	Sequence 315110,
268	8.8	33.8	12	1	US-10-257-017B-315369	Sequence 315369,
269	8.8	33.8	12	1	US-10-257-017B-315967	Sequence 315967,
C 270	8.8	33.8	12	1	US-10-257-017B-317533	Sequence 317533,
271	8.8	33.8	12	1	US-10-257-017B-319294	Sequence 319294,
272	8.8	33.8	12	1	US-10-257-017B-320903	Sequence 320903,
C 273	8.8	33.8	12	1	US-10-257-017B-322792	Sequence 322792,
274	8.8	33.8	12	1	US-10-257-017B-323185	Sequence 323185,
275	8.8	33.8	12	1	US-10-257-017B-323187	Sequence 323187,
C 276	8.8	33.8	12	1	US-10-257-017B-326521	Sequence 326521,
C 277	8.8	33.8	12	1	US-10-257-017B-327842	Sequence 327842,
278	8.8	33.8	12	1	US-10-257-017B-328615	Sequence 328615,
279	8.8	33.8	12	1	US-10-257-017B-329701	Sequence 329701,
280	8.8	33.8	12	1	US-10-257-017B-334701	Sequence 334701,
281	8.8	33.8	12	1	US-10-257-017B-335615	Sequence 335615,
C 282	8.8	33.8	12	1	US-10-257-017B-337282	Sequence 337282,
C 283	8.8	33.8	12	1	US-10-257-017B-339583	Sequence 339583,
C 284	8.8	33.8	12	1	US-10-257-017B-344435	Sequence 344435,
285	8.8	33.8	12	1	US-10-257-017B-344922	Sequence 344922,
C 286	8.8	33.8	12	1	US-10-257-017B-348072	Sequence 348072,
C 287	8.8	33.8	12	1	US-10-257-017B-349107	Sequence 349107,
C 288	8.8	33.8	12	1	US-10-257-017B-349377	Sequence 349377,
C 289	8.8	33.8	12	1	US-10-257-017B-350201	Sequence 350201,
C 290	8.8	33.8	12	1	US-10-257-017B-350285	Sequence 350285,
291	8.8	33.8	12	1	US-10-257-017B-350759	Sequence 350759,
292	8.8	33.8	12	1	US-10-257-017B-354578	Sequence 354578,
C 293	8.8	33.8	12	1	US-10-257-017B-356323	Sequence 356323,
C 294	8.8	33.8	12	1	US-10-257-017B-357355	Sequence 357355,
295	8.8	33.8	12	1	US-10-257-017B-357650	Sequence 357650,
296	8.8	33.8	12	1	US-10-257-017B-358254	Sequence 358254,
C 297	8.8	33.8	12	1	US-10-257-017B-359463	Sequence 359463,
C 298	8.8	33.8	12	1	US-10-257-017B-360360	Sequence 360360,
C 299	8.8	33.8	12	1	US-10-257-017B-362746	Sequence 362746,
C 300	8.8	33.8	12	1	US-10-257-017B-364264	Sequence 364264,
C 301	8.8	33.8	12	1	US-10-257-017B-368210	Sequence 368210,
302	8.8	33.8	12	1	US-10-257-017B-370744	Sequence 370744,
303	8.8	33.8	12	1	US-10-257-017B-371049	Sequence 371049,
C 304	8.8	33.8	12	1	US-10-257-017B-372640	Sequence 372640,
305	8.8	33.8	12	1	US-10-257-017B-373933	Sequence 373933,
C 306	8.8	33.8	12	1	US-10-257-017B-374652	Sequence 374652,
307	8.8	33.8	12	1	US-10-257-017B-378396	Sequence 378396,
308	8.8	33.8	12	1	US-10-257-017B-381325	Sequence 381325,
309	8.8	33.8	12	1	US-10-257-017B-381966	Sequence 381966,

## ALIGNMENTS

RESULT 1  
US-09-904-968A-4  
; Sequence 4, Application US/09904968A  
; Publication No. US20030008288A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: GERMINO, Gregory  
; APPLICANT: WATNICK, Terry  
; APPLICANT: PHAKDEKITCHAREEN, Bunyong  
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE  
; FILE REFERENCE: JHU1680-2

; CURRENT APPLICATION NUMBER: US/09/904,968A  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/283,691  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/218,261  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer BPR9  
US-09-904-968A-4

Query Match 100.0%; Score 26; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.52;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCTTAAGCAT 26  
Db 1 CCACCTCATCGCCCTTCTTAAGCAT 26

RESULT 2  
US-10-455-229-6/c  
; Sequence 6, Application US/10455229  
; Publication No. US20040016030A1  
; GENERAL INFORMATION:  
; APPLICANT: LOWE, BRENDA A.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF MAIZE LINES  
; FILE REFERENCE: DEKM:195US  
; CURRENT APPLICATION NUMBER: US/10/455,229  
; PRIOR APPLICATION NUMBER: 2003-06-05  
; PRIOR FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-455-229-6

Query Match 55.4%; Score 14.4; DB 1; Length 20;  
Best Local Similarity 93.8%; Pred. No. 25;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCTTCTTA 21  
Db 20 TCATCGCCCTTCTTA 5

RESULT 3  
US-08-983-605-11  
; Sequence 11, Application US/08983605A  
; Publication No. US20020066118A1  
; GENERAL INFORMATION:  
; APPLICANT: Roder, Marion  
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species  
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticaceae and the Use of  
; FILE REFERENCE: 2936.10400  
; CURRENT APPLICATION NUMBER: US/08/983,605A  
; CURRENT FILING DATE: 1998-05-01  
; EARLIER APPLICATION NUMBER: DE 195 25 284.5  
; EARLIER FILING DATE: 1995-06-28

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; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-11
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Query Match          49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      1 CCACCTCATCGCCCT 16
        |||||
Db      2 CGACCTGATCGCCCT 17
```

## RESULT 4

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US-10-697-527-11
; Sequence 11, Application US/10697527
; Publication No. US20040146898A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: MICROSATELLITE MARKERS FOR PLANTS OF THE SPECIES TRITICUM AESTIVU
; FILE REFERENCE: US 08/983,605
; CURRENT APPLICATION NUMBER: US/10/697,527
; PRIOR FILING DATE: 1996-06-27
; PRIOR APPLICATION NUMBER: PCT/DE96/01185
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Triticum sp.
US-10-697-527-11
```

```
Query Match          49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 CCACCTCATCGCCCT 16
        |||||
Db      2 CGACCTGATCGCCCT 17
```

## RESULT 5

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US-09-866-108-242
; Sequence 242, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 242
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-242
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Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy      4 CCTCATCGCCCTTCCT 20
        |||||
Db      1 CATCCTCGCCCTCCT 17
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## RESULT 6

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US-09-866-108-755/C
; Sequence 755, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
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```
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7555
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-7555
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```
Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY          9 TCGCCCTTCTAGCA 25
Db          17 TGGCCCGTCATAGCA 1
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```
RESULT 7
US-09-780-533A-2547/c
; Sequence 2547, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2547
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2547
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```
Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY          5 CTCATGCCCCCTTCTA 21
Db          17 CTCATGCGCTTCTATA 1
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RESULT 8
US-10-723-361-242
; Sequence 242, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
```

```
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 242
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-242
```

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Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          4 CCTCATGCCCCCTTCTT 20
Db          1 CATCCTGCCCCCTTCTT 17
```

```
RESULT 9
US-10-723-361-7555/c
; Sequence 7555, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 7555
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-7555

Query Match          46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      9 TCGCCCTTCTCTAGCA 25
        ||||| |||||
Db      17 TGGCCCCGTCTATAGCA 1

RESULT 10
US-10-257-017B-109215/c
; Sequence 109215, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109215
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109215

Query Match          43.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 67;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
        ||||| |||||
Db      13 ACCTCATCCCCC 1

RESULT 11
US-10-257-017B-109216
; Sequence 109216, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 109216
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109216

Query Match          43.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 67;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
        ||||| |||||
Db      1 ACCTCATCCCCC 13

RESULT 12
US-10-604-944-105/c
; Sequence 105, Application US/10604944
; Publication No. US20040219515A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL HIV REGULATORY GENES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 55008
; CURRENT APPLICATION NUMBER: US/10/604,944
; CURRENT FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 406
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus 1
US-10-604-944-105

Query Match          43.1%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCCCT 16
        ||||| |||||
Db      16 CAACTCATCTCCCT 1

RESULT 13
US-10-056-414-33
; Sequence 33, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth G.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; FILE REFERENCE: NF-KB
; CURRENT APPLICATION NUMBER: 830
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; SUITE: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/10/056,414  
FILING DATE: 23-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-10-056-414-33

Query Match 41.5%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 78.6%; Pred. No. 79;  
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGGCC 14  
Db 2 CCACCUCACCGGCC 15

RESULT 14  
US-10-056-414-126  
Sequence 126, Application US/10056414  
Publication No. US20030003469A1  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
Draper, Kenneth G.  
McSwigen, James  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
RELATED TO LEVELS OF  
NF-KB  
NUMBER OF SEQUENCES: 830  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056,414  
FILING DATE: 23-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 126:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 126:  
US-10-056-414-126

Query Match 41.5%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 64.3%; Pred. No. 79;  
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAGC 24  
Db 1 GUCCCUUCUCAGC 14

RESULT 15  
US-10-056-414-153  
Sequence 153, Application US/10056414  
Publication No. US20030003469A1  
GENERAL INFORMATION:  
APPLICANT: Stinchcomb, Dan T.  
Draper, Kenneth G.  
McSwigen, James  
TITLE OF INVENTION: RIBOZYME TREATMENT OF  
DISEASES OR CONDITIONS  
RELATED TO LEVELS OF  
NF-KB  
NUMBER OF SEQUENCES: 830  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/056,414  
FILING DATE: 23-Jan-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/291,932A  
FILING DATE: August 15, 1994  
APPLICATION NUMBER: 08/245,466  
FILING DATE: May 18, 1994  
APPLICATION NUMBER: 07/987,132  
FILING DATE: December 7, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 208/157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

```
; INFORMATION FOR SEQ ID NO: 153:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 15 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 153:
US-10-056-414-153

Query Match          41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 79;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      11 GCCCCTTCCTAAGC 24
        |||::||:||||
Db       1 GUCCCTUCCUCACG 14

RESULT 16
US-10-056-414-158
; Sequence 158, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
;   APPLICANT: Stinchcomb, Dan T.
;               Draper, Kenneth G.
;               McSwiggen, James
;   TITLE OF INVENTION: RIBOZYME TREATMENT OF
;                       DISEASES OR CONDITIONS
;                       RELATED TO LEVELS OF
;                       NF-KB
;   NUMBER OF SEQUENCES: 830
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Lyon & Lyon
;       STREET: 633 West Fifth Street
;               Suite 4700
;       CITY: Los Angeles
;       STATE: California
;       COUNTRY: U.S.A.
;       ZIP: 90071-2066
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: 3.5" Diskette, 1.44 MB
;       storage
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: IBM P.C. DOS 5.0
;   SOFTWARE: Word Perfect 5.1
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/056,414
;       FILING DATE: 23-Jan-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/08/291,932A
;       FILING DATE: August 15, 1994
;       APPLICATION NUMBER: 08/245,466
;       FILING DATE: May 18, 1994
;       APPLICATION NUMBER: 07/987,132
;       FILING DATE: December 7, 1992
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Warburg, Richard J.
;       REGISTRATION NUMBER: 32,327
;       REFERENCE/DOCKET NUMBER: 208/157
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (213) 489-1600
;       TELEFAX: (213) 955-0440
;       TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 158:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 158:
US-10-056-414-158
```

```
Query Match          41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 79;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      11 GCCCCTTCCTAAGC 24
        |||::||:||||
Db       2 GUCCCTUCCUCACG 15

RESULT 17
US-10-056-414-162
; Sequence 162, Application US/10056414
; Publication No. US20030003469A1
; GENERAL INFORMATION:
;   APPLICANT: Stinchcomb, Dan T.
;               Draper, Kenneth G.
;               McSwiggen, James
;   TITLE OF INVENTION: RIBOZYME TREATMENT OF
;                       DISEASES OR CONDITIONS
;                       RELATED TO LEVELS OF
;                       NF-KB
;   NUMBER OF SEQUENCES: 830
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Lyon & Lyon
;       STREET: 633 West Fifth Street
;               Suite 4700
;       CITY: Los Angeles
;       STATE: California
;       COUNTRY: U.S.A.
;       ZIP: 90071-2066
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: 3.5" Diskette, 1.44 MB
;       storage
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: IBM P.C. DOS 5.0
;   SOFTWARE: Word Perfect 5.1
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/056,414
;       FILING DATE: 23-Jan-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/08/291,932A
;       FILING DATE: August 15, 1994
;       APPLICATION NUMBER: 08/245,466
;       FILING DATE: May 18, 1994
;       APPLICATION NUMBER: 07/987,132
;       FILING DATE: December 7, 1992
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Warburg, Richard J.
;       REGISTRATION NUMBER: 32,327
;       REFERENCE/DOCKET NUMBER: 208/157
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (213) 489-1600
;       TELEFAX: (213) 955-0440
;       TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 162:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-10-056-414-162

Query Match          41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATGCCCTTCCT 20
        ||:||||::||:
Db       2 CAUGGUCCUCU 15
```

```
RESULT 18
US-10-257-017B-303995/c
; Sequence 303995, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303995
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020735
US-10-257-017B-303995

Query Match
Best Local Similarity 40.0%; Score 10.4; DB 1; Length 12;
Matches 11; Conservativity 91.7%; Pred. No. 92;
Mismatches 0; Indels 1; Gaps 0;

QY 12 CCCCTTCCTAG 23
Db 12 CCCCTTCCTAG 1

RESULT 19
US-10-257-017B-308420/c
; Sequence 308420, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 308420
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0023007
US-10-257-017B-308420

Query Match
Best Local Similarity 40.0%; Score 10.4; DB 1; Length 12;
Matches 11; Conservativity 91.7%; Pred. No. 92;
Mismatches 0; Indels 1; Gaps 0;

QY 14 CCTTCCTAAGCA 25
Db 12 CCTTCCTAAGCA 1

RESULT 20
US-10-257-017B-2227/c
; Sequence 2227, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 2227
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000901
US-10-257-017B-2227

Query Match
Best Local Similarity 40.0%; Score 10.4; DB 1; Length 13;
Matches 11; Conservativity 91.7%; Pred. No. 91;
Mismatches 0; Indels 1; Gaps 0;

QY 14 CCTTCCTAAGCA 25
Db 12 CCTTCCTAAGCA 1

RESULT 21
US-10-257-017B-2228
; Sequence 2228, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 2228
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000901
US-10-257-017B-2228

Query Match
Best Local Similarity 40.0%; Score 10.4; DB 1; Length 13;
Matches 11; Conservativity 91.7%; Pred. No. 91;
Mismatches 0; Indels 1; Gaps 0;

QY 14 CCTTCCTAAGCA 25
Db 2 CCTTCCTAAGCA 13

RESULT 22
US-10-257-017B-11629/c
; Sequence 11629, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11629
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002818
US-10-257-017B-11629

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATCGCCCC 15
        | |||||
Db      13 CTTCATCGCCCC 2

RESULT 23
US-10-257-017B-11630
; Sequence 11630, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11630
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002818
US-10-257-017B-11630

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATCGCCCC 15
        | |||||
Db      1 CTTCATCGCCCC 12

RESULT 24
US-10-257-017B-63253/c
; Sequence 63253, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63253
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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---

```
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016710
US-10-257-017B-63253

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATCGCCCC 15
        | |||||
Db      12 CCTCATCCCCC 1

RESULT 25
US-10-257-017B-63254
; Sequence 63254, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63254
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016710
US-10-257-017B-63254

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 CCTCATCGCCCC 15
        | |||||
Db      2 CCTCATCCCCC 13

RESULT 26
US-10-257-017B-86351/c
; Sequence 86351, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86351
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021689
US-10-257-017B-86351

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



QY 4 CCTCATCGCCCC 15  
| | | | |  
Db 13 CCTCACC GCCC 2

## RESULT 27

US-10-257-017B-86352  
; Sequence 86352, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 86352  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021689  
US-10-257-017B-86352

Query Match 40.0%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 91;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15  
| | | | |  
Db 1 CCTCACC GCCC 12

## RESULT 28

US-10-257-017B-171701/c  
; Sequence 171701, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 171701  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042797  
US-10-257-017B-171701

Query Match 40.0%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 91;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15  
| | | | |  
Db 12 CCTCATCTCCCC 1

## RESULT 29

US-10-257-017B-171702

; Sequence 171702, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 171702  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042797  
US-10-257-017B-171702

Query Match 40.0%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 91;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15  
| | | | |  
Db 2 CCTCATCTCCCC 13

## RESULT 30

US-10-257-017B-182255/c  
; Sequence 182255, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 182255  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045047  
US-10-257-017B-182255

Query Match 40.0%; Score 10.4; DB 1; Length 13;  
Best Local Similarity 91.7%; Pred. No. 91;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CATCGCCCTTC 18  
| | | | |  
Db 13 CATCGCCCTTC 2

## RESULT 31

US-10-257-017B-182256  
; Sequence 182256, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 182256
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045047
US-10-257-017B-182256

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CATGCCCTTC 18
        |||||
Db      1 CATGCCCTTC 12

RESULT 32
US-10-257-017B-209367/c
; Sequence 209367, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 209367
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051131
US-10-257-017B-209367

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TCGCCCTTCCT 20
        |||||
Db      13 TCACCCCTTCCT 2

RESULT 33
US-10-257-017B-209368
; Sequence 209368, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 209368
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051131
US-10-257-017B-209368

Query Match          40.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TCGCCCTTCCT 20
        |||||
Db      1 TCACCCCTTCCT 12

RESULT 34
US-10-257-017B-303994/c
; Sequence 303994, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303994
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020735
US-10-257-017B-303994

Query Match          38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCTA 21
        |||||
Db      12 CCCCTTCCTA 3

RESULT 35
US-10-257-017B-307435
; Sequence 307435, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307435
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022495
US-10-257-017B-307435
```

Query Match 38.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 CCCTTCCTA 21  
|||||  
Db 3 CCCTTCCTA 12

## RESULT 36

US-10-257-017B-315233  
; Sequence 315233, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 315233  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026790  
US-10-257-017B-315233

Query Match 38.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCACCTCATC 10  
|||||  
Db 2 CCACCTCATC 11

## RESULT 37

US-10-257-017B-321799/c  
; Sequence 321799, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 321799  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030498  
US-10-257-017B-321799

Query Match 38.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CCCTTCCTAA 22  
|||||

Db 12 CCCTTCCTAA 3

## RESULT 38

US-10-257-017B-322509  
; Sequence 322509, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 322509  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer  
US-10-257-017B-322509

Query Match 38.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CCCTTCCTAA 22  
|||||  
Db 1 CCCTTCCTAA 10

## RESULT 39

US-10-257-017B-348675/c  
; Sequence 348675, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 348675  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045700  
US-10-257-017B-348675

Query Match 38.5%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CCCTTCCTAA 22  
|||||  
Db 12 CCCTTCCTAA 3

## RESULT 40

US-10-257-017B-357467  
; Sequence 357467, Application US/10257017B  
; Publication No. US20040241651A1

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357467
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050637
US-10-257-017B-357467

Query Match          38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
DB      1 CCCTTCCTAA 10

RESULT 41
US-10-257-017B-374592
; Sequence 374592, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 374592
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060789
US-10-257-017B-374592

Query Match          38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
DB      3 CCCTTCCTAA 12

RESULT 42
US-10-257-017B-381693
; Sequence 381693, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 381693
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064489
US-10-257-017B-381693

Query Match          38.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCTA 21
DB      2 CCCCTTCCTA 11

RESULT 43
US-10-257-017B-1599/c
; Sequence 1599, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 1599
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000579
US-10-257-017B-1599

Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
DB      13 CCCTTCCTAA 4

RESULT 44
US-10-257-017B-1600
; Sequence 1600, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 1600
; LENGTH: 13
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000579
US-10-257-017B-1600
```

```
Query Match
Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Matches 10; Conservativity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 13 CCCTTCCTAA 22
      |||||
Db 1 CCCTTCCTAA 10
```

```
RESULT 45
US-10-257-017B-24289/c
; Sequence 24289, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 24289
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0005767
US-10-257-017B-24289
```

```
Query Match
Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Matches 10; Conservativity 83.3%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 11 GCCCCTTCCTAA 22
      :|||
Db 13 RCCCCATCCTAA 2
```

```
RESULT 46
US-10-257-017B-24290
; Sequence 24290, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 24290
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0005767
US-10-257-017B-24290
```

Query Match 38.5%; Score 10; DB 1; Length 13;

```
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 11 GCCCCTTCCTAA 22
      :|||
Db 1 RCCCCATCCTAA 12
```

```
RESULT 47
US-10-257-017B-30023/c
; Sequence 30023, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 30023
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009041
US-10-257-017B-30023
```

```
Query Match
Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Matches 10; Conservativity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 7 CATCGCCCT 16
      |||||
Db 13 CATCGCCCT 4
```

```
RESULT 48
US-10-257-017B-30024
; Sequence 30024, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 30024
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009041
US-10-257-017B-30024
```

```
Query Match
Best Local Similarity 38.5%; Score 10; DB 1; Length 13;
Matches 10; Conservativity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 7 CATCGCCCT 16
      |||||
Db 1 CATCGCCCT 10
```



```
RESULT 49
US-10-257-017B-51035/c
; Sequence 51035, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51035
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014276
US-10-257-017B-51035

Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
|||||
Db 10 CCCTTCCTAA 1

RESULT 50
US-10-257-017B-51036
; Sequence 51036, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 51036
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014276
US-10-257-017B-51036

Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
|||||
Db 4 CCCTTCCTAA 13

RESULT 51
US-10-257-017B-78483/c
; Sequence 78483, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 78483
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019989
US-10-257-017B-78483

Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
|||||
Db 11 CCACCTCATC 2

RESULT 52
US-10-257-017B-78484
; Sequence 78484, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 78484
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019989
US-10-257-017B-78484

Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
|||||
Db 3 CCACCTCATC 12

RESULT 53
US-10-257-017B-80875/c
; Sequence 80875, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
```

```
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 80875
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020490
US-10-257-017B-80875

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
Db 10 CCCTTCCTAA 1

RESULT 54
US-10-257-017B-80876
; Sequence 80876, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 80876
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0020490
US-10-257-017B-80876

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
Db 4 CCCTTCCTAA 13

RESULT 55
US-10-257-017B-133103/c
; Sequence 133103, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 133103
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208
US-10-257-017B-133103

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
Db 11 CCCTTCCTAA 2

RESULT 56
US-10-257-017B-133104
; Sequence 133104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 133104
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208
US-10-257-017B-133104

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTAA 22
Db 3 CCCTTCCTAA 12

RESULT 57
US-10-257-017B-133107/c
; Sequence 133107, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 133107
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208
US-10-257-017B-133107

Query Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Oy 13 CCCTTCCTAA 22  
| | | | |  
Db 11 CCCTTCCTAA 2

## RESULT 58

US-10-257-017B-133108  
; Sequence 133108, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 133108  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0033208  
US-10-257-017B-133108

Query Match 38.5%; Score 10; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 CCCTTCCTAA 22  
| | | | |  
Db 3 CCCTTCCTAA 12

## RESULT 59

US-10-257-017B-193907/c  
; Sequence 193907, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 193907  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047683  
US-10-257-017B-193907

Query Match 38.5%; Score 10; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 CCCTTCCTAA 22  
| | | | |  
Db 13 CCCTTCCTAA 4

## RESULT 60

US-10-257-017B-193908  
; Sequence 193908, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 193908  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047683  
US-10-257-017B-193908

Query Match 38.5%; Score 10; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 CCCTTCCTAA 22  
| | | | |  
Db 1 CCCTTCCTAA 10

## RESULT 61

US-10-257-017B-237207/c  
; Sequence 237207, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 237207  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057853  
US-10-257-017B-237207

Query Match 38.5%; Score 10; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 CCCTTCCTAA 22  
| | | | |  
Db 12 CCCTTCCTAA 3

## RESULT 62

US-10-257-017B-237208  
; Sequence 237208, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 237208
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0057853
US-10-257-017B-237208

Query Match          38.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCTAA 22
Db      2 CCCTTCCTAA 11

RESULT 63
US-09-997-672-39/c
; Sequence 39, Application US/09997672
; Publication No. US20030061632A1
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; APPLICANT: Ceres, Inc.
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; FILE REFERENCE: 023070-115810US
; CURRENT APPLICATION NUMBER: US/09/997,672
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,672
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:H-AP56 forward
US-09-997-672-39

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAGCAT 26
Db      13 CCTTCATAGCTT 1

RESULT 64
US-10-257-017B-5801/c
; Sequence 5801, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5801
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001882
US-10-257-017B-5801

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CCTCATCGCCCT 16
Db      13 CCTCATCGTACT 1

RESULT 65
US-10-257-017B-5802
; Sequence 5802, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5802
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001882
US-10-257-017B-5802

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CCTCATCGCCCT 16
Db      1 CCTCATCGTACT 13

RESULT 66
US-10-257-017B-16407/c
; Sequence 16407, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 16407
; LENGTH: 13
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003579
US-10-257-017B-16407
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 8 ATGCCCCCTTCT 20
    ||| ||| |||
Db 13 ATCTCCCCCTCT 1
```

```
RESULT 67
US-10-257-017B-16408
; Sequence 16408, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 16408
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003579
US-10-257-017B-16408
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 8 ATGCCCCCTTCT 20
    ||| ||| |||
Db 1 ATCTCCCCCTCT 13
```

```
RESULT 68
US-10-257-017B-31007/c
; Sequence 31007, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 31007
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009549
US-10-257-017B-31007
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;

Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 14 CCTTCCTAAGCAT 26
    ||| ||| |||
Db 13 CCTTCCTATCCAT 1
```

```
RESULT 69
US-10-257-017B-31008
; Sequence 31008, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 31008
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009549
US-10-257-017B-31008
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 14 CCTTCCTAAGCAT 26
    ||| ||| |||
Db 1 CCTTCCTATCCAT 13
```

```
RESULT 70
US-10-257-017B-58775/c
; Sequence 58775, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 58775
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015747
US-10-257-017B-58775
```

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 2 CACCTCATCGCC 14
    ||| ||| |||
Db 13 CACCCATCCCCC 1
```



```
RESULT 71
US-10-257-017B-58776
; Sequence 58776, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 58776
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015747
US-10-257-017B-58776

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CACCTCATGCCCC 14
Db      1 CACCCCATCCCCC 13

RESULT 72
US-10-257-017B-103101/c
; Sequence 103101, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103101
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025784
US-10-257-017B-103101

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATGCCCCCTTCC 19
Db      13 CATCCCCCATCC 1

RESULT 73
US-10-257-017B-103102
; Sequence 103102, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

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; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103102
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025784
US-10-257-017B-103102

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATGCCCCCTTCC 19
Db      1 CATCCCCCATCC 13

RESULT 74
US-10-257-017B-109217/c
; Sequence 109217, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109217
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109217

Query Match      37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATGCCCC 15
Db      13 ACCTCAACCCCC 1

RESULT 75
US-10-257-017B-109218
; Sequence 109218, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
```

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; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 109218
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027329
US-10-257-017B-109218

Query Match
Best Local Similarity 37.7%; Score 9.8; DB 1; Length 13;
Matches 11; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCC 15
Db 1 ACCTCAACCCCC 13

RESULT 76
US-10-257-017B-111859/c
; Sequence 111859, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111859
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027920
US-10-257-017B-111859

Query Match
Best Local Similarity 37.7%; Score 9.8; DB 1; Length 13;
Matches 11; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCTTAA 22
Db 13 CCCCCCTACTTAA 1

RESULT 77
US-10-257-017B-111860
; Sequence 111860, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 111860
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028646
US-10-257-017B-114403

Query Match
Best Local Similarity 37.7%; Score 9.8; DB 1; Length 13;
Matches 11; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCC 15
Db 13 ACCTCATCTCTCC 1

RESULT 78
US-10-257-017B-114403/c
; Sequence 114403, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 114403
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028646
US-10-257-017B-114403

Query Match
Best Local Similarity 37.7%; Score 9.8; DB 1; Length 13;
Matches 11; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCC 15
Db 13 ACCTCATCTCTCC 1

RESULT 79
US-10-257-017B-114404
; Sequence 114404, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 114404
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028646
US-10-257-017B-114404

Query Match
Best Local Similarity 37.7%; Score 9.8; DB 1; Length 13;
Matches 11; Conservativity 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 3 ACCTCATCGCCCC 15  
| | | | | | | | | |  
Db 1 ACCTCATCTCTCC 13

## RESULT 80

US-10-257-017B-142679/c  
; Sequence 142679, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 142679  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035782  
US-10-257-017B-142679

## Query Match

37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCAT 26  
| | | | | | | | | |  
Db 13 CCTTCATAAACAT 1

## RESULT 81

US-10-257-017B-142680  
; Sequence 142680, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 142680  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0035782  
US-10-257-017B-142680

## Query Match

37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCAT 26  
| | | | | | | | | |  
Db 1 CCTTCATAAACAT 13

## RESULT 82

US-10-257-017B-146283/c  
; Sequence 146283, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 146283  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036853  
US-10-257-017B-146283

## Query Match

37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCCTTCCTAAGCA 25  
| | | | | | | | | |  
Db 13 CCCTTCCCAACA 1

## RESULT 83

US-10-257-017B-146284  
; Sequence 146284, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 146284  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036853  
US-10-257-017B-146284

## Query Match

37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCCTTCCTAAGCA 25  
| | | | | | | | | |  
Db 1 CCCTTCCCAACA 13

## RESULT 84

US-10-257-017B-160217/c  
; Sequence 160217, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160217
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040348
US-10-257-017B-160217

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCCTAA 22
      |||||
Db      13 CACTCCTCCTAA 1

RESULT 85
US-10-257-017B-160218
; Sequence 160218, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160218
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040348
US-10-257-017B-160218

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCCTAA 22
      |||||
Db      1 CACTCCTTCCTAA 13

RESULT 86
US-10-257-017B-178305/c
; Sequence 178305, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 178305
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044162
US-10-257-017B-178305

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 CCCTTCCTAGCA 25
      |||||
Db      13 CCTTCCTAGCA 1

RESULT 87
US-10-257-017B-178306
; Sequence 178306, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 178306
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044162
US-10-257-017B-178306

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 CCCTTCCTAGCA 25
      |||||
Db      1 CCTTCCTAGCA 13

RESULT 88
US-10-257-017B-205671/c
; Sequence 205671, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205671
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008146
```

US-10-257-017B-205671

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCAT 26  
||| ||||| |||  
Db 13 CCTCCCTAATCAT 1

RESULT 89

US-10-257-017B-205672  
; Sequence 205672, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 205672  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0008146  
US-10-257-017B-205672

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCAT 26  
||| ||||| |||  
Db 1 CCTCCCTAATCAT 13

RESULT 90

US-10-257-017B-220613/c  
; Sequence 220613, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 220613  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053694  
US-10-257-017B-220613

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCCTTCCTAAGCA 25

Db 13 CCCTTACTAACC A 1  
||||| ||||| ||

RESULT 91

US-10-257-017B-220614  
; Sequence 220614, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 220614  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053694  
US-10-257-017B-220614

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCCTTCCTAAGCA 25  
||||| ||||| ||  
Db 1 CCCTTACTAACC A 13

RESULT 92

US-10-257-017B-230287/c  
; Sequence 230287, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 230287  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056170  
US-10-257-017B-230287

Query Match 37.7%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 1.1e+02;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCAT 26  
||| ||||| |||  
Db 13 CCTCCCTAACCAT 1

RESULT 93

US-10-257-017B-230288  
; Sequence 230288, Application US/10257017B



```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 230288
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056170
US-10-257-017B-230288

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGCAT 26
      ||| ||||| |||
Db      1 CCTCCCTAACCAT 13

RESULT 94
US-10-257-017B-263207/c
; Sequence 263207, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263207
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000489
US-10-257-017B-263207

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGCAT 26
      ||| ||||| |||
Db      13 CATTCCTAACCAT 1

RESULT 95
US-10-257-017B-263208
; Sequence 263208, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263208
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0000489
US-10-257-017B-263208

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGCAT 26
      ||| ||||| |||
Db      1 CATTCCTAACCAT 13

RESULT 96
US-10-984-919-1296
; Sequence 1296, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1296
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-984-919-1296

Query Match          37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAGC 24
      ||| ||||| |||
Db      1 CTCCTCCTAGC 13

RESULT 97
US-10-836-670-18
; Sequence 18, Application US/10836670
; Publication No. US20040235031A1
; GENERAL INFORMATION:
; APPLICANT: Schultz, Gregory Scott
; APPLICANT: Lewin, Alfred Samuel
; APPLICANT: Blalock, Timothy D.
; TITLE OF INVENTION: ANTI-SCARRING RIBOZYMES AND METHODS
; FILE REFERENCE: 5853-303
; CURRENT APPLICATION NUMBER: US/10/836,670
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 57
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Human adenovirus type 1
US-10-836-670-18
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 CTCATCGCCC 14
         ||||| |||||
Db       1 CCTCCTCGCCC 11
```

## RESULT 98

```
US-10-257-017B-276286
; Sequence 276286, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 276286
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004140
US-10-257-017B-276286
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 CTCATCGCCC 15
         ||||| |||||
Db       2 CTCATCACCAC 12
```

## RESULT 99

```
US-10-257-017B-283032/c
; Sequence 283032, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 283032
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004140
US-10-257-017B-283032
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 CCTCATCGCCC 14
         ||||| |||||
Db       12 CCTCATCGCAC 2
```

## RESULT 100

```
US-10-257-017B-283033/c
; Sequence 283033, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 283033
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0011109
US-10-257-017B-283033
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 CCTCATCGCCC 14
         ||||| |||||
Db       12 CCTCATCGCGC 2
```

## RESULT 101

```
US-10-257-017B-288035
; Sequence 288035, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 288035
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013344
US-10-257-017B-288035
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 CTCATCGCCC 14
         ||||| |||||
Db       1 CTCACCGCCC 11
```

```
RESULT 102
US-10-257-017B-290681/c
; Sequence 290681, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290681
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014470
US-10-257-017B-290681

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CCTCCTAAGC 24
DB 12 CCTCCTAAGC 2

RESULT 103
US-10-257-017B-291350/c
; Sequence 291350, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 291350
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014761
US-10-257-017B-291350

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGCAT 26
DB 12 TTCCTAAGCAT 2

RESULT 104
US-10-257-017B-300973
; Sequence 300973, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300973
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019284
US-10-257-017B-300973

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
DB 2 CCCCTTCCTAA 12

RESULT 105
US-10-257-017B-305394
; Sequence 305394, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305394
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021425
US-10-257-017B-305394

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
DB 2 CCCCTTCCTAA 12

RESULT 106
US-10-257-017B-306843/c
; Sequence 306843, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306843
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021425
US-10-257-017B-306843/c

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
DB 2 CCCCTTCCTAA 12
```

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306843
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022198
US-10-257-017B-306843

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
   ||| ||| ||| |||
Db 11 CTCCTTCCTAA 1

RESULT 107
US-10-257-017B-307267
; Sequence 307267, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307267
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022406
US-10-257-017B-307267

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGCAT 26
   ||| ||| ||| |||
Db 2  TTCCTAAGCAT 12

RESULT 108
US-10-257-017B-307408/c
; Sequence 307408, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307408
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022484
US-10-257-017B-307408

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
   ||| ||| ||| |||
Db 11 CCTTCCTCTAA 1

RESULT 109
US-10-257-017B-313315/c
; Sequence 313315, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 313315
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025663
US-10-257-017B-313315

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
   ||| ||| ||| |||
Db 12 CCTTCCTCTAA 2

RESULT 110
US-10-257-017B-316732
; Sequence 316732, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 316732
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027582
US-10-257-017B-316732

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
```

```
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 CTTCTAAGCA 25
   |||||
Db 2 CTTCTAACCA 12
```

```
RESULT 111
US-10-257-017B-317750/c
; Sequence 317750, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317750
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028225
US-10-257-017B-317750
```

```
Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 12 CCCCTTCCTAA 22
   |||||
Db 12 CCCCTTCCTTA 2
```

```
RESULT 112
US-10-257-017B-324000/c
; Sequence 324000, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324000
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031723
US-10-257-017B-324000
```

```
Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 12 CCCCTTCCTAA 22
   |||||
Db 12 CCCCTACTTAA 2
```

```
RESULT 113
US-10-257-017B-324164
; Sequence 324164, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324164
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031842
US-10-257-017B-324164
```

```
Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 14 CCTTCCTAAGC 24
   |||||
Db 1 CCTTCCTTAAC 11
```

```
RESULT 114
US-10-257-017B-330982
; Sequence 330982, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 330982
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035890
US-10-257-017B-330982
```

```
Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 12 CCCCTTCCTAA 22
   |||||
Db 2 CCCCTTCCTTA 12
```

```
RESULT 115
US-10-257-017B-341250
; Sequence 341250, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```



```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341250
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0041948
US-10-257-017B-341250

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 CATGCCCTT 17
        |||||
Db      1 CATGCCCTT 11

RESULT 116
US-10-257-017B-341938/c
; Sequence 341938, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 341938
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042302
US-10-257-017B-341938

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      15 CTTCTAAGCA 25
        |||||
Db      12 CTTCTAAGCA 2

RESULT 117
US-10-257-017B-344659
; Sequence 344659, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 344659
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043651
US-10-257-017B-344659

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CTTCTAAGC 24
        |||||
Db      1 CTTCTAAGC 11

RESULT 118
US-10-257-017B-349772
; Sequence 349772, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349772
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046308
US-10-257-017B-349772

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATGCC 14
        |||||
Db      2 CCTCATGCC 12

RESULT 119
US-10-257-017B-351147
; Sequence 351147, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 351147
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0047122
US-10-257-017B-351147

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CTCATCGCCCC 15
        ||| ||| |||
Db       1 CTCCTCGCCCC 11

RESULT 120
US-10-257-017B-353448
; Sequence 353448, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 353448
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0048524
US-10-257-017B-353448

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
        ||| ||| |||
Db       1 CACCTTCCTAA 11

RESULT 121
US-10-257-017B-376045
; Sequence 376045, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376045
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061586
US-10-257-017B-376045

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
        ||| ||| |||
Db       2 CACCTCATCTC 12

RESULT 122
US-10-257-017B-377399
; Sequence 377399, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 377399
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010447
US-10-257-017B-377399

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
        ||| ||| |||
Db       1 CCCCTTCCTAA 11

RESULT 123
US-10-994-626-31
; Sequence 31, Application US/10994626
; Publication No. US20050112677A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A substrate having an oxide layer, method for detecting a target
; FILE REFERENCE: PN051212
; CURRENT FILING DATE: 2004-11-22
; CURRENT APPLICATION NUMBER: US/10/994,626
; CURRENT FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 31
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe oligonucleotide
US-10-994-626-31

Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 CGCCCTTCCT 20
        ||| ||| |||
Db       2 CGCCCTTCCT 12

RESULT 124
US-11-078-601-53
; Sequence 53, Application US/11078601
; Publication No. US20050202492A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A microarray having probe polynucleotide spots binding to a same
; TITLE OF INVENTION: target polynucleotide fragment maximally apart therebetween and
; TITLE OF INVENTION: method of producing the same
; FILE REFERENCE: P052961
; CURRENT APPLICATION NUMBER: US/11/078,601
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 53
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe polynucleotide
US-11-078-601-53
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      10 CGCCCTTCTTCT 20
        |||||
Db       2 CGCCCTTCTTCT 12
```

## RESULT 125

```
US-10-257-017B-5883/c
; Sequence 5883, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5883
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001890
US-10-257-017B-5883
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CACCTCATCGC 12
        |||||
Db       11 CACCTAATCGC 1
```

## RESULT 126

```
US-10-257-017B-5884
; Sequence 5884, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
```

```
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 5884
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0001890
US-10-257-017B-5884
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CACCTCATCGC 12
        |||||
Db       3 CACCTAATCGC 13
```

## RESULT 127

```
US-10-257-017B-11473/c
; Sequence 11473, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11473
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0002797
US-10-257-017B-11473
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CACCTCATCGC 12
        |||||
Db       11 CACTTCATCGC 1
```

## RESULT 128

```
US-10-257-017B-11474
; Sequence 11474, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 11474
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC002797
US-10-257-017B-11474

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
        ||| |||||
Db       3 CACTTCATCGC 13

RESULT 129
US-10-257-017B-33623/c
; Sequence 33623, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 33623
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010714
US-10-257-017B-33623

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TCATCGCCCT 16
        ||||| |||
Db       11 TCATCGCCTCT 1

RESULT 130
US-10-257-017B-33624
; Sequence 33624, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 33624
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010714
US-10-257-017B-33624

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 TCATCGCCCT 16
        ||||| |||
Db       3 TCATCGCCTCT 13

RESULT 131
US-10-257-017B-37115/c
; Sequence 37115, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 37115
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011591
US-10-257-017B-37115

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 TTCCTAAGCAT 26
        ||||| |||
Db       13 TTCCTAACCAT 3

RESULT 132
US-10-257-017B-37116
; Sequence 37116, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 37116
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011591
US-10-257-017B-37116

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      16 TTCCTAAGCAT 26
        ||||| |||
Db       1  TTCCTAACCAT 11

RESULT 133
US-10-257-017B-47113/c
```

```
; Sequence 47113, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 47113
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013556
US-10-257-017B-47113

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTCTAA 22
Db      11 CCCCTTACTTAA 1

RESULT 134
US-10-257-017B-47114
; Sequence 47114, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 47114
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0013556
US-10-257-017B-47114

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTCTAA 22
Db      3 CCCCTTACTTAA 13

RESULT 135
US-10-257-017B-55917/c
; Sequence 55917, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
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; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 55917
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015221
US-10-257-017B-55917

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CTCATCGCCCC 15
Db      13 CTCCTCGCCCC 3

RESULT 136
US-10-257-017B-55918
; Sequence 55918, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 55918
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0015221
US-10-257-017B-55918

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CTCATCGCCCC 15
Db      1 CTCCTCGCCCC 11

RESULT 137
US-10-257-017B-74019/c
; Sequence 74019, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```



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; SEQ ID NO 74019
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019042
US-10-257-017B-74019

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
       :||||| |||||
Db      13 RCCTCCTCCCCC 1

RESULT 138
US-10-257-017B-74020
; Sequence 74020, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 74020
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019042
US-10-257-017B-74020

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCCC 15
       :||||| |||||
Db      1 RCCTCCTCCCCC 13

RESULT 139
US-10-257-017B-87741/c
; Sequence 87741, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87741
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87741

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCCC 14
       |||||||
Db      13 CCACATCGCCC 3

RESULT 140
US-10-257-017B-87742
; Sequence 87742, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87742
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87742

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCCC 14
       |||||||
Db      1 CCACATCGCCC 11

RESULT 141
US-10-257-017B-87751/c
; Sequence 87751, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87751
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87751

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CCTCATCGCCC 14
       |||||||
```

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Db          13 CCGCATCGCCC 3

RESULT 142
US-10-257-017B-87752
; Sequence 87752, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 87752
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022068
US-10-257-017B-87752

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 CCTCATCGCCC 14
Db          1 CCGCATCGCCC 11

RESULT 143
US-10-257-017B-88487/C
; Sequence 88487, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88487
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022233
US-10-257-017B-88487

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TCGCCCTTCC 19
Db          13 TCTCCCTTCC 3

RESULT 144
US-10-257-017B-88488
; Sequence 88488, Application US/10257017B
; Publication No. US20040241651A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88488
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022233
US-10-257-017B-88488

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TCGCCCTTCC 19
Db          1 TCTCCCTTCC 11

RESULT 145
US-10-257-017B-97321/C
; Sequence 97321, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 97321
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024141
US-10-257-017B-97321

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          12 CCCCTTCTTAA 22
Db          12 CCCCTTCCAA 2

RESULT 146
US-10-257-017B-97322
; Sequence 97322, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
```

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; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 97322
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024141
US-10-257-017B-97322

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
        |||||
Db       2 CCCCTTCCAAA 12

RESULT 147
US-10-257-017B-97389/c
; Sequence 97389, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 97389
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024174
US-10-257-017B-97389

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
        |||||
Db       13 CACCTCATCTC 3

RESULT 148
US-10-257-017B-97390
; Sequence 97390, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 97390
; LENGTH: 13

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024174
US-10-257-017B-97390

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
        |||||
Db       13 CACCTCATCTC 3

RESULT 149
US-10-257-017B-99113/c
; Sequence 99113, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 99113
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024611
US-10-257-017B-99113

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TCGCCCTTCC 19
        |||||
Db       12 TCGCCCTTCC 2

RESULT 150
US-10-257-017B-99114
; Sequence 99114, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 99114
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024611
US-10-257-017B-99114

Query Match          36.2%; Score 9.4; DB 1; Length 13;
```

Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTTCC 19  
| | | | | | | |  
Db 2 TCGCCCTTCC 12

## RESULT 151

US-10-257-017B-100941/c  
; Sequence 100941, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 100941  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025123  
US-10-257-017B-100941

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCTCCT 20  
| | | | | | | |  
Db 11 CTCCCTTCTCCT 1

## RESULT 152

US-10-257-017B-100942  
; Sequence 100942, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 100942  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0025123  
US-10-257-017B-100942

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCTCCT 20  
| | | | | | | |  
Db 3 CTCCCTTCTCCT 13

## RESULT 153

US-10-257-017B-109443/c  
; Sequence 109443, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 109443  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027383  
US-10-257-017B-109443

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGCAT 26  
| | | | | | | |  
Db 11 TTCCTAATCAT 1

## RESULT 154

US-10-257-017B-109444  
; Sequence 109444, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 109444  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0027383  
US-10-257-017B-109444

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGCAT 26  
| | | | | | | |  
Db 3 TTCCTAATCAT 13

## RESULT 155

US-10-257-017B-112773/c  
; Sequence 112773, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 112773
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028182
US-10-257-017B-112773

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      12 CACCTTCCTAA 2

RESULT 156
US-10-257-017B-112774
; Sequence 112774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 112774
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028182
US-10-257-017B-112774

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      2 CACCTTCCTAA 12

RESULT 157
US-10-257-017B-117647/c
; Sequence 117647, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
```

```
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117647
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029417
US-10-257-017B-117647

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      13 CCACTTCCTAA 3

RESULT 158
US-10-257-017B-117648
; Sequence 117648, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117648
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029417
US-10-257-017B-117648

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
Db      1 CCACTTCCTAA 11

RESULT 159
US-10-257-017B-126495/c
; Sequence 126495, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 126495
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
```



```
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031652
US-10-257-017B-126495

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      15 CTTCTTAAGCA 25
      |||||
Db      13 CTTCTTAATCA 3

RESULT 160
US-10-257-017B-126496
; Sequence 126496, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 126496
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0031652
US-10-257-017B-126496

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      15 CTTCTTAAGCA 25
      |||||
Db      1 CTTCTTAATCA 11

RESULT 161
US-10-257-017B-131503/c
; Sequence 131503, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131503
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032822
US-10-257-017B-131503

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 CACCTCATCGC 12
      |||||
Db      12 CACCTCATCAC 2

RESULT 162
US-10-257-017B-131504
; Sequence 131504, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131504
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032822
US-10-257-017B-131504

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
      |||||
Db      2 CACCTCATCAC 12

RESULT 163
US-10-257-017B-131881/c
; Sequence 131881, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131881
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131881

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATGCCCCCTTCT 20
      :|||
Db      13 RTCTCACCTTCT 1

RESULT 164
```

```
US-10-257-017B-131882
; Sequence 131882, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131882
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131882

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATCGCCCTTCTTCT 20
      :||| |||||
Db      1 RTCTCACCCTTCT 13

RESULT 165
US-10-257-017B-131885/c
; Sequence 131885, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131885
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131885

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATCGCCCTTCTTCT 20
      :||| |||||
Db      13 RTCTCGCCTTCT 1

RESULT 166
US-10-257-017B-131886
; Sequence 131886, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 131886
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0032929
US-10-257-017B-131886

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 ATCGCCCTTCTTCT 20
      :||| |||||
Db      1 RTCTCGCCTTCT 13

RESULT 167
US-10-257-017B-149605/c
; Sequence 149605, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 149605
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037765
US-10-257-017B-149605

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCTTAA 22
      |||||
Db      13 CCACTTCTTAA 3

RESULT 168
US-10-257-017B-149606
; Sequence 149606, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 149606
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0037765
US-10-257-017B-149606

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 13;
Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
Db 1 CCACTTCCTAA 11

RESULT 169
US-10-257-017B-154545/c
; Sequence 154545, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 154545
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0039062
US-10-257-017B-154545

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 13;
Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATGCCCC 15
Db 13 RCTCATCTCTCC 1

RESULT 170
US-10-257-017B-154546
; Sequence 154546, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 154546
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0039062
```

```
US-10-257-017B-154546

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 13;
Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATGCCCC 15
Db 1 RCTCATCTCTCC 13

RESULT 171
US-10-257-017B-160177/c
; Sequence 160177, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160177
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040333
US-10-257-017B-160177

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 13;
Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATCGC 12
Db 11 CACCTCATCAC 1
```

```
RESULT 172
US-10-257-017B-160178
; Sequence 160178, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 160178
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040333
US-10-257-017B-160178

Query Match
Best Local Similarity 36.2%; Score 9.4; DB 1; Length 13;
Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATCGC 12
```

Db 3 CACCTCATCAC 13

## RESULT 173

US-10-257-017B-160495/c  
; Sequence 160495, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 160495  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040405  
US-10-257-017B-160495

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19  
||| |||||  
Db 13 TCCCCCTTCC 3

## RESULT 174

US-10-257-017B-160496  
; Sequence 160496, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 160496  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0040405  
US-10-257-017B-160496

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19  
||| |||||  
Db 1 TCCCCCTTCC 11

## RESULT 175

US-10-257-017B-167797/c  
; Sequence 167797, Application US/10257017B

; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 167797  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010656  
US-10-257-017B-167797

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCCCTTCTTAA 22  
||| |||||  
Db 12 CCCATTCTTAA 2

## RESULT 176

US-10-257-017B-167798  
; Sequence 167798, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 167798  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0010656  
US-10-257-017B-167798

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCCCTTCTTAA 22  
||| |||||  
Db 2 CCCATTCTTAA 12

## RESULT 177

US-10-257-017B-169489/c  
; Sequence 169489, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 169489
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042339
US-10-257-017B-169489

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGC 24
        |||||
        11 CCTTCCTAATC 1

RESULT 178
US-10-257-017B-169490
; Sequence 169490, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 169490
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042339
US-10-257-017B-169490

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGC 24
        |||||
        3 CCTTCCTAATC 13

RESULT 179
US-10-257-017B-171151/c
; Sequence 171151, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171151
```

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009084
US-10-257-017B-171151

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
        |||||
        12 CCTCTTCCTAA 2

RESULT 180
US-10-257-017B-171152
; Sequence 171152, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171152
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0009084
US-10-257-017B-171152

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCCTAA 22
        |||||
        2 CCTCTTCCTAA 12

RESULT 181
US-10-257-017B-171713/c
; Sequence 171713, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 171713
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042804
US-10-257-017B-171713
```



Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20  
| |||||  
Db 13 CTCCTTCCT 3

RESULT 182

US-10-257-017B-171714  
; Sequence 171714, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 171714  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0042804  
US-10-257-017B-171714

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20  
| |||||  
Db 1 CTCCTTCCT 11

RESULT 183

US-10-257-017B-180561/c  
; Sequence 180561, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 180561  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044693  
US-10-257-017B-180561

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22  
| |||||  
Db 13 CCCCTACTAA 3

RESULT 184  
US-10-257-017B-180562

; Sequence 180562, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 180562  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044693  
US-10-257-017B-180562

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22  
| |||||  
Db 1 CCCCTACTAA 11

RESULT 185

US-10-257-017B-187479/c  
; Sequence 187479, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 187479  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046214  
US-10-257-017B-187479

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22  
| |||||  
Db 12 CCCTTCCTAA 2

RESULT 186

US-10-257-017B-187480  
; Sequence 187480, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:

```
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 187480
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0046214
US-10-257-017B-187480
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      12 CCCCTTCCTAA 22
        ||| ||||| |||
Db       2 CCCTTTCCTAA 12
```

## RESULT 187

```
US-10-257-017B-193135/c
; Sequence 193135, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 193135
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047508
US-10-257-017B-193135
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 ACCTCATCGCC 13
        ||||| ||| ||
Db       11 ACCTCATCTCC 1
```

## RESULT 188

```
US-10-257-017B-193136
; Sequence 193136, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 193136
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0047508
US-10-257-017B-193136
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 ACCTCATCGCC 13
        ||||| ||| ||
Db       3 ACCTCATCTCC 13
```

## RESULT 189

```
US-10-257-017B-205333/c
; Sequence 205333, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205333
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0050342
US-10-257-017B-205333
```

```
Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      16 TTCCTTAAGCAT 26
        ||||| ||| |||
Db       13 TTCCTAATCAT 3
```

## RESULT 190

```
US-10-257-017B-205334
; Sequence 205334, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 205334
; LENGTH: 13
; TYPE: DNA
```

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0050342  
US-10-257-017B-205334

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCCTAAGCAT 26  
| | | | | | | | | |  
Db 1 TTCTTATCAT 11

RESULT 191  
US-10-257-017B-212563/c  
; Sequence 212563, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 212563  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051772  
US-10-257-017B-212563

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTCCTAAGCA 25  
| | | | | | | | | |  
Db 11 CTTCCTAACA 1

RESULT 192  
US-10-257-017B-212564  
; Sequence 212564, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 212564  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0051772  
US-10-257-017B-212564

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTCCTAAGCA 25  
| | | | | | | | | |  
Db 3 CTTCCTAACA 13

RESULT 193  
US-10-257-017B-240965/c  
; Sequence 240965, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 240965  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058763  
US-10-257-017B-240965

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CATGCCCTT 17  
| | | | | | | | | |  
Db 11 CATGCTCCTT 1

RESULT 194  
US-10-257-017B-240966  
; Sequence 240966, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 240966  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0058763  
US-10-257-017B-240966

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CATGCCCTT 17  
| | | | | | | | | |  
Db 3 CATGCTCCTT 13

```
RESULT 195
US-10-257-017B-244719/c
; Sequence 244719, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 244719
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059747
US-10-257-017B-244719

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGC 24
Db      12 CCTTCCTAAGC 2

RESULT 196
US-10-257-017B-244720
; Sequence 244720, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 244720
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0059747
US-10-257-017B-244720

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGC 24
Db      2 CCTTCCTAAGC 12

RESULT 197
US-10-257-017B-263651/c
; Sequence 263651, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
```

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263651
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063915
US-10-257-017B-263651

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
Db      12 CACCTCATCGC 2

RESULT 198
US-10-257-017B-263652
; Sequence 263652, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 263652
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0063915
US-10-257-017B-263652

Query Match          36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
Db      2 CACCTCATCGC 12

RESULT 199
US-10-984-919-1297
; Sequence 1297, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
```

; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: EP 97 101 531.8  
; PRIOR FILING DATE: 1997-01-31  
; NUMBER OF SEQ ID NOS: 1764  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1297  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: antisense oligonucleotide  
US-10-984-919-1297

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CCTCCTAAGC 24  
|||  
Db 1 CCCTCCTAAGC 11

## RESULT 200

US-11-116-252-2  
; Sequence 2, Application US/11116252  
; Publication No. US20050186632A1  
; GENERAL INFORMATION:  
; APPLICANT: KATAOKA, Kohsuke  
; TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR  
; FILE REFERENCE: Q69817  
; CURRENT APPLICATION NUMBER: US/11/116,252  
; PRIOR FILING DATE: 2005-04-28  
; PRIOR APPLICATION NUMBER: US/10/129,192  
; PRIOR FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: PCT/JP00/00841  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: JP 1999-314335  
; PRIOR FILING DATE: 1999-11-04  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Maf recognition element  
US-11-116-252-2

Query Match 36.2%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 1.2e+02;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTCCTAAGCA 25  
|||  
Db 3 CTTCCTAAGCA 13

## RESULT 201

US-09-783-338A-2/c  
; Sequence 2, Application US/09783338A  
; Patent No. US20020028922A1  
; GENERAL INFORMATION:  
; APPLICANT: Glazer, Peter M.  
; ; Havre, Pamela A.  
; TITLE OF INVENTION: Chemically Modified Oligonucleotide for  
; ; Site-Directed Mutagenesis  
; ;  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 1100 Peachtree Street, Suite 2800  
; CITY: Atlanta  
; STATE: Georgia

; COUNTRY: USA  
; ZIP: 30309-4530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/783,338A  
; FILING DATE: 14-Feb-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/083,088  
; FILING DATE: 25-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: YU109  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-815-6508  
; TELEFAX: (404)-815-6555  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-783-338A-2

Query Match 34.6%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20  
|||  
Db 9 CCCCTTCCT 1

## RESULT 202

US-09-978-333B-1/c  
; Sequence 1, Application US/09978333B  
; Publication No. US2003032768A1  
; GENERAL INFORMATION:  
; APPLICANT: Glazer, Peter M.  
; TITLE OF INVENTION: Triple-Helix forming Oligonucleotides for Targeted Mutagenesis  
; FILE REFERENCE: YU 132  
; CURRENT APPLICATION NUMBER: US/09/978,333B  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: US 09/411,291  
; PRIOR FILING DATE: 1999-10-04  
; PRIOR APPLICATION NUMBER: US 08/476,712  
; PRIOR FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide Ag10  
US-09-978-333B-1

Query Match 34.6%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20  
|||  
Db 9 CCCCTTCCT 1



```
RESULT 203
US-10-033-145-1976
; Sequence 1976, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1976
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1976

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCTTAG 23
Db 2 CTTCTTAG 10

RESULT 204
US-10-055-713-51/c
; Sequence 51, Application US/10055713
; Publication No. US20030044957A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: LI, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; TITLE OF INVENTION: REGULATION IN PLANTS
; FILE REFERENCE: 8325-0026 / S26-US1
; CURRENT APPLICATION NUMBER: US/10/055,713
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP 5 target sequence
US-10-055-713-51

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 10 CCCCTTCCT 2

RESULT 205
US-10-055-711-55/c
; Sequence 55, Application US/10055711
; Publication No. US20030108880A1
; GENERAL INFORMATION:
; APPLICANT: LI, Guofu
; APPLICANT: LIU, Qiang
```

```
; APPLICANT: REBAR, Edward
; APPLICANT: JAMIESON, Andrew
; TITLE OF INVENTION: MODIFIED ZINC FINGER BINDING PROTEINS
; FILE REFERENCE: 8325-0025
; CURRENT APPLICATION NUMBER: US/10/055,711
; CURRENT FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP #5 target
US-10-055-711-55

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 10 CCCCTTCCT 2

RESULT 206
US-10-418-552-37/c
; Sequence 37, Application US/10418552
; Publication No. US2003023672A1
; GENERAL INFORMATION:
; APPLICANT: LI, Guofu
; APPLICANT: LIU, Qiang
; APPLICANT: JAMIESON, Andrew
; APPLICANT: REBAR, Edward
; APPLICANT: VAN BENENNAAM, Alison
; APPLICANT: VENKATRAMESH, Mylavarapu
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR REGULATION OF PLANT GAMMA-
; TITLE OF INVENTION: TOCOPHEROL METHYLTRANSFERASE
; FILE REFERENCE: 8325-0029 (S29-US1)
; CURRENT APPLICATION NUMBER: US/10/418,552
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 60/373,488
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/385,992
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/442,470
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: AGMT5 target
US-10-418-552-37

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 10 CCCCTTCCT 2

RESULT 207
US-10-650-454-56/c
; Sequence 56, Application US/10650454
; Publication No. US20040091990A1
; GENERAL INFORMATION:
; APPLICANT: LI, Guofu
; APPLICANT: LIU, Qiang
```

```
; APPLICANT: JAMIESON, Andrew
; APPLICANT: REBAR, Edward
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION OF PLANT GAMMA-TOCOPHEROL
; TITLE OF INVENTION: METHYLTRANSFERASE
; FILE REFERENCE: 8325-0029.30 (S29-US2)
; CURRENT APPLICATION NUMBER: US/10/650,454
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/406,849
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ZFP5 target
US-10-650-454-56

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
        |||||
Db       10 CCCCTTCCT 2

RESULT 208
US-10-470-180-51/c
; Sequence 51, Application US/10470180
; Publication No. US20040128717A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: LI, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; TITLE OF INVENTION: REGULATION IN PLANTS
; FILE REFERENCE: 8325-0026.30 / S26-US2
; CURRENT APPLICATION NUMBER: US/10/470,180
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: PCT/US02/01906
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ZFP 5 target sequence
US-10-470-180-51

Query Match          34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
        |||||
Db       10 CCCCTTCCT 2

RESULT 209
US-09-783-338A-1/c
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
; APPLICANT: Havre, Pamela A.
; TITLE OF INVENTION: Chemically Modified Oligonucleotide for
; NUMBER OF SEQUENCES: 13
; Site-Directed Mutagenesis
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,338A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,088
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU109
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 11
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-783-338A-1

Query Match          34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
        |||||
Db       10 CCCCTTCCT 2

RESULT 210
US-10-450-797-877
; Sequence 877, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 877
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-877

Query Match          34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
        |||||
Db       3 CCCCTTCCT 11

RESULT 211
```

```
US-10-257-017B-270857
; Sequence 270857, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 270857
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002302
US-10-257-017B-270857

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
Db      4 CCTTCCTAA 12

RESULT 212
US-10-257-017B-271330/c
; Sequence 271330, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 271330
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002471
US-10-257-017B-271330

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
Db      11 CCCCTTCCT 3

RESULT 213
US-10-257-017B-292092/c
; Sequence 292092, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 292092
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015081
US-10-257-017B-292092

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
Db      10 CCTTCCTAA 2

RESULT 214
US-10-257-017B-295660
; Sequence 295660, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295660
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016678
US-10-257-017B-295660

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
Db      4 CCTTCCTAA 12

RESULT 215
US-10-257-017B-296570/c
; Sequence 296570, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
```

```
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 296570
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0017152
US-10-257-017B-296570

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 CGCCCTTC 18
        |||||
Db       11 CGCCCTTC 3

RESULT 216
US-10-257-017B-302250/c
; Sequence 302250, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302250
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019887
US-10-257-017B-302250

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CATGCCCC 15
        |||||
Db       9 CATGCCCC 1

RESULT 217
US-10-257-017B-306989/c
; Sequence 306989, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306989
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022284
```

```
US-10-257-017B-306989

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CCTTCCTAA 22
        |||||
Db       9 CCTTCCTAA 1

RESULT 218
US-10-257-017B-307276/c
; Sequence 307276, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307276
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022412
US-10-257-017B-307276

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
        |||||
Db       12 CCCCTTCT 4

RESULT 219
US-10-257-017B-307786
; Sequence 307786, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 307786
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022686
US-10-257-017B-307786

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCTTA 21
```

Db 2 CCCTTCCTA 10

RESULT 220

US-10-257-017B-317371/c  
; Sequence 317371, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 317371  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027956  
US-10-257-017B-317371

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCTTCCTAA 22  
Db 12 CCTTCCTAA 4

RESULT 221

US-10-257-017B-318871  
; Sequence 318871, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 318871  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028928  
US-10-257-017B-318871

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20  
Db 3 CCCCTTCCT 11

RESULT 222

US-10-257-017B-319500/c  
; Sequence 319500, Application US/10257017B

; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 319500  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029262  
US-10-257-017B-319500

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCTTCCTAA 22  
Db 10 CCTTCCTAA 2

RESULT 223

US-10-257-017B-321861  
; Sequence 321861, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 321861  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030535  
US-10-257-017B-321861

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9  
Db 1 CCACCTCAT 9

RESULT 224

US-10-257-017B-323643/c  
; Sequence 323643, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 323643  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030535  
US-10-257-017B-323643/c



```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323643
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031518
US-10-257-017B-323643

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCCCCCTTC 18
Db 9 CGCCCCCTTC 1

RESULT 225
US-10-257-017B-324895/C
; Sequence 324895, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324895
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0032282
US-10-257-017B-324895

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCTTCCTAA 22
Db 10 CCTTCCTAA 2

RESULT 226
US-10-257-017B-331316
; Sequence 331316, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331316

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0036120
US-10-257-017B-331318

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACCTCATCG 11
Db 4 ACCTCATCG 12

RESULT 227
US-10-257-017B-331318
; Sequence 331318, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 331318
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039455
US-10-257-017B-336647

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACCTCATCG 11
Db 4 ACCTCATCG 12

RESULT 228
US-10-257-017B-336647
; Sequence 336647, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 336647
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039455
US-10-257-017B-336647
```

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTA 21  
Db 1 CCCTTCCTA 9

## RESULT 229

US-10-257-017B-339949  
; Sequence 339949, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 339949  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007933  
US-10-257-017B-339949

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCCCCCTTC 18  
Db 2 CGCCCCCTTC 10

## RESULT 230

US-10-257-017B-347634/c  
; Sequence 347634, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 347634  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045197  
US-10-257-017B-347634

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTA 21  
Db 9 CCCTTCCTA 1

RESULT 231  
US-10-257-017B-351281/c

; Sequence 351281, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 351281  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0047204  
US-10-257-017B-351281

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTA 21  
Db 10 CCCTTCCTA 2

## RESULT 232

US-10-257-017B-362364/c  
; Sequence 362364, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 362364  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053186  
US-10-257-017B-362364

Query Match 34.6%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCTTCCT 20  
Db 11 CCCTTCCT 3

## RESULT 233

US-10-257-017B-368993  
; Sequence 368993, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:

```
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 368993
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057391
US-10-257-017B-368993

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTA 21
Db 3 CCCTTCCTA 11

RESULT 234
US-10-257-017B-368994
; Sequence 368994, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 368994
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0057391
US-10-257-017B-368994

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCTA 21
Db 3 CCCTTCCTA 11

RESULT 235
US-10-257-017B-372951
; Sequence 372951, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
```

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 372951
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0059746
US-10-257-017B-372951

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCTTCCTAA 22
Db 4 CCTTCCTAA 12

RESULT 236
US-10-257-017B-376095/C
; Sequence 376095, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 376095
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0061608
US-10-257-017B-376095

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9
Db 11 CCACCTCAT 3

RESULT 237
US-10-257-017B-379937
; Sequence 379937, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 379937
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0063546
US-10-257-017B-379937

Query Match          34.6%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
Db      2 CCCCTTCT 10

RESULT 238
US-10-661-165-565/c
; Sequence 565, Application US/10661165
; Publication No. US20040137470A1
; GENERAL INFORMATION:
; APPLICANT: Dhallan, Ravinder S.
; TITLE OF INVENTION: METHODS FOR DETECTION OF GENETIC
; FILE REFERENCE: 543312000420
; CURRENT APPLICATION NUMBER: US/10/661,165
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: PCT/US03/06198
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/378,354
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 10/093,618
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/360,232
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: PCT/US03/27308
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 10/376,770
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 565
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-661-165-565

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TCGCCCTTCT 20
Db      12 TTGCCCTTCT 1

RESULT 239
US-10-836-670-34
; Sequence 34, Application US/10836670
; Publication No. US20040235031A1
; GENERAL INFORMATION:
; APPLICANT: Schultz, Gregory Scott
; APPLICANT: Lewin, Alfred Samuel
; APPLICANT: Bialock, Timothy D.
; TITLE OF INVENTION: ANTI-SCARRING RIBOZYMES AND METHODS
; FILE REFERENCE: 5853-303
; CURRENT APPLICATION NUMBER: US/10/836,670
; CURRENT FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 12
; TYPE: DNA

; ORGANISM: Human adenovirus type 1
US-10-836-670-34

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CCCCTTCTAAG 23
Db      1 CCCCTTCCCGAG 12

RESULT 240
US-10-257-017B-268660/c
; Sequence 268660, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 268660
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001285
US-10-257-017B-268660

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      15 CTTCTAAGCAT 26
Db      12 CTTCTAACCCT 1

RESULT 241
US-10-257-017B-269228
; Sequence 269228, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269228
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001671
US-10-257-017B-269228

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 5 CTCATCGCCCT 16  
| | | | |  
Db 1 CTCATCTACCCT 12

## RESULT 242

US-10-257-017B-270998/c  
; Sequence 270998, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 270998  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002355  
US-10-257-017B-270998

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCGCCCTTCT 20  
| | | | |  
Db 12 TCGACCTACCCT 1

## RESULT 243

US-10-257-017B-276248/c  
; Sequence 276248, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 276248  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004128  
US-10-257-017B-276248

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATCGCCCTTC 18  
| | | | |  
Db 12 CCTCGCCCTTC 1

## RESULT 244

US-10-257-017B-277116

; Sequence 277116, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 277116  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004389  
US-10-257-017B-277116

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATGCCC 14  
| | | | |  
Db 1 ACCTCATATCCC 12

## RESULT 245

US-10-257-017B-278152/c  
; Sequence 278152, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 278152  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005715  
US-10-257-017B-278152

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCTTA 22  
| | | | |  
Db 12 GCCCCTCCCTTA 1

## RESULT 246

US-10-257-017B-278353/c  
; Sequence 278353, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine



```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 278353
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005916
US-10-257-017B-278353

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCGCCCTTCCT 20
Db 12 TCCCCCTACCT 1

RESULT 247
US-10-257-017B-280327
; Sequence 280327, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 280327
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008491
US-10-257-017B-280327

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCTA 21
Db 1 CCCCCCTACCTA 12

RESULT 248
US-10-257-017B-281811
; Sequence 281811, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 281811
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010079
US-10-257-017B-281811

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CTTCTTAAGCA 25
Db 1 CTTCCCAACCA 12

RESULT 249
US-10-257-017B-286583
; Sequence 286583, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 286583
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012738
US-10-257-017B-286583

Query Match
Best Local Similarity 33.8%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATGCCC 14
Db 1 ACCTCATACCC 12

RESULT 250
US-10-257-017B-287738/c
; Sequence 287738, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 287738
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013227
US-10-257-017B-287738
```

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CGCCCTTCTCTA 21  
| | | | | | | |  
Db 12 CGAACCTTCTCTA 1

RESULT 251

US-10-257-017B-290339/c  
; Sequence 290339, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 290339  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014311  
US-10-257-017B-290339

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 CCCTTCTTAAGC 24  
| | | | | | | |  
Db 12 CCCTTCCAAAC 1

RESULT 252

US-10-257-017B-292113  
; Sequence 292113, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 292113  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0015089  
US-10-257-017B-292113

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 CTTCCTAAGCAT 26  
| | | | | | | |

Db 1 CTTCCTAAAAAT 12

RESULT 253

US-10-257-017B-295712  
; Sequence 295712, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 295712  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016696  
US-10-257-017B-295712

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 CCCTTCTTAAGC 24  
| | | | | | | |  
Db 1 CCCTTCTTAAC 12

RESULT 254

US-10-257-017B-298724  
; Sequence 298724, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; PRIOR FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 298724  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018250  
US-10-257-017B-298724

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 CGCCCTTCTCTA 21  
| | | | | | | |  
Db 1 CCCACCTTCTCTA 12

RESULT 255

US-10-257-017B-299865/c  
; Sequence 299865, Application US/10257017B  
; Publication No. US20040241651A1

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299865
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018786
US-10-257-017B-299865

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCCTA 21
Db      12 CTCCTCTCCCA 1

RESULT 256
US-10-257-017B-300302/c
; Sequence 300302, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 300302
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018963
US-10-257-017B-300302

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTCATCGC 12
Db      12 CAACCTCATCCC 1

RESULT 257
US-10-257-017B-302104/c
; Sequence 302104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
```

```
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 302104
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0019796
US-10-257-017B-302104

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 CCCTTCCTAAGC 24
Db      12 CCATCCTTAAC 1

RESULT 258
US-10-257-017B-303551/c
; Sequence 303551, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303551
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020529
US-10-257-017B-303551

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATGCCC 14
Db      12 ACCTATCATCCC 1

RESULT 259
US-10-257-017B-304348
; Sequence 304348, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 304348
; LENGTH: 12
```

;  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020881  
US-10-257-017B-304348

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCCCTTCCTA 21  
| | | | | | | |  
Db 1 CTCCTTACTA 12

RESULT 260  
US-10-257-017B-306913  
; Sequence 306913, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 306913  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022244  
US-10-257-017B-306913

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15  
| | | | | | | |  
Db 1 CCTAATCCCCCC 12

RESULT 261  
US-10-257-017B-313065/c  
; Sequence 313065, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 313065  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025454  
US-10-257-017B-313065

Query Match 33.8%; Score 8.8; DB 1; Length 12;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCC 14  
| | | | | | | |  
Db 12 ACCACCTCGCCC 1

RESULT 262  
US-10-257-017B-313798/c  
; Sequence 313798, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 313798  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0025975  
US-10-257-017B-313798

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATCGCCCTTC 18  
| | | | | | | |  
Db 12 CATCTCCCTCC 1

RESULT 263  
US-10-257-017B-314753  
; Sequence 314753, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 314753  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548  
US-10-257-017B-314753

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCC 14  
| | | | | | | |  
Db 1 ACATCATCGCAC 12

```
RESULT 264
US-10-257-017B-314756
; Sequence 314756, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314756
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548
US-10-257-017B-314756

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCC 14
Db 1 ACATCATCGCGC 12

RESULT 265
US-10-257-017B-314759
; Sequence 314759, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314759
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548
US-10-257-017B-314759

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCC 14
Db 1 ACATCATCGCGC 12

RESULT 266
US-10-257-017B-314762
; Sequence 314762, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

```
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314762
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026548
US-10-257-017B-314762

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCC 14
Db 1 ACATCATCGCGC 12

RESULT 267
US-10-257-017B-315110/c
; Sequence 315110, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 315110
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026719
US-10-257-017B-315110

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATCGCCCTTC 18
Db 12 CATACCCCTTC 1

RESULT 268
US-10-257-017B-315369
; Sequence 315369, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
```



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; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 315369
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026872
US-10-257-017B-315369

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      14 CCTCCTAAGCA 25
      |||||
Db      1 CCTTCTAACCA 12

RESULT 269
US-10-257-017B-315967
; Sequence 315967, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 315967
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027203
US-10-257-017B-315967

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACCTCATCGC 12
      |||||
Db      1 CCACTTCATCAC 12

RESULT 270
US-10-257-017B-317533/c
; Sequence 317533, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317533
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0028084
US-10-257-017B-317533

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      8 ATCGCCCTTCC 19
      |||||
Db      12 ATCTCCCATCC 1

RESULT 271
US-10-257-017B-319294
; Sequence 319294, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 319294
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029155
US-10-257-017B-319294

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      9 TCGCCCTTCTCT 20
      |||||
Db      1 TCGCCCTTAAC 12

RESULT 272
US-10-257-017B-320903
; Sequence 320903, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methyations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 320903
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029956
US-10-257-017B-320903

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

OY 13 CCTTCTTAAGC 24  
|||  
Db 1 CCTTCTTAACC 12

## RESULT 273

US-10-257-017B-322792/c  
; Sequence 322792, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 322792  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031068  
US-10-257-017B-322792

## Query Match

33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 9 TCGCCCTTCT 20  
|||  
Db 12 TCACCCCTTCTT 1

## RESULT 274

US-10-257-017B-323185  
; Sequence 323185, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 323185  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031247  
US-10-257-017B-323185

## Query Match

33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCTCATCGCCCC 15  
|||  
Db 1 CCCATCGCCCC 12

## RESULT 275

US-10-257-017B-323187  
; Sequence 323187, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 323187  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031247  
US-10-257-017B-323187

## Query Match

33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 CCTCATCGCCCC 15  
|||  
Db 1 CCCGATCGCCCC 12

## RESULT 276

US-10-257-017B-326521/c  
; Sequence 326521, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 326521  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033109  
US-10-257-017B-326521

## Query Match

33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 14 CCTTCTTAAGCA 25  
|||  
Db 12 CCATCCTTAAGCA 1

## RESULT 277

US-10-257-017B-327842/c  
; Sequence 327842, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 327842
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033930
US-10-257-017B-327842

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGCA 25
        |||||
Db       12 CCTCCTACCCA 1

RESULT 278
US-10-257-017B-328615
; Sequence 328615, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 328615
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0034416
US-10-257-017B-328615

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 CCTCATGCCCC 15
        |||
Db       1 CCCCTCGCCCC 12

RESULT 279
US-10-257-017B-329701
; Sequence 329701, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329701
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038921
US-10-257-017B-334701

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATCGCCCTTC 18
        |||||
Db       1 CATCTCCTTTC 12

RESULT 280
US-10-257-017B-334701
; Sequence 334701, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 334701
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038351
US-10-257-017B-335615

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      13 CCCTTCCTAAGC 24
        |||||
Db       1 CCCTACCTTAAC 12

RESULT 281
US-10-257-017B-335615
; Sequence 335615, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 335615
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0038921
```

US-10-257-017B-335615

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCCCCCTTC 18  
Db 1 CACCGCCCCCTC 12

RESULT 282

US-10-257-017B-337282/c  
; Sequence 337282, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 337282  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0039782  
US-10-257-017B-337282

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCCCCCTTC 18  
Db 12 CATACCCCTTC 1

RESULT 283

US-10-257-017B-339583/c  
; Sequence 339583, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 339583  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0041083  
US-10-257-017B-339583

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATCGCCCTTC 19

Db 12 ATCACCCCTACC 1

RESULT 284

US-10-257-017B-344435/c  
; Sequence 344435, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 344435  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043536  
US-10-257-017B-344435

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAA 22  
Db 12 GCCCACCCTAA 1

RESULT 285

US-10-257-017B-344922  
; Sequence 344922, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 344922  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0043771  
US-10-257-017B-344922

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATCGCCCT 16  
Db 1 CTCATAACCCCT 12

RESULT 286

US-10-257-017B-348072/c  
; Sequence 348072, Application US/10257017B

```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 348072
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0010192
US-10-257-017B-348072

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCCTCA 21
      ||| ||| ||| |||
Db       12 CTCCTCTTCCTCA 1

RESULT 287
US-10-257-017B-349107/c
; Sequence 349107, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349107
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0045920
US-10-257-017B-349107

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CACCTCATCGCC 13
      ||| ||| ||| |||
Db       12 CACTTCATCTCC 1

RESULT 288
US-10-257-017B-349377
; Sequence 349377, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 349377
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046101
US-10-257-017B-349377

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCCC 14
      ||| ||| ||| |||
Db       1 ACCTCATTCCCC 12

RESULT 289
US-10-257-017B-350201/c
; Sequence 350201, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350201
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046561
US-10-257-017B-350201

Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAGCA 25
      ||| ||| ||| |||
Db       12 CCTCCCTAATCA 1

RESULT 290
US-10-257-017B-350285/c
; Sequence 350285, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350285
```



```

; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046584
US-10-257-017B-350285
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 ACCTCATCGCCC 14
        |||||
Db       12 ACCTCATACCCC 1
```

## RESULT 291

```
US-10-257-017B-350759
; Sequence 350759, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350759
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046864
US-10-257-017B-350759
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 CACCTCATCGCC 13
        |||||
Db       1 CACCTCAACCCC 12
```

## RESULT 292

```
US-10-257-017B-354578
; Sequence 354578, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 354578
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0049156
US-10-257-017B-354578
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      14 CCTCCTAAGCA 25
        |||||
Db       1 CCTACCTAACA 12
```

## RESULT 293

```
US-10-257-017B-356323/c
; Sequence 356323, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 356323
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050058
US-10-257-017B-356323
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      3 ACCTCATCGCCC 14
        |||||
Db       12 ACCTCTTCGCTC 1
```

## RESULT 294

```
US-10-257-017B-357335/c
; Sequence 357335, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357335
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0050568
US-10-257-017B-357335
```

```
Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      15 CTCCTAAGCAT 26
        |||||
Db       12 CTCCTAACCAT 1
```

```
RESULT 295
US-10-257-017B-357650
; Sequence 357650, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 357650
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007066
US-10-257-017B-357650

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      7 CATGCCCCCTTC 18
Db      1 CATCTCCCCCTCC 12

RESULT 296
US-10-257-017B-358254
; Sequence 358254, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 358254
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0007531
US-10-257-017B-358254

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGCA 25
Db      1 CCCTCCTAACA 12

RESULT 297
US-10-257-017B-359463/c
; Sequence 359463, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359463
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0051615
US-10-257-017B-359463

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      9 TCGCCCCCTTCT 20
Db      12 TCTCCCTTCTCT 1

RESULT 298
US-10-257-017B-360360/c
; Sequence 360360, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 360360
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0052046
US-10-257-017B-360360

Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTCATCGC 12
Db      12 CCACCTCCTCTC 1

RESULT 299
US-10-257-017B-362746/c
; Sequence 362746, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257, 017B
```

```
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 362746
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0053413
US-10-257-017B-362746

Query Match
  33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCCTTCCTAAGC 24
Db 12 CACTTCCTAATC 1

RESULT 300
US-10-257-017B-364264
; Sequence 364264, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364264
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0005484
US-10-257-017B-364264

Query Match
  33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACCTCATCGCC 13
Db 1 CACATCACCGCC 12

RESULT 301
US-10-257-017B-368210/c
; Sequence 368210, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 368210
; LENGTH: 12
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0056866
US-10-257-017B-368210

Query Match
  33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCCTAAGCAT 26
Db 12 CTTCATTAACAT 1

RESULT 302
US-10-257-017B-370744
; Sequence 370744, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 370744
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058361
US-10-257-017B-370744

Query Match
  33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TCGCCCTTCTCT 20
Db 1 TCCCTCTTCTCT 12

RESULT 303
US-10-257-017B-371049
; Sequence 371049, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 371049
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0058537
US-10-257-017B-371049

Query Match
  33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
```

Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATGCCCCCTTCC 19  
| | | | | | | | | |  
Db 1 ATCTACCCCTTCC 12

RESULT 304  
US-10-257-017B-372640/c  
; Sequence 372640, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 372640  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0059513  
US-10-257-017B-372640

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCA 25  
| | | | | | | | | |  
Db 12 CCTTCCTATTCA 1

RESULT 305  
US-10-257-017B-373933  
; Sequence 373933, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 373933  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060397  
US-10-257-017B-373933

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACCTCATCGCC 13  
| | | | | | | | | |  
Db 1 CACCTCCTCTCC 12

RESULT 306  
US-10-257-017B-374652/c  
; Sequence 374652, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 374652  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0060825  
US-10-257-017B-374652

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCC 14  
| | | | | | | | | |  
Db 12 ACCTCATCCAC 1

RESULT 307  
US-10-257-017B-378396  
; Sequence 378396, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 378396  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008704  
US-10-257-017B-378396

Query Match 33.8%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATGCCCCCTTCC 19  
| | | | | | | | | |  
Db 1 ATCTCCCATCC 12

RESULT 308  
US-10-257-017B-381325  
; Sequence 381325, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock

```
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 381325
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064280
US-10-257-017B-381325
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Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      14 CCTTCCTAGCA 25
      |||||
Db       1 CCATCCTATCA 12
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## RESULT 309

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US-10-257-017B-381966
; Sequence 381966, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 381966
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0064656
US-10-257-017B-381966
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Query Match          33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      4 CCTCATCGCCCC 15
      |||||
Db       1 CCTCACCACCCC 12
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Search completed: May 9, 2006, 16:59:40  
Job time : 0.001 secs



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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:55:34 ; Search time 0.001 Seconds  
(without alignments)  
23.920 Million cell updates/sec

Title: US-09-904-968A-4-COPY  
Perfect score: 26  
Sequence: 1 ccacctcatcgcccttcctaagcat 26

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 25 seqs, 460 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 25 summaries

Database : pubnewdb4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15.6	60.0	22	1	US-10-310-914A-1031100 Sequence 1031100,
C 2	15.2	58.5	20	1	US-10-310-914A-66874 Sequence 66874, A
C 3	14.8	56.9	19	1	US-11-101-244-788791 Sequence 788791,
C 4	14.8	56.9	19	1	US-11-083-784-788791 Sequence 788791,
C 5	14.2	54.6	19	1	US-10-310-914A-1300864 Sequence 1300864,
C 6	14.2	54.6	20	1	US-10-310-914A-74927 Sequence 74927, A
C 7	14.2	54.6	20	1	US-10-310-914A-1166831 Sequence 1166831,
C 8	13.8	53.1	18	1	US-10-310-914A-74926 Sequence 74926, A
C 9	13.8	53.1	18	1	US-10-310-914A-627529 Sequence 627529,
C 10	13.4	51.5	18	1	US-10-310-914A-258747 Sequence 258747,
C 11	13.4	51.5	18	1	US-10-310-914A-258760 Sequence 258760,
C 12	13.4	51.5	18	1	US-10-310-914A-526385 Sequence 526385,
C 13	13.4	51.5	18	1	US-10-310-914A-634307 Sequence 634307,
C 14	13.4	51.5	18	1	US-10-310-914A-1117030 Sequence 1117030,
C 15	13.4	51.5	19	1	US-10-310-914A-634308 Sequence 634308,
C 16	13.4	51.5	19	1	US-11-101-244-100792 Sequence 100792,
C 17	13.4	51.5	19	1	US-11-101-244-100799 Sequence 100799,
C 18	13.4	51.5	19	1	US-11-083-784-100792 Sequence 100792,
C 19	13.4	51.5	19	1	US-11-083-784-100799 Sequence 100799,
C 20	13.2	50.8	18	1	US-10-310-914A-126258 Sequence 126258,
C 21	13.2	50.8	18	1	US-10-310-914A-755151 Sequence 755151,
C 22	13.2	50.8	18	1	US-10-310-914A-1097078 Sequence 1097078,
C 23	12.8	49.2	18	1	US-10-310-914A-616514 Sequence 616514,
C 24	12.8	49.2	18	1	US-10-310-914A-1008058 Sequence 1008058,
C 25	9	34.6	10	1	US-11-035-105-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-10-310-914A-1031100/c  
; Sequence 1031100, Application US/10310914A

; Publication No. US200600003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1031100  
; LENGTH: 22  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-1031100

Query Match 60.0%; Score 15.6; DB 1; Length 22;  
Best Local Similarity 81.8%; Pred. No. 3.8;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

4 CCTCATCGCCCTTCCTAAGCA 25  
||||| ||||||| |||  
22 CCTCAGCTCCCTTCCTCTGCA 1

RESULT 2

US-10-310-914A-66874/c  
; Sequence 66874, Application US/10310914A  
; Publication No. US200600003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; TITLE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 66874  
; LENGTH: 20  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-66874

Query Match 58.5%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 4.6;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

2 CACCTCATCGCCCTTCCTA 21  
||||| |||||| |||  
20 CACCTCCTCGCCCTTCTTA 1

Db

RESULT 3

US-11-101-244-788791  
; Sequence 788791, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137

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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 788791
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-788791

Query Match          56.9%; Score 14.8; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 5.3;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACCTCATCGCCCTTC 18
    ||||:|||||:|
Db 1 CCACCUCACCGCCCAUUC 18

RESULT 4
US-11-083-784-788791
; Sequence 788791, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 788791
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-788791

Query Match          56.9%; Score 14.8; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 5.3;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACCTCATCGCCCTTC 18
    ||||:|||||:|
Db 1 CCACCUCACCGCCCAUUC 18

RESULT 5
US-10-310-914A-1300864
; Sequence 1300864, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1300864
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-310-914A-1300864
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; ORGANISM: Human
US-10-310-914A-1300864

Query Match          54.6%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 6.1;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCCTTCCTAA 22
    ||:|:|||||:|:|
Db 1 CCUCCUGGCCCAUCCUAA 19

RESULT 6
US-10-310-914A-74927/c
; Sequence 74927, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74927
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-74927

Query Match          54.6%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CACCTCATCGCCCTTCCT 20
    ||||| || ||||| |||
Db 20 CCCCTCCTCACCCCTTCCT 2

RESULT 7
US-10-310-914A-1166831/c
; Sequence 1166831, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1166831
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1166831

Query Match          54.6%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCACCTCATCGCCCTTC 19
    ||||| || ||||| |||
Db 19 CCACCTCCTCGCCCGGCC 1

RESULT 8
US-10-310-914A-74926/c
; Sequence 74926, Application US/10310914A
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; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 634307
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-634307

Query Match      51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 7.7;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAAGCA 25
   |||||:||||
Db 3 GCCCCUCCUCAGCA 17

RESULT 14
US-10-310-914A-1117030
; Sequence 1117030, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1117030
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1117030

Query Match      51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 7.7;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAAGCA 25
   |||||:||||
Db 3 GCCCCUCCUCAGCA 17

RESULT 14
US-10-310-914A-1117030
; Sequence 1117030, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1117030
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1117030

Query Match      51.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 7.7;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTTC 18
   ||:|||||:|
Db 1 CCUCAUGCCCCUCC 15

RESULT 15
US-10-310-914A-634308
; Sequence 634308, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 634308
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-634308
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Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 7.3;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAAGCA 25
   |||||:||||
Db 3 GCCCCUCCUCAGCA 17

RESULT 16
US-11-101-244-100792/c
; Sequence 100792, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100792
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-100792

Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCTTCCT 20
   ||||| |||||
Db 19 TCATCGGCCCTTCCT 5

RESULT 17
US-11-101-244-100799/c
; Sequence 100799, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100799
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-100799
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Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TCATCGCCCCCTTCCT 20
      18 TCATCGGCCCTTCCT 4
Db

RESULT 18
US-11-083-784-100792/c
; Sequence 100792, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100792
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-100792

Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TCATCGCCCCCTTCCT 20
      19 TCATCGGCCCTTCCT 5
Db

RESULT 19
US-11-083-784-100799/c
; Sequence 100799, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 100799
; LENGTH: 19
; TYPE: RNA
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; ORGANISM: Homo sapiens
US-11-083-784-100799

Query Match      51.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 7.3;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 TCATCGCCCCCTTCCT 20
      18 TCATCGGCCCTTCCT 4
Db

RESULT 20
US-10-310-914A-126258
; Sequence 126258, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126258
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-126258

Query Match      50.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 8.1;
Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCACCTCATCGCCCTTC 18
      1 CAACCCUCCUCCUCCUUC 18
Db

RESULT 21
US-10-310-914A-755151/c
; Sequence 755151, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 755151
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-755151

Query Match      50.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      5 CTCATCGCCCTTCCTAA 22
      18 CTCACCGCCCTTCCTTA 1
Db

RESULT 22
US-10-310-914A-1097078/c
; Sequence 1097078, Application US/10310914A
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; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1097078
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1097078

Query Match 50.8%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCC 19
Db 18 CATCTCATTCCTCTTCC 1

RESULT 23
US-10-310-914A-616514/c
; Sequence 616514, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 616514
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-616514

Query Match 49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 8.9;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAAGCAT 26
Db 17 GCCCCTTCCTGAGCCT 2

RESULT 24
US-10-310-914A-1008058
; Sequence 1008058, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1008058
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human

US-10-310-914A-1008058

Query Match 49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 8.9;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCCTAAGCAT 26
Db 2 GCCCCUUCUCAGCCU 17

RESULT 25
US-11-035-105-31
; Sequence 31, Application US/11035105
; Publication No. US20050255498A1
; GENERAL INFORMATION:
; APPLICANT: Aerssens, Jeroen
; APPLICANT: Athanasiou, Maria
; APPLICANT: Brain, Carlos
; APPLICANT: Cohen, Nadine
; APPLICANT: Dain, Bradley
; APPLICANT: Denton, R. Rex
; APPLICANT: Judson, Richard S.
; APPLICANT: Ozdemir, Vural
; APPLICANT: Reed, Carol R.
; TITLE OF INVENTION: APOC1 Genetic Markers Associated with Age of Onset of Alzheimer's
; TITLE OF INVENTION: Disease
; FILE REFERENCE: 2300.0120001
; CURRENT APPLICATION NUMBER: US/11/035,105
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: US 60/538,606
; PRIOR FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Forward Primer Extension Oligonucleotide for Detecting Alleles a
; OTHER INFORMATION: PSs in Haplotypes Comprising Preferred Embodiments of Age of
; OTHER INFORMATION: Onset Markers I and II
US-11-035-105-31

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 1 CCCCTTCCT 9

Search completed: May 9, 2006, 16:55:34
Job time : 0.001 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:44:42 ; Search time 0.001 Seconds  
(without alignments)  
7.030 Million cell updates/sec

Title: US-09-904-968A-19-COPY  
Perfect score: 19  
Sequence: 1 ggtcgcgctgtggcgaagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 16 seqs, 185 residues

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 16 summaries

Database : estdb19:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	10.8	56.8	15	1	BM396199	ACCESSION:BM396199
2	9.8	51.6	13	1	BM396884	ACCESSION:BM396884
3	9.8	51.6	13	1	BM397041	ACCESSION:BM397041
4	8.8	46.3	12	1	BM395931	ACCESSION:BM395931
5	8.8	46.3	12	1	BM400217	ACCESSION:BM400217
6	8.4	44.2	12	1	AJ655540	ACCESSION:AJ655540
7	8	42.1	11	1	BM395226	ACCESSION:BM395226
8	7.8	41.1	11	1	AJ679435	ACCESSION:AJ679435
9	7.8	41.1	11	1	AJ681247	ACCESSION:AJ681247
10	7.8	41.1	11	1	AJ683713	ACCESSION:AJ683713
11	7.8	41.1	11	1	AJ686459	ACCESSION:AJ686459
12	7.8	41.1	11	1	BM395786	ACCESSION:BM395786
13	7.8	41.1	11	1	BM398154	ACCESSION:BM398154
14	7.8	41.1	11	1	BM401300	ACCESSION:BM401300
15	7.4	38.9	10	1	BM396011	ACCESSION:BM396011
16	7.4	38.9	10	1	BM398849	ACCESSION:BM398849

ALIGNMENTS

RESULT 1  
BM396199  
LOCUS  
DEFINITION  
5009-0-18-G04.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION  
BM396199  
VERSION  
BM396199.1 GI:18196252  
KEYWORDS  
EST.  
SOURCE  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

BM396199 15 bp mRNA linear EST 17-JAN-2002

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 15)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source

Location/Qualifiers  
1..15  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 56.8%; Score 10.8; DB 1; Length 15;  
Best Local Similarity 85.7%; Pred. No. 1.4;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCGA 16

Db 1 TCACGCGGTGGCGA 14

RESULT 2  
BM396884

LOCUS

DEFINITION

BM396884 13 bp mRNA linear EST 17-JAN-2002  
5009-0-26-Cl1.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 13)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source

Location/Qualifiers  
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/mol\_type="mRNA"  
/strain="CU428.1"  
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/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 2.2;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15  
| | | | | | | | | |  
Db 1 TCACGCGGTGGCG 13

RESULT 3  
BM397041  
LOCUS 13 bp mRNA linear EST 17-JAN-2002  
DEFINITION 5009-0-28-C12.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM397041  
VERSION BM397041.1 GI:18197094  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1. .13  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
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preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES  
source  
Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 2.2;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15  
| | | | | | | | | |  
Db 1 TCACGCGGTGGCG 13

RESULT 4  
BM395931  
LOCUS 12 bp mRNA linear EST 17-JAN-2002  
DEFINITION 5009-0-14-D04.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM395931  
VERSION BM395931.1 GI:18195984  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1. .12  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
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/db\_xref="taxon:5911"  
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/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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source  
Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 3.4;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGC 14  
| | | | | | | | | |  
Db 1 TCACGCGGTGGC 12

RESULT 5  
BM400217  
LOCUS 12 bp mRNA linear EST 17-JAN-2002  
DEFINITION 5009-0-7-B09.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM400217  
VERSION BM400217.1 GI:18200270  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1. .12  
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preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

FEATURES  
source  
Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 3.4;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGC 14  
| | | | | | | | | |  
Db 1 TCACGCGGTGGC 12

RESULT 6  
AJ655540  
LOCUS 12 bp mRNA linear EST 28-JUN-2004  
DEFINITION AJ655540 KN277 Sus scrofa cDNA clone C0005190\_G13, mRNA sequence.  
ACCESSION AJ655540  
VERSION AJ655540.1 GI:49339572





VERSION AJ681247.1 GI:49413837  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.  
FEATURES  
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/organism="Sus scrofa"  
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/clone="C0001795\_I24"  
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/clone\_lib="CSEQRAN04"  
/note="Vector: pBlueScriptII(KS+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 5.4;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 CGCGCTGTGGC 14  
| ||| |||||  
Db 1 CCCGCGGTGGC 11  
RESULT 10  
AJ683713  
LOCUS AJ683713 CSEQRAN04 Sus scrofa cDNA clone C0001802\_O06, mRNA  
DEFINITION sequence.  
ACCESSION AJ683713  
VERSION AJ683713.1 GI:49416303  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

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Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 5.4;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 CGCGCTGTGGC 14  
| ||| |||||  
Db 1 CCCGCGGTGGC 11  
RESULT 11  
AJ686459  
LOCUS AJ686459 CSEQRAN04 Sus scrofa cDNA clone C0001811\_K23, mRNA  
DEFINITION sequence.  
ACCESSION AJ686459  
VERSION AJ686459.1 GI:49419049  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 11)  
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle  
JOURNAL Unpublished (2004)  
COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.  
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/organism="Sus scrofa"  
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/db\_xref="taxon:9823"  
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Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 5.4;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 CGCGCTGTGGC 14  
| ||| |||||  
Db 1 CCCGCGGTGGC 11  
RESULT 12  
BM395786

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LOCUS      BM395786                      11 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION  5009-0-11-G09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM395786
VERSION     BM395786.1  GI:18195839
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
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Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      3  TCGCGCTGTGG 13
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 5.4;
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QY      3  TCGCGCTGTGG 13
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Db      1  TCACGCGGTGG 11

RESULT 13
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LOCUS      BM398154                      11 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION  5009-0-41-D10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398154
VERSION     BM398154.1  GI:18198207
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Db      1  TCACGCGGTGG 11

RESULT 15
BM396011
LOCUS      BM396011                      10 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION  5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM396011
VERSION     BM396011.1  GI:18196064
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Best Local Similarity 81.8%;  Pred. No. 5.4;
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      |||||
Db      1  TCACGCGGTGG 11

RESULT 14
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LOCUS      BM401300                      11 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION  5009-0-85-E01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM401300
VERSION     BM401300.1  GI:18201353
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 11)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE       EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL     Unpublished (2002)
COMMENT     Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..11
/organism="Tetrahymena thermophila"
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/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 5.4;
Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      3  TCGCGCTGTGG 13
      |||||
Db      1  TCACGCGGTGG 11

RESULT 15
BM396011
LOCUS      BM396011                      10 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION  5009-0-15-E12.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM396011
VERSION     BM396011.1  GI:18196064
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
ORGANISM    Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 10)
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AUTHORS

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.

TITLE

EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL

Unpublished (2002)

COMMENT

Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES

source

1..10

Location/Qualifiers

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

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Query Match

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Best Local Similarity 88.9%; Pred. No. 6.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db

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RESULT 16

BM398849

LOCUS

5009-0-5-G06.t.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION

10 bp mRNA linear EST 17-JAN-2002

ACCESSION

BM398849

VERSION

BM398849.1 GI:18198902

KEYWORDS

EST.

SOURCE

Tetrahymena thermophila

ORGANISM

Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.  
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REFERENCE

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.

AUTHORS

EST from Tetrahymena thermophila, strain CU428.1, growing cells

TITLE

Unpublished (2002)

JOURNAL

Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
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COMMENT

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Best Local Similarity 88.9%; Pred. No. 6.1;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

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Db

2 CGCGGTGGC 10

Db

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|||||

Search completed: May 9, 2006, 15:44:42

Job time : 0.001 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: May 9, 2006, 15:46:51 ; Search time 0.001 Seconds  
(without alignments)  
68.894 Million cell updates/sec

Title: US-09-904-968A-19-COPY  
Perfect score: 19  
Sequence: 1 ggtcgcgctgtggaagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 173 seqs, 1813 residues

Total number of hits satisfying chosen parameters: 346

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 173 summaries

Database : gedbl9:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 8	9	47.4	10	1	AR201469
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ALIGNMENTS

RESULT 1

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LOCUS	AX440515	Sequence 19 from Patent WO0206529.	19 bp	DNA	linear	PAT 28-JUN-2002
DEFINITION	AX440515	Sequence 19 from Patent WO0206529.	19 bp	DNA	linear	PAT 28-JUN-2002
ACCESSION	AX440515	Sequence 19 from Patent WO0206529.	19 bp	DNA	linear	PAT 28-JUN-2002
VERSION	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
KEYWORDS	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
SOURCE	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
ORGANISM	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
REFERENCE	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
AUTHORS	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
TITLE	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
JOURNAL	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
FEATURES	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
source	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
Query Match	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
Best Local Similarity	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
Matches	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
Qy	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
Db	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
RESULT 2	AX440515.1	GI:21665318	19 bp	DNA	linear	PAT 28-JUN-2002
AR364760	AR364760	Sequence 4 from patent US 5427929.	14 bp	DNA	linear	PAT 03-SEP-2003
LOCUS	AR364760	Sequence 4 from patent US 5427929.	14 bp	DNA	linear	PAT 03-SEP-2003
DEFINITION	AR364760	Sequence 4 from patent US 5427929.	14 bp	DNA	linear	PAT 03-SEP-2003
ACCESSION	AR364760	Sequence 4 from patent US 5427929.	14 bp	DNA	linear	PAT 03-SEP-2003
VERSION	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
KEYWORDS	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
SOURCE	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
ORGANISM	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
REFERENCE	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
AUTHORS	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
TITLE	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
JOURNAL	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
FEATURES	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
source	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
Query Match	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
Best Local Similarity	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
Matches	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
Qy	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
Db	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
RESULT 3	AR364760.1	GI:34427756	14 bp	DNA	linear	PAT 03-SEP-2003
AR408022	AR408022	Sequence 115 from patent US 6632057.	14 bp	RNA	linear	PAT 18-DEC-2003
LOCUS	AR408022	Sequence 115 from patent US 6632057.	14 bp	RNA	linear	PAT 18-DEC-2003
DEFINITION	AR408022	Sequence 115 from patent US 6632057.	14 bp	RNA	linear	PAT 18-DEC-2003
ACCESSION	AR408022	Sequence 115 from patent US 6632057.	14 bp	RNA	linear	PAT 18-DEC-2003
VERSION	AR408022.1	GI:40158009	14 bp	RNA	linear	PAT 18-DEC-2003
KEYWORDS	AR408022.1	GI:40158009	14 bp	RNA	linear	PAT 18-DEC-2003
SOURCE	AR408022.1	GI:40158009	14 bp	RNA	linear	PAT 18-DEC-2003
ORGANISM	AR408022.1	GI:40158009	14 bp	RNA	linear	PAT 18-DEC-2003
REFERENCE	AR408022.1	GI:40158009	14 bp	RNA	linear	PAT 18-DEC-2003
AUTHORS	AR408022.1	GI:40158009	14 bp	RNA	linear	PAT 18-DEC-2003
TITLE	AR408022.1	GI:40158009	14 bp	RNA	linear	PAT 18-DEC-2003



JOURNAL Patent: US 6632057-A 115 14-OCT-2003;  
GFI Aerospace; Paris;  
FRX;

FEATURES source Location/Qualifiers  
1. .14  
/organism="unknown"  
/mol\_type="unassigned RNA"

Query Match 54.7%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 91.7%; Pred. No. 16;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAGG 19  
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Db 1 CTGTGGAGAAGG 12

RESULT 4  
LOCUS BD225399 14 bp DNA linear PAT 17-JUL-2003  
DEFINITION Targeting antisense library.  
ACCESSION BD225399  
VERSION BD225399.1 GI:33035169  
KEYWORDS JP 2002509733-A/33.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Ruffner,D.E., Pierce,M.L. and Chen,Z.  
TITLE Targeting antisense library  
JOURNAL Patent: JP 2002509733-A 33 02-APR-2002;  
UNIVERSITY OF UTAH RESEARCH FOUNDATION  
COMMENT OS Herpes simplex virus  
PN JP 2002509733-A/33  
PD 02-APR-2002  
PF 28-MAR-1999 JP 2000541344  
PR 28-MAR-1998 US 60/079792,06-NOV-1998 US 60/107504 PI  
DUANE E RUFFNER,MICHAEL L PIERCE,ZHIDONG CHEN PC  
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CC Targeting antisense library  
FH Key Location/Qualifiers  
FT source 1. .14  
FT /organism='Herpes simplex virus'.

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Query Match 51.6%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 84.6%; Pred. No. 23;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTGGC 14  
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Db 2 GTGGCGCTGGGC 14

RESULT 5  
AR349597  
LOCUS AR349597 14 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 33 from patent US 6586180.  
ACCESSION AR349597  
VERSION AR349597.1 GI:33750395  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Ruffner,D.E., Pierce,M.L. and Chen,Z.  
TITLE Directed antisense libraries  
JOURNAL Patent: US 6586180-A 33 01-JUL-2003;  
University of Utah; Salt Lake City, UT

FEATURES source Location/Qualifiers  
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Query Match 51.6%; Score 9.8; DB 1; Length 14;  
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Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTGGC 14  
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Db 2 GTGGCGCTGGGC 14

RESULT 6  
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LOCUS AR103443 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 18 from patent US 6087477.  
ACCESSION AR103443  
VERSION AR103443.1 GI:12815031  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease  
JOURNAL Patent: US 6087477-A 18 11-JUL-2000;  
FEATURES source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
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Db 10 GTGGCGAAG 2

RESULT 7  
BD223041/c  
LOCUS BD223041 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Compositions and methods for the treatment and diagnosis of cardiovascular disease.  
ACCESSION BD223041  
VERSION BD223041.1 GI:33032811  
KEYWORDS JP 2002521679-A/12.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease  
JOURNAL Patent: JP 2002521679-A 12 16-JUL-2002;  
COMMENT MILLENNIUM PHARMACEUTICALS INC  
OS Artificial Sequence  
PN JP 2002521679-A/12  
PD 16-JUL-2002  
PF 30-JUL-1999 JP 2000562059  
PR 30-JUL-1998 US 09/126640  
PI DEAN A FALB  
PC  
G01N33/50,A61K31/711,A61K39/395,A61K45/00,A61K48/00, PC  
A61P7/00,  
PC  
A61P9/08,A61P9/10,A61P9/12,A61P9/14,A61P27/02,A61P29/00,A61P35/ PC  
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PC G01N33/15,G01N33/566,G01N33/68//C12N15/09,C12N15/00 CC

Primer  
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FT Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 8  
AR201469/c  
LOCUS AR201469 18 from patent US 6359194. linear PAT 20-APR-2002  
DEFINITION AR201469  
ACCESSION AR201469  
VERSION AR201469.1 GI:20252357  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Galvin,K., Falb,D.A., Donovan,M.J., Huszar,D. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease  
JOURNAL Patent: US 6359194-A 18 19-MAR-2002;  
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source Location/Qualifiers  
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Query Match 47.4%; Score 9; DB 1; Length 10;  
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 9  
AR265162/c  
LOCUS AR265162 18 from patent US 6492126. linear PAT 10-APR-2003  
DEFINITION AR265162  
ACCESSION AR265162  
VERSION AR265162.1 GI:29693564  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease  
JOURNAL Patent: US 6492126-A 18 10-DEC-2002;  
FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 10  
AR562046/c  
LOCUS AR562046 18 from patent US 6759210. linear PAT 08-OCT-2004  
DEFINITION AR562046  
ACCESSION AR562046  
VERSION AR562046.1 GI:53975863  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using fehd545 as a target  
JOURNAL Patent: US 6759210-A 18 06-JUL-2004;  
FEATURES  
source Location/Qualifiers  
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Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 11  
AR590095/c  
LOCUS AR590095 11 from patent US 6803215. linear PAT 15-DEC-2004  
DEFINITION AR590095  
ACCESSION AR590095  
VERSION AR590095.1 GI:56637588  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Shaw,P.-C., Wang,J., But,P.P.H., Ha,W.-Y. and Yau,F.C.F.  
TITLE Sequence characterized amplified region (SCAR) test for the authentication of traditional Chinese medicinal materials  
JOURNAL Patent: US 6803215-A 11 12-OCT-2004;  
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source Location/Qualifiers  
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Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 12  
AX630373  
LOCUS AX630373 11 bp DNA PAT 21-FEB-2003  
DEFINITION AX630373  
ACCESSION AX630373  
VERSION AX630373.1 GI:28458411  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.  
AUTHORS Method for determining homeostasis of the skin  
TITLE Patent: WO 02053774-A 7414 11-JUL-2002;  
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 47.4%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 GCGCTGTGG 13  
|||||  
Db 3 GCGCTGTGG 11  
RESULT 13  
ATH524760  
LOCUS  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 081C08.  
ACCESSION AJ524760  
VERSION AJ524760.1 GI:26792996  
KEYWORDS left border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1  
REFERENCE Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
PUBMED 12446565  
REFERENCE 2 (bases 1 to 12)  
AUTHORS Balzergue,S.  
TITLE Direct Submision  
JOURNAL Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).  
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/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/ecotype="Wassilewskija"  
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1. .12  
/note="T-DNA flanking sequence  
left border"

Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 33;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 5 GCGCTGTGGCGA 16  
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Db 1 GCGCTATGGTGA 12  
RESULT 14  
BD161333/c  
LOCUS BD161333  
DEFINITION Human activated Th1 and Th2 cell expression genes.  
ACCESSION BD161333  
VERSION BD161333.1 GI:27867091  
KEYWORDS JP 2002186482-A/155.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
REFERENCE Nagai,S., Matsushima,K. and Hashimoto,S.  
AUTHORS Human activated Th1 and Th2 cell expression genes  
TITLE Patent: JP 2002186482-A 155 02-JUL-2002;  
JOURNAL JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002186482-A/155  
PD 02-JUL-2002  
PF 19-DEC-2000 JP 2000385816  
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human activated Th1 and Th2 cell expression genes FH Key  
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FEATURES Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 34;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCTG 10  
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Db 10 GGGCGCGCTG 1  
RESULT 15  
BD238832/c  
LOCUS BD238832  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238832  
VERSION BD238832.1 GI:33048602  
KEYWORDS JP 2002534056-A/250.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 10)  
REFERENCE Roberts,B.L. and Shankara,S.  
AUTHORS Preparation and use of superior vaccines  
TITLE Patent: JP 2002534056-A 250 15-OCT-2002;  
JOURNAL GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/250  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749

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PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/53,G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
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Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTG 10
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Db 10 GGGCGCGCTG 1

RESULT 16
BD238855
LOCUS BD238855 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238855
VERSION BD238855.1 GI:33048625
KEYWORDS JP 2002534056-A/273.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 273 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/273
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1. .10
FT /organism='Homo sapiens (human)'.

FEATURES
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Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
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Db 1 CGCTGTGGCG 10

RESULT 17
AX152988/c
LOCUS AX152988 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 903 from Patent WO0138577.
ACCESSION AX152988
VERSION AX152988.1 GI:14534639
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 903 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
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Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCTG 10
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Db 10 GGGCGCGCTG 1

RESULT 18
BD124474
LOCUS BD124474 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124474
VERSION BD124474.1 GI:23219419
KEYWORDS JP 2002503460-A/305.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
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AUTHORS Katz,E.H.  
TITLE Compositions and method for healing wound  
JOURNAL Patent: JP 2002503460-A 305 05-FEB-2002;  
THE WISTAR INSTITUTE  
COMMENT OS Mus musculus (mouse)  
PN JP 2002503460-A/305  
PD 05-FEB-2002  
PF 12-FEB-1999 JP 2000531545  
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR  
28-SEP-1998 US 60/102051  
PI ELLEN HEBER KATZ  
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC  
C12N5/00  
CC Compositions and method for healing wound  
FH Key Location/Qualifiers  
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FT Location/Qualifiers  
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Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GCTGTGGCGA 16  
Db 1 GCTGTGGCCA 10  
RESULT 19  
CQ832827  
LOCUS 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 198 from Patent WO2004059002.  
ACCESSION CQ832827  
VERSION CQ832827.1 GI:50832434  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 198 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 9 TGTGGCGAAG 18  
Db 1 TGTGGCAAAG 10  
RESULT 20  
CQ833102/c  
LOCUS 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 473 from Patent WO2004059002.  
ACCESSION CQ833102  
VERSION CQ833102.1 GI:50832709  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 473 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCTG 10  
Db 10 GGGCGCGCTG 1  
RESULT 21  
CQ833458  
LOCUS 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 829 from Patent WO2004059002.  
ACCESSION CQ833458  
VERSION CQ833458.1 GI:50833065  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 829 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
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source Location/Qualifiers  
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Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 GCGCTGTGGC 14  
Db 2 GGGCTGTGGC 11  
RESULT 22  
CQ835173/c  
LOCUS 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 231 from Patent WO2004059001.  
ACCESSION CQ835173  
VERSION CQ835173.1 GI:50834707  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
Conradt,M. and Hofmann,K.



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TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 231 15-JUL-2004;
           Henkel Kommanditgesellschaft auf Aktien (DE)
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           /db_xref="taxon:9606"

Query Match      44.2%;   Score 8.4;   DB 1;   Length 11;
Best Local Similarity 90.0%;   Pred. No. 37;
Matches      9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      5 GCGCTGTGGC 14
Db      11 GCGCAGTGGC 2

RESULT 23
CQ837127/c
LOCUS      CQ837127      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 2185 from Patent WO2004059001.
ACCESSION  CQ837127
VERSION     CQ837127.1 GI:50836661
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining markers of human facial skin
JOURNAL     Patent: WO 2004059001-A 2185 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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           /db_xref="taxon:9606"

Query Match      44.2%;   Score 8.4;   DB 1;   Length 11;
Best Local Similarity 90.0%;   Pred. No. 37;
Matches      9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      10 GTGGCGAAGG 19
Db      11 GTGGAGAAGG 2

RESULT 24
CQ838018
LOCUS      CQ838018      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 3076 from Patent WO2004059001.
ACCESSION  CQ838018
VERSION     CQ838018.1 GI:50837552
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining markers of human facial skin
JOURNAL     Patent: WO 2004059001-A 3076 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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           /db_xref="taxon:9606"

Query Match      44.2%;   Score 8.4;   DB 1;   Length 11;
Best Local Similarity 90.0%;   Pred. No. 37;
Matches      9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      5 GCGCTGTGGC 14
Db      2 GCGCTGTGGC 11

RESULT 25
CQ838061
LOCUS      CQ838061      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 3119 from Patent WO2004059001.
ACCESSION  CQ838061
VERSION     CQ838061.1 GI:50837595
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining markers of human facial skin
JOURNAL     Patent: WO 2004059001-A 3119 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      44.2%;   Score 8.4;   DB 1;   Length 11;
Best Local Similarity 90.0%;   Pred. No. 37;
Matches      9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      6 CGCTGTGGCG 15
Db      1 CGCTGTGGGG 10

RESULT 26
CS058641/c
LOCUS      CS058641      11 bp      DNA      linear      PAT 13-APR-2005
DEFINITION Sequence 538 from Patent WO2005028671.
ACCESSION  CS058641
VERSION     CS058641.1 GI:62551824
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
TITLE       Method for determining hair cycle markers
JOURNAL     Patent: WO 2005028671-A 538 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      44.2%;   Score 8.4;   DB 1;   Length 11;
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Matches      9;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      5 GCGCTGTGGC 14

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Db 11 GCGCGGTGGC 2  
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RESULT 27 AR301724 linear PAT 12-JUN-2003  
LOCUS AR301724 11 bp DNA  
DEFINITION Sequence 305 from patent US 6538173.  
ACCESSION AR301724  
VERSION AR301724.1 GI:31689526  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 11)  
AUTHORS Heber-Katz,E.  
TITLE Compositions and methods for wound healing  
JOURNAL Patent: US 6538173-A 305 25-MAR-2003;  
The Wistar Institute; Philadelphia, PA;  
WOX;  
FEATURES Location/Qualifiers  
source 1..11  
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Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GCTGTGGCGCA 16  
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Db 1 GCTGTGGCCA 10  
RESULT 28 AX470439 linear PAT 09-AUG-2002  
LOCUS AX470439 11 bp DNA  
DEFINITION Sequence 16 from Patent WO02053773.  
ACCESSION AX470439  
VERSION AX470439.1 GI:22205564  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 16 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
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Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
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Db 1 GTGGCGAATG 10  
RESULT 29 AX471346/c linear PAT 09-AUG-2002  
LOCUS AX471346 11 bp DNA  
DEFINITION Sequence 923 from Patent WO02053773.  
ACCESSION AX471346  
VERSION AX471346.1 GI:22206471  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 923 11-JUL-2002;  
HENKEL KGAA (DE)  
FEATURES Location/Qualifiers  
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Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
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Db 11 GTGGAGAAGG 2  
RESULT 30 AX623088 linear PAT 21-FEB-2003  
LOCUS AX623088 11 bp DNA  
DEFINITION Sequence 129 from Patent WO02053774.  
ACCESSION AX623088  
VERSION AX623088.1 GI:28451029  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 129 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1..11  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 37;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
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Db 1 GTGGCGAATG 10  
RESULT 31 AX624098 linear PAT 21-FEB-2003  
LOCUS AX624098 11 bp DNA  
DEFINITION Sequence 1139 from Patent WO02053774.  
ACCESSION AX624098  
VERSION AX624098.1 GI:28452039  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1139 11-JUL-2002;

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    Best Local Similarity
      90.0%; Pred. No. 37;
    Matches
      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  10 GTGGCGAAGG 19
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  Db
  1 GTGGCGAATG 10

RESULT 32
AX624741
LOCUS
  AX624741 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 1782 from Patent WO02053774.
ACCESSION
  AX624741
VERSION
  AX624741.1 GI:28452682
KEYWORDS
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SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 1782 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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QY
  6 CGCTGTGGCG 15
    |||||
  Db
  2 CGATGTGGCG 11

RESULT 33
AX626676
LOCUS
  AX626676 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 3717 from Patent WO02053774.
ACCESSION
  AX626676
VERSION
  AX626676.1 GI:28454714
KEYWORDS
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SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 3717 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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      90.0%; Pred. No. 37;
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QY
  6 CGCTGTGGCG 15
    |||||
  Db
  2 CGATGTGGCG 11

RESULT 34
AX626754/c
LOCUS
  AX626754 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 3795 from Patent WO02053774.
ACCESSION
  AX626754
VERSION
  AX626754.1 GI:28454792
KEYWORDS
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SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 3795 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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      90.0%; Pred. No. 37;
    Matches
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QY
  5 GCGCTGTGGC 14
    |||||
  Db
  11 GCGCAGTGGC 2

RESULT 35
AX628541
LOCUS
  AX628541 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 5582 from Patent WO02053774.
ACCESSION
  AX628541
VERSION
  AX628541.1 GI:28456579
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 5582 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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    Best Local Similarity
      90.0%; Pred. No. 37;
    Matches
      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  5 GCGCTGTGGC 14
    |||||
  Db
  2 GGGCTGTGGC 11

RESULT 36
AX629565
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FEATURES
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    Henkel Kommanditgesellschaft auf Aktien (DE)
    Location/Qualifiers
      1. .11
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

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      44.2%; Score 8.4; DB 1; Length 11;
    Best Local Similarity
      90.0%; Pred. No. 37;
    Matches
      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  9 TGTCGCGAAG 18
    |||||
  Db
  1 TGTCGCAAAAG 10

RESULT 34
AX626754/c
LOCUS
  AX626754 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 3795 from Patent WO02053774.
ACCESSION
  AX626754
VERSION
  AX626754.1 GI:28454792
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 3795 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    1. .11
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

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      44.2%; Score 8.4; DB 1; Length 11;
    Best Local Similarity
      90.0%; Pred. No. 37;
    Matches
      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  5 GCGCTGTGGC 14
    |||||
  Db
  11 GCGCAGTGGC 2

RESULT 35
AX628541
LOCUS
  AX628541 11 bp DNA linear PAT 21-FEB-2003
DEFINITION
  Sequence 5582 from Patent WO02053774.
ACCESSION
  AX628541
VERSION
  AX628541.1 GI:28456579
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 5582 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    1. .11
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

    Query Match
      44.2%; Score 8.4; DB 1; Length 11;
    Best Local Similarity
      90.0%; Pred. No. 37;
    Matches
      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
  5 GCGCTGTGGC 14
    |||||
  Db
  2 GGGCTGTGGC 11

RESULT 36
AX629565
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LOCUS      AX629565                      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6606 from Patent WO02053774.
ACCESSION  AX629565
VERSION    AX629565.1  GI:28457603
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6606 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  CGCTGTGGCG 15
        |||||
Db      1  CGCTGTGGG 10

RESULT 37
AX629817/c
LOCUS      AX629817                      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6858 from Patent WO02053774.
ACCESSION  AX629817
VERSION    AX629817.1  GI:28457855
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 6858 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
        |||||
Db      11 GTGGAGAAGG 2

RESULT 38
AX630364/c
LOCUS      AX630364                      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7405 from Patent WO02053774.
ACCESSION  AX630364
VERSION    AX630364.1  GI:28458402
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7405 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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              /db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GGTCGCGCTG 10
        |||||
Db      10 GGGCGGCGTG 1

RESULT 39
AX630509
LOCUS      AX630509                      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7550 from Patent WO02053774.
ACCESSION  AX630509
VERSION    AX630509.1  GI:28458547
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7550 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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              /mol_type="unassigned DNA"
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Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
        |||||
Db      1  GTGGCGAATG 10

RESULT 40
AX631519
LOCUS      AX631519                      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8561 from Patent WO02053774.
ACCESSION  AX631519
VERSION    AX631519.1  GI:28459585
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 8561 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
    ||| ||| ||| |||
Db 1 GTGGCGAATG 10

RESULT 41
AX632162
LOCUS AX632162 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9204 from Patent WO02053774.
ACCESSION AX632162
VERSION AX632162.1 GI:28467777
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE Hominidae; Homo.
JOURNAL Petersohn,D., Conradt,M. and Hofmann,K.
METHOD for determining homeostasis of the skin
PATENT: WO 02053774-A 9204 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
    || ||| ||| |||
Db 2 CGATGTGGCG 11

RESULT 42
A71524/c
LOCUS A71524 12 bp DNA linear PAT 07-MAY-1999
DEFINITION Sequence 83 from Patent WO9813521.
ACCESSION A71524
VERSION A71524.1 GI:4775136
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 unclassified sequences.
AUTHORS 1 (bases 1 to 12)
TITLE Fesce,R. and Consalez,G.
METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
JOURNAL PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
PATENT: WO 9813521-A 83 02-APR-1998;
FEATURES Location/Qualifiers
source 1..12
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
    ||| ||| ||| |||
Db 12 GTGACGAAGG 3
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RESULT 43
AR172146
LOCUS AR172146 12 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6303293.
ACCESSION AR172146
VERSION AR172146.1 GI:17911637
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 Unclassified.
AUTHORS 1 (bases 1 to 12)
TITLE Patterson,D.R., Puskas,J.A., Song,K. and Linnen,J.M.
JOURNAL Oligonucleotide reverse transcription primers for efficient
FEATURES detection of HIV-1 and HIV-2 and methods of use thereof
source Patent: US 6303293-A 2 16-OCT-2001;
Location/Qualifiers
1..12
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
    | ||| ||| |||
Db 1 CCCTGTGGCG 10

RESULT 44
AR678905/c
LOCUS AR678905 12 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 50 from patent US 6902894.
ACCESSION AR678905
VERSION AR678905.1 GI:67620099
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 Unclassified.
AUTHORS 1 (bases 1 to 12)
TITLE Yang,M. and Woo,H.S.
JOURNAL Mutation detection on RNA polymerase beta subunit gene having
rifampin resistance
PATENT: US 6902894-A 50 07-JUN-2005;
Genetel Pharmaceuticals Ltd.; Hong Kong;
CNX;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 41;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
    ||| ||| |||
Db 11 GCGCTGGGC 2

RESULT 45
BD000788
LOCUS BD000788 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Oligonucleotide reverse transcription primers for efficient
ACCESSION detection of HIV-1 and HIV-2 and methods of use thereof.
VERSION BD000788.1 GI:18623901
KEYWORDS BD000788
SOURCE JP 2000342274-A/2.
ORGANISM synthetic construct
other sequences; artificial sequences.
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REFERENCE 1 (bases 1 to 12)  
AUTHORS Patterson,D.R., Puscus,J.A., Son,K. and Lynen,J.M.  
TITLE Oligonucleotide reverse transcription primers for efficient  
detection of HIV-1 and HIV-2 and methods of use thereof  
JOURNAL Patent: JP 2000342274-A 2 12-DEC-2000;  
ORTHO CLINICAL DIAGNOSTICS INC  
COMMENT OS Artificial Sequence  
PN JP 2000342274-A/2  
PD 12-DEC-2000  
PF 02-FEB-2000 JP 2000025419  
PR 02-FEB-1999 US 60/118417  
PI DAVID R PATTERSON,JOHN A PUSCUS,KEMIN SON,JEFFREY M LYNEN PC  
C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,G01N33/569, PC  
C12N15/00  
CC  
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FT /organism='Artificial Sequence'.  
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1..12  
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/db\_xref="taxon:32630"  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 41;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 6 CGCTGTGGCG 15  
Db 1 CCCTGTGGCG 10  
RESULT 46  
BD083127  
LOCUS Human matured/activated dendritic cell expression genes.  
DEFINITION BD083127  
ACCESSION BD083127.1 GI:22628737  
VERSION JP 2001327293-A/48.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.  
TITLE Human matured/activated dendritic cell expression genes  
JOURNAL Patent: JP 2001327293-A 48 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001327293-A/48  
PD 27-NOV-2001  
PF 22-MAY-2000 JP 2000150562  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI  
NAGAI  
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00  
CC  
FH Key Location/Qualifiers  
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FT /mol\_type="genomic DNA"  
FT /db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 CTGTGGCG 15  
Db 2 CTGTGGCG 9  
RESULT 47  
BD083229  
LOCUS Human matured/activated dendritic cell expression genes.  
DEFINITION BD083229  
ACCESSION BD083229.1 GI:22628839  
VERSION JP 2001327293-A/150.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.  
TITLE Human matured/activated dendritic cell expression genes  
JOURNAL Patent: JP 2001327293-A 150 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001327293-A/150  
PD 27-NOV-2001  
PF 22-MAY-2000 JP 2000150562  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI  
NAGAI  
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00  
CC  
FH Key Location/Qualifiers  
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FT /mol\_type="genomic DNA"  
FT /db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 CTGTGGCG 15  
Db 2 CTGTGGCG 9  
RESULT 48  
BD240116  
LOCUS Preparation and use of superior vaccines.  
DEFINITION BD240116  
ACCESSION BD240116  
VERSION BD240116.1 GI:33049886  
KEYWORDS JP 2002534056-A/1534.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 1534 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/1534  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR  
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR  
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR  
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR

REFERENCE 1 (bases 1 to 12)  
AUTHORS Patterson,D.R., Puscus,J.A., Son,K. and Lynen,J.M.  
TITLE Oligonucleotide reverse transcription primers for efficient  
detection of HIV-1 and HIV-2 and methods of use thereof  
JOURNAL Patent: JP 2000342274-A 2 12-DEC-2000;  
ORTHO CLINICAL DIAGNOSTICS INC  
COMMENT OS Artificial Sequence  
PN JP 2000342274-A/2  
PD 12-DEC-2000  
PF 02-FEB-2000 JP 2000025419  
PR 02-FEB-1999 US 60/118417  
PI DAVID R PATTERSON,JOHN A PUSCUS,KEMIN SON,JEFFREY M LYNEN PC  
C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,G01N33/569, PC  
C12N15/00  
CC  
FH Key Location/Qualifiers  
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source Location/Qualifiers  
1..12  
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Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 41;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 6 CGCTGTGGCG 15  
Db 1 CCCTGTGGCG 10  
RESULT 46  
BD083127  
LOCUS Human matured/activated dendritic cell expression genes.  
DEFINITION BD083127  
ACCESSION BD083127  
VERSION BD083127.1 GI:22628737  
KEYWORDS JP 2001327293-A/48.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.  
TITLE Human matured/activated dendritic cell expression genes  
JOURNAL Patent: JP 2001327293-A 48 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001327293-A/48  
PD 27-NOV-2001  
PF 22-MAY-2000 JP 2000150562  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI  
NAGAI  
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00  
CC  
FH Key Location/Qualifiers  
FT source 1..10  
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FT /mol\_type="genomic DNA"  
FT /db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 CTGTGGCG 15  
Db 2 CTGTGGCG 9  
RESULT 47  
BD083229  
LOCUS Human matured/activated dendritic cell expression genes.  
DEFINITION BD083229  
ACCESSION BD083229.1 GI:22628839  
VERSION JP 2001327293-A/150.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.  
TITLE Human matured/activated dendritic cell expression genes  
JOURNAL Patent: JP 2001327293-A 150 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001327293-A/150  
PD 27-NOV-2001  
PF 22-MAY-2000 JP 2000150562  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI  
NAGAI  
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00  
CC  
FH Key Location/Qualifiers  
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FT /mol\_type="genomic DNA"  
FT /db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 CTGTGGCG 15  
Db 2 CTGTGGCG 9  
RESULT 48  
BD240116  
LOCUS Preparation and use of superior vaccines.  
DEFINITION BD240116  
ACCESSION BD240116  
VERSION BD240116.1 GI:33049886  
KEYWORDS JP 2002534056-A/1534.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 1534 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/1534  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR  
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR  
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR  
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR



REFERENCE 1  
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.  
TITLE Tumor markers in ovarian cancer  
JOURNAL Patent: WO 0175177-A 108 11-OCT-2001;  
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
FEATURES  
source  
1. .10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 TCGCGCTG 10  
|||||  
Db 2 TCGCGCTG 9  
RESULT 53  
BD007778  
LOCUS 10 bp DNA linear PAT 31-JAN-2002  
DEFINITION LPS activated human monocyte expressing genes.  
ACCESSION BD007778  
VERSION BD007778.1 GI:18636151  
KEYWORDS JP 2001069993-A/54.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.  
TITLE LPS activated human monocyte expressing genes  
JOURNAL Patent: JP 2001069993-A 54 21-MAR-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001069993-A/54  
PD 21-MAR-2001  
PF 28-APR-2000 JP 2000131079  
PR  
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC  
C12N15/09, C07K14/47, C07K16/18, G01N33/50, G01N33/53//A61K45/00, PC  
A61P29/00,  
PC A61P31/00, C12P21/08, C12N15/00  
CC  
FH key Location/Qualifiers  
FT source 1. .10  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
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1. .10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CTGTGGCG 15  
|||||  
Db 2 CTGTGGCG 9  
RESULT 54  
CS058186/c  
LOCUS 11 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 83 from Patent WO2005028671.  
ACCESSION CS058186  
VERSION CS058186.1 GI:62551138  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and Kessler-Becker,D.  
TITLE Method for determining hair cycle markers  
JOURNAL Patent: WO 2005028671-A 83 31-MAR-2005;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GCTGTGGC 14  
|||||  
Db 8 GCTGTGGC 1  
RESULT 55  
AX623147/c  
LOCUS 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 188 from Patent WO02053774.  
ACCESSION AX623147  
VERSION AX623147.1 GI:28451088  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 188 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES  
source  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GCTGTGGC 14  
|||||  
Db 8 GCTGTGGC 1  
RESULT 56  
AX628349/c  
LOCUS 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 5390 from Patent WO02053774.  
ACCESSION AX628349  
VERSION AX628349.1 GI:28456387  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin

JOURNAL Patent: WO 02053774-A 5390 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGC 14  
|||||  
Db 8 GCTGTGGC 1  
  
RESULT 57  
AX630568/c  
LOCUS AX630568 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 7609 from Patent WO02053774.  
ACCESSION AX630568  
VERSION AX630568.1 GI:28458606  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Conradt,M. and Hofmann,K.  
AUTHORS Method for determining homeostasis of the skin  
TITLE Patent: WO 02053774-A 7609 11-JUL-2002;  
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGC 14  
|||||  
Db 8 GCTGTGGC 1  
  
RESULT 58  
BD269102  
LOCUS BD269102 11 bp DNA linear PAT 17-JUL-2003  
DEFINITION Directed evolution of microorganisms.  
ACCESSION BD269102  
VERSION BD269102.1 GI:33078870  
KEYWORDS JP 2002543834-A/6.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
1 (bases 1 to 11)  
REFERENCE Schellenberger,V., Liu,A.D. and Selifonova,O.V.  
AUTHORS Directed evolution of microorganisms  
TITLE Patent: JP 2002543834-A 6 24-DEC-2002;  
JOURNAL GENENCOR INTERNATIONAL INC  
COMMENT OS Artificial Sequence  
PN JP 2002543834-A/6  
PD 24-DEC-2002  
PF 15-MAY-2000 JP 2000618443  
PR 19-MAY-1999 US 09/314847  
PI VOLKER SCHELLENBERGER,AMY D LIU,OLGA V SELIFONOVA PC  
C12N15/09,C12N1/21,C12N15/01/(C12N1/21,C12R1:185),C12N15/00, PC  
C12N15/00  
CC pos102 mutd mutated gene

FEATURES FH Key Location/Qualifiers  
source 1. .11  
/organism='Artificial Sequence'.  
FT source 1. .11  
FT Location/Qualifiers  
1. .11  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 GTGGCGCTGTG 12  
|||  
Db 1 GTGGCGCTGTG 11  
  
RESULT 59  
CQ833123  
LOCUS CQ833123 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 494 from Patent WO2004059002.  
ACCESSION CQ833123  
VERSION CQ833123.1 GI:50832730  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
AUTHORS Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 494 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 9 TGTGGCGAAGG 19  
|||||  
Db 1 TGTGGGGAAG 11  
  
RESULT 60  
CQ833801  
LOCUS CQ833801 11 bp DNA linear PAT 29-JUL-2004  
DEFINITION Sequence 1172 from Patent WO2004059002.  
ACCESSION CQ833801  
VERSION CQ833801.1 GI:50833408  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,  
AUTHORS Conradt,M. and Hofmann,K.  
TITLE Method for determining the homeostasis of hairy skin  
JOURNAL Patent: WO 2004059002-A 1172 15-JUL-2004;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"

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/db_xref="taxon:9606"

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 15
   |||||
Db 1 GGGCTGTGGAG 11

RESULT 61
CQ837135/c
LOCUS      CQ837135      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 2193 from Patent WO2004059001.
ACCESSION  CQ837135
VERSION    CQ837135.1 GI:50836669
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
           Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 2193 15-JUL-2004;
           Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCGCGCTGT 11
   |||||
Db 11 GGTACCCCTGT 1

RESULT 62
AR203918
LOCUS      AR203918      11 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 8 from patent US 6365410.
ACCESSION  AR203918
VERSION    AR203918.1 GI:21500430
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS    Schellenberger,V., Liu,A.D. and Selifonova,O.V.
TITLE      Directed evolution of microorganisms
JOURNAL    Patent: US 6365410-A 8 02-APR-2002;
           Location/Qualifiers
FEATURES   Location/Qualifiers
            source
              1..11
              /organism="unknown"
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Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
   |||||
Db 1 GTGCCGCTGTG 11

RESULT 63
AX471274/c
LOCUS      AX471274      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 851 from Patent WO02053773.
ACCESSION  AX471274
VERSION    AX471274.1 GI:22206399
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
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AR487539
LOCUS      AR487539      11 bp      DNA      linear      PAT 14-MAY-2004
DEFINITION Sequence 10 from patent US 6706503.
ACCESSION  AR487539
VERSION    AR487539.1 GI:47252783
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 11)
AUTHORS    Schellenberger,V., Liu,A.D. and Selifonova,O.V.
TITLE      Directed evolution of microorganisms
JOURNAL    Patent: US 6706503-A 10 16-MAR-2004;
           Genencor International, Inc.; Palo Alto, CA
FEATURES   Location/Qualifiers
            source
              1..11
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Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
   |||||
Db 1 GTGCCGCTGTG 11

RESULT 64
AX049397
LOCUS      AX049397      11 bp      DNA      linear      PAT 12-JAN-2001
DEFINITION Sequence 8 from Patent WO0070037.
ACCESSION  AX049397
VERSION    AX049397.1 GI:12226137
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Schellenberger,V., Liu,A.D. and Selifonova,O.V.
TITLE      Directed evolution of microorganisms
JOURNAL    Patent: WO 0070037-A 8 23-NOV-2000;
           GENENCOR INTERNATIONAL, INC. (US)
FEATURES   Location/Qualifiers
            source
              1..11
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="pos102 mutD mutated gene"

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
   |||||
Db 1 GTGCCGCTGTG 11

RESULT 65
AX471274/c
LOCUS      AX471274      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION Sequence 851 from Patent WO02053773.
ACCESSION  AX471274
VERSION    AX471274.1 GI:22206399
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Hofmann,K., Conradt,M. and Petersohn,D.
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TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 851 11-JUL-2002;  
HENKEL KGAA (DE)

FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14  
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Db 11 CTCGCTGGGC 1

RESULT 66  
AX471408/c  
LOCUS AX471408 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 985 from Patent WO02053773.  
ACCESSION AX471408  
VERSION AX471408.1 GI:22206533  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1

REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 985 11-JUL-2002;  
HENKEL KGAA (DE)

FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 18  
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Db 11 CTGGGGCTAAG 1

RESULT 67  
AX471445  
LOCUS AX471445 11 bp DNA linear PAT 09-AUG-2002  
DEFINITION Sequence 1022 from Patent WO02053773.  
ACCESSION AX471445  
VERSION AX471445.1 GI:22206570  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1

REFERENCE 1  
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.  
TITLE Method for determining skin stress or skin ageing in vitro  
JOURNAL Patent: WO 02053773-A 1022 11-JUL-2002;  
HENKEL KGAA (DE)

FEATURES  
source Location/Qualifiers  
1. .11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 18  
| | | | | | | |  
Db 1 CTGGGGCGAAG 11

RESULT 68  
AX622989  
LOCUS AX622989 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 30 from Patent WO02053774.  
ACCESSION AX622989  
VERSION AX622989.1 GI:28450930  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 30 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source Location/Qualifiers  
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Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14  
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Db 1 CACGCAGTGGC 11

RESULT 69  
AX624192/c  
LOCUS AX624192 11 bp DNA linear PAT 21-FEB-2003  
DEFINITION Sequence 1233 from Patent WO02053774.  
ACCESSION AX624192  
VERSION AX624192.1 GI:28452133  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1

REFERENCE 1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 1233 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES  
source Location/Qualifiers  
1. .11  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 51;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 18  
| | | | | | | |  
Db 11 CTGGGGCTAAG 1

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RESULT 70
AX626026
LOCUS      AX626026               11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 3067 from Patent WO02053774.
ACCESSION  AX626026
VERSION     AX626026.1  GI:28454064
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3067 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 51;
Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      8 CTGTGGCGGAAG 18
        |||||
Db      1 CTGGGGGGAAG 11

RESULT 71
AX627479
LOCUS      AX627479               11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 4520 from Patent WO02053774.
ACCESSION  AX627479
VERSION     AX627479.1  GI:28455517
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4520 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 51;
Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      8 CTGTGGCGGAAG 18
        |||||
Db      1 CTGGGGGGAAG 11

RESULT 72
AX628487/c
LOCUS      AX628487               11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 5528 from Patent WO02053774.
ACCESSION  AX628487
VERSION     AX628487.1  GI:28456525
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5528 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 51;
Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      8 CTGTGGCGGAAG 18
        |||||
Db      1 CTGTGTCCAAG 11

RESULT 73
AX629205/c
LOCUS      AX629205               11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 6246 from Patent WO02053774.
ACCESSION  AX629205
VERSION     AX629205.1  GI:28457243
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 6246 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 51;
Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      4 CGCGCTGTGGC 14
        |||||
Db      11 CTCGCTGGGC 1

RESULT 74
AX630410
LOCUS      AX630410               11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 7451 from Patent WO02053774.
ACCESSION  AX630410
VERSION     AX630410.1  GI:28458448
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7451 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5528 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 51;
Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      4 CGCGCTGTGGC 14
        |||||
Db      11 CTCGCTGGGC 1

RESULT 73
AX629205/c
LOCUS      AX629205               11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 6246 from Patent WO02053774.
ACCESSION  AX629205
VERSION     AX629205.1  GI:28457243
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 6246 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source          1..11
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

Query Match      41.1%;  Score 7.8;  DB 1;  Length 11;
Best Local Similarity 81.8%;  Pred. No. 51;
Matches 9;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      1 GGTCGCGCTGT 11
        |||||
Db      11 GGTCACCCCTGT 1

RESULT 74
AX630410
LOCUS      AX630410               11 bp      DNA          linear      PAT 21-FEB-2003
DEFINITION Sequence 7451 from Patent WO02053774.
ACCESSION  AX630410
VERSION     AX630410.1  GI:28458448
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7451 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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source      1. .11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
    |||||
Db 1 CACGCAGTGGC 11

RESULT 75
AX631613/c
LOCUS AX631613 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8655 from Patent WO02053774.
ACCESSION AX631613
VERSION AX631613.1 GI:28459689
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8655 11-JUL-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAG 18
    |||||
Db 11 CTGGGGCTAAG 1

RESULT 76
AX632853/c
LOCUS AX632853 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9895 from Patent WO02053774.
ACCESSION AX632853
VERSION AX632853.1 GI:28468468
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9895 11-JUL-2002;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 9 TGTGGCCAAGG 19
    |||||
Db 11 TGTGGCCAAGG 1

RESULT 77
AR098894/c
LOCUS AR098894 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6077685.
ACCESSION AR098894
VERSION AR098894.1 GI:12808660
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 30 20-JUN-2000;
FEATURES Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16
    |||||
Db 10 CTGTGGCGA 2

RESULT 78
AR098900/c
LOCUS AR098900 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 36 from patent US 6077685.
ACCESSION AR098900
VERSION AR098900.1 GI:12808666
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 36 20-JUN-2000;
FEATURES Location/Qualifiers
1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16
    |||||
Db 10 CTGTGGCGA 2

RESULT 79
AR167218
LOCUS AR167218 10 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 52 from patent US 6284466.
ACCESSION AR167218
VERSION AR167218.1 GI:16243729
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Benson,A.
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TITLE Method of detecting genetic polymorphisms using over represented sequences  
JOURNAL Patent: US 6284466-A 52 04-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17  
| | | | | | | |  
Db 2 TCTGGCGAA 10

RESULT 80  
BD083089  
LOCUS BD083089 10 bp DNA linear PAT 27-AUG-2002  
DEFINITION Human matured/activated dendritic cell expression genes.  
ACCESSION BD083089  
VERSION BD083089.1 GI:22628699  
KEYWORDS JP 2001327293-A/10.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
1 (bases 1 to 10)  
Matsushima,K., Hashimoto,S., Suzuki,T. and Nagai,S.  
Human matured/activated dendritic cell expression genes  
Patent: JP 2001327293-A 10 27-NOV-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
OS Homo sapiens (human)  
PN JP 2001327293-A/10  
PD 27-NOV-2001  
PF 22-MAY-2000 JP 2000150562  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI  
NAGAI  
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00  
CC  
FH Key Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
| | | | | | | | | |  
Db 2 TGGTGAAGG 10

RESULT 81  
BD166770  
LOCUS BD166770 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD166770  
VERSION BD166770.1 GI:27872582  
KEYWORDS JP 2002209591-A/315.  
SOURCE unidentified  
ORGANISM unidentified  
1 (bases 1 to 10)  
Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
Human liver disease-expressing genes  
Patent: JP 2002209591-A 315 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT OS Homo sapiens (human)  
PN JP 2002209591-A/315  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI  
YAMASHITA  
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,  
C12P21/08,  
PC C12N15/00  
CC Human liver disease-expressing genes  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
| | | | | | | |  
Db 2 GGACGCGCT 10

RESULT 82  
BD166788  
LOCUS BD166788 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD166788  
VERSION BD166788.1 GI:27872600  
KEYWORDS JP 2002209591-A/333.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
1 (bases 1 to 10)  
Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
Human liver disease-expressing genes  
Patent: JP 2002209591-A 333 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
OS Homo sapiens (human)  
PN JP 2002209591-A/333  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI  
YAMASHITA  
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,  
C12P21/08,  
PC C12N15/00  
CC Human liver disease-expressing genes  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
| | | | | | | |  
Db 2 GGACGCGCT 10

RESULT 83  
BD166960

LOCUS BD166960 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD166960  
VERSION BD166960.1 GI:27872772  
KEYWORDS JP 2002209591-A/505.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
TITLE Human liver disease-expressing genes  
JOURNAL Patent: JP 2002209591-A 505 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002209591-A/505  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI  
YAMASHITA  
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,  
PC C12P21/08,  
PC C12N15/00  
CC Human liver disease-expressing genes  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCT 9  
||| |||||  
Db 2 GGACGCGCT 10  
RESULT 84  
LOCUS BD166975 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD166975  
VERSION BD166975.1 GI:27872787  
KEYWORDS JP 2002209591-A/520.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
TITLE Human liver disease-expressing genes  
JOURNAL Patent: JP 2002209591-A 520 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002209591-A/520  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI  
YAMASHITA  
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,  
PC C12P21/08,  
PC C12N15/00  
CC Human liver disease-expressing genes  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
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/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCT 9  
||| |||||  
Db 2 GGACGCGCT 10  
RESULT 84  
LOCUS BD166975 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD166975  
VERSION BD166975.1 GI:27872787  
KEYWORDS JP 2002209591-A/520.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
TITLE Human liver disease-expressing genes  
JOURNAL Patent: JP 2002209591-A 520 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002209591-A/520  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI  
YAMASHITA  
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,  
PC C12P21/08,  
PC C12N15/00  
CC Human liver disease-expressing genes  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unidentified"  
/mol\_type="genomic DNA"

/db\_xref="taxon:32644"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCT 9  
||| |||||  
Db 2 GGACGCGCT 10  
RESULT 85  
LOCUS BD167006 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD167006  
VERSION BD167006.1 GI:27872818  
KEYWORDS JP 2002209591-A/551.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
TITLE Human liver disease-expressing genes  
JOURNAL Patent: JP 2002209591-A 551 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002209591-A/551  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328  
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI  
YAMASHITA  
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,  
PC C12P21/08,  
PC C12N15/00  
CC Human liver disease-expressing genes  
FH Key Location/Qualifiers  
FT source 1..10  
FT /organism='Homo sapiens (human)'.  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unidentified"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCT 9  
||| |||||  
Db 2 GGACGCGCT 10  
RESULT 86  
LOCUS BD167029 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human liver disease-expressing genes.  
ACCESSION BD167029  
VERSION BD167029.1 GI:27872841  
KEYWORDS JP 2002209591-A/574.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.  
TITLE Human liver disease-expressing genes  
JOURNAL Patent: JP 2002209591-A 574 30-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002209591-A/574  
PD 30-JUL-2002  
PF 19-JAN-2001 JP 2001012328





Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
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Db 2 GGACGCGCT 10

RESULT 90  
BD167232

LOCUS BD167232 10 bp DNA linear PAT 17-JAN-2003

DEFINITION Human liver disease-expressing genes.

ACCESSION BD167232

VERSION BD167232.1 GI:27873044

KEYWORDS JP 2002209591-A/777.

SOURCE unidentified

ORGANISM unidentified

REFERENCE unclassified.

AUTHORS 1 (bases 1 to 10)

TITLE Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.

JOURNAL Human liver disease-expressing genes

Patent: JP 2002209591-A 777 30-JUL-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

COMMENT OS Homo sapiens (human)

PN JP 2002209591-A/777

PD 30-JUL-2002

PF 19-JAN-2001 JP 2001012328

PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI YAMASHITA

PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,

PC C12P21/08,

PC C12N15/00

CC Human liver disease-expressing genes

FH Key Location/Qualifiers

FT source 1..10

FT /organism='Homo sapiens (human)'.  
Location/Qualifiers  
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source

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
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Db 2 TGGTGAAGG 10

RESULT 91  
BD239791/c

LOCUS BD239791 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD239791

VERSION BD239791.1 GI:33049561

KEYWORDS JP 2002534056-A/1209.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1 (bases 1 to 10)

AUTHORS Roberts,B.L. and Shankara,S.

TITLE Preparation and use of superior vaccines

JOURNAL Patent: JP 2002534056-A 1209 15-OCT-2002;

GENZYME CORP

COMMENT OS Homo sapiens (human)

PN JP 2002534056-A/1209

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR

19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR

19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC G01N37/00,

PC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FH Key Location/Qualifiers

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Location/Qualifiers  
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Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
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Db 10 TGGAGAAGG 2

RESULT 92  
BD240084/c

LOCUS BD240084 10 bp DNA linear PAT 17-JUL-2003

DEFINITION Preparation and use of superior vaccines.

ACCESSION BD240084

VERSION BD240084.1 GI:33049854

KEYWORDS JP 2002534056-A/1502.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1 (bases 1 to 10)

AUTHORS Roberts,B.L. and Shankara,S.

TITLE Preparation and use of superior vaccines

JOURNAL Patent: JP 2002534056-A 1502 15-OCT-2002;

GENZYME CORP

COMMENT OS Homo sapiens (human)

PN JP 2002534056-A/1502

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR

19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR

19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

08-DEC-1998 US 60/1111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,  
PC C12N15/00,C12N5/00,C12N15/00  
CC Preparation and use of superior vaccines  
FH Key Location/Qualifiers  
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FT Location/Qualifiers  
/organism='Homo sapiens (human)'.  
1..10

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source

/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15  
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Db 10 GCTGTGGGG 2

RESULT 93  
BD240490

LOCUS BD240490 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD240490  
VERSION BD240490.1 GI:33050260  
KEYWORDS JP 2002534056-A/1908.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1 (bases 1 to 10)

ROBERTS,B.L. and Shankara,S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 1908 15-OCT-2002;

GENZYME CORP

OS Homo sapiens (human)

PN JP 2002534056-A/1908

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR

19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR

19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,

PC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FH Key Location/Qualifiers

FT source 1..10

FT Location/Qualifiers  
/organism='Homo sapiens (human)'.  
1..10

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source

1..10

/organism="Homo sapiens"  
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Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15  
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Db 2 GCTGTGGGG 10

RESULT 94  
BD240685

LOCUS BD240685 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD240685

VERSION BD240685.1 GI:33050455

KEYWORDS JP 2002534056-A/2103.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 10)

ROBERTS,B.L. and Shankara,S.

Preparation and use of superior vaccines

Patent: JP 2002534056-A 2103 15-OCT-2002;

GENZYME CORP

OS Homo sapiens (human)

PN JP 2002534056-A/2103

PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749

PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR

19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR

19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR

19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR

19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR

19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR

19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR

19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR

19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR

19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR

19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

08-DEC-1998 US 60/111715

PI BRUCE L ROBERTS,SRINIVAS SHANKARA

PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,

PC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FH Key Location/Qualifiers

FT source 1..10

FT Location/Qualifiers  
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1..10

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source

/organism="Homo sapiens"

/mol\_type="genomic DNA"

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Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13  
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Db 2 GGGCTGTGG 10

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RESULT 95
CQ889057
LOCUS      CQ889057              10 bp      DNA      linear      PAT 19-OCT-2004
DEFINITION Sequence 3 from Patent WO2004062555.
ACCESSION  CQ889057
VERSION    CQ889057.1  GI:54304970
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Rappold-Hoerbrand,G. and Haecker,B.
TITLE      Use of natriuretic peptides for the treatment of stature disorders
            related to the shox gene
JOURNAL    Patent: WO 2004062555-A 3 29-JUL-2004;
            Rappold-Hoerbrand, Gudrun (DE)
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            Best Local Similarity 88.9%;  Pred. No. 57;
            Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      11  TGGCGAAGG 19
        ||| |||||
Db      1  TGGGGAAGG 9

RESULT 96
E39471
LOCUS      E39471              10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39471
VERSION    E39471.1  GI:18621562
KEYWORDS   JP 2000279181-A/4.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1  (bases 1 to 10)
AUTHORS    Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE      Genes with human dendritic cell expression
JOURNAL    Patent: JP 2000279181-A 4 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT    OS  Homo sapiens (human)
            PN  JP 2000279181-A/4
            PD  10-OCT-2000
            PF  01-APR-1999  JP 1999095481
            PR
            PI  SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC

FEATURES   Location/Qualifiers
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            Query Match      38.9%;  Score 7.4;  DB 1;  Length 10;
            Best Local Similarity 88.9%;  Pred. No. 57;
            Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      11  TGGCGAAGG 19
        ||| |||||
Db      1  TGGGGAAGG 9

RESULT 97
E39633/c
LOCUS      E39633              10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39633
VERSION    E39633.1  GI:18621724
KEYWORDS   JP 2000279181-A/166.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1  (bases 1 to 10)
AUTHORS    Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE      Genes with human dendritic cell expression
JOURNAL    Patent: JP 2000279181-A 166 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT    OS  Homo sapiens (human)
            PN  JP 2000279181-A/166
            PD  10-OCT-2000
            PF  01-APR-1999  JP 1999095481
            PR
            PI  SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC

FEATURES   Location/Qualifiers
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            Query Match      38.9%;  Score 7.4;  DB 1;  Length 10;
            Best Local Similarity 88.9%;  Pred. No. 57;
            Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      11  TGGCGAAGG 19
        ||| |||||
Db      10  TGGAGAAGG 2

RESULT 98
E39676
LOCUS      E39676              10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Genes with human dendritic cell expression.
ACCESSION  E39676
VERSION    E39676.1  GI:18621767
KEYWORDS   JP 2000279181-A/209.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1  (bases 1 to 10)
AUTHORS    Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE      Genes with human dendritic cell expression
JOURNAL    Patent: JP 2000279181-A 209 10-OCT-2000;
            SCIENCE & TECH AGENCY
COMMENT    OS  Homo sapiens (human)
            PN  JP 2000279181-A/209
            PD  10-OCT-2000
            PF  01-APR-1999  JP 1999095481
            PR
            PI  SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC

FEATURES   Location/Qualifiers
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            Query Match      38.9%;  Score 7.4;  DB 1;  Length 10;
            Best Local Similarity 88.9%;  Pred. No. 57;
            Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      11  TGGCGAAGG 19
        ||| |||||
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Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGCA 16  
Db 10 CTGTGGCGCA 2

RESULT 103  
AR261814/c  
LOCUS AR261814 10 bp DNA linear PAT 29-JAN-2003  
DEFINITION Sequence 240 from patent US 6322995.  
ACCESSION AR261814  
VERSION AR261814.1 GI:28072954  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hohmann,H.-P., Humbelin,M., van Loon,A. and Schurter,W.  
TITLE Riboflavin production  
JOURNAL Patent: US 6322995-A 240 27-NOV-2001;  
F. Hoffmann-La Roche AG; Basel;  
EPX;

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source Location/Qualifiers  
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Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGCGCTGTG 12  
Db 9 CGCGCTGGG 1

RESULT 104  
AR477257/c  
LOCUS AR477257 10 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 9 from patent US 6696274.  
ACCESSION AR477257  
VERSION AR477257.1 GI:47234570  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.  
TITLE Ligand for enhancing oral and CNS delivery of biological agents  
JOURNAL Patent: US 6696274-A 9 24-FEB-2004;  
Supratek Pharma, Inc.;;  
WOX;

FEATURES  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGGCGCT 9  
Db 10 GGTGGCGCT 2

RESULT 105  
AR533687/c  
LOCUS AR533687 10 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 12 from patent US 6733755.  
ACCESSION AR533687

VERSION AR533687.1 GI:53923681  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.  
TITLE Ligand for vascular endothelial growth factor receptor  
JOURNAL Patent: US 6733755-A 12 11-MAY-2004;  
Supratek Pharma, Inc.;;  
WOX;

FEATURES  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGGCGCT 9  
Db 10 GGTGGCGCT 2

RESULT 106  
AR630145  
LOCUS AR630145 10 bp DNA linear PAT 14-FEB-2005  
DEFINITION Sequence 199 from patent US 6838556.  
ACCESSION AR630145  
VERSION AR630145.1 GI:59762469  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,  
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,  
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.  
TITLE Promoters for regulated gene expression  
JOURNAL Patent: US 6838556-A 199 04-JAN-2005;  
Genelabs Technologies, Inc.; Redwood City, CA

FEATURES  
source Location/Qualifiers  
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Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCGCGCTG 10  
Db 1 GGCGCGCTG 9

RESULT 107  
AR642556/c  
LOCUS AR642556 10 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 29 from patent US 6864052.  
ACCESSION AR642556  
VERSION AR642556.1 GI:62779710  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.  
TITLE Enhanced sequencing by hybridization using pools of probes  
JOURNAL Patent: US 6864052-A 29 08-MAR-2005;  
Callida Genomics, Inc.; Sunnyvale, CA

FEATURES  
source Location/Qualifiers  
1..10

/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16  
| | | | | | | |  
Db 10 CTGTGGCAA 2

RESULT 108  
AR642557/c

LOCUS AR642557 10 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 30 from patent US 6864052.  
ACCESSION AR642557  
VERSION AR642557.1 GI:62779711  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.  
TITLE Enhanced sequencing by hybridization using pools of probes  
JOURNAL Patent: US 6864052-A 30 08-MAR-2005;  
Callida Genomics, Inc.; Sunnyvale, CA

FEATURES  
source  
1. .10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16  
| | | | | | | |  
Db 9 CTGTGGCAA 1

RESULT 109  
AR649447/c

LOCUS AR649447 10 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 92 from patent US 6875606.  
ACCESSION AR649447  
VERSION AR649447.1 GI:62790108  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 10)  
AUTHORS Leonard,S. and Freedman,R.  
TITLE Human .alpha.-7 nicotinic receptor promoter  
JOURNAL Patent: US 6875606-A 92 05-APR-2005;  
The United States of America as represented by the Department of  
Veterans Affairs; Washington, DC

FEATURES  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16  
| | | | | | | |  
Db 10 CTGTGGAGA 2

RESULT 110  
AX113023

LOCUS AX113023 10 bp DNA linear PAT 01-MAY-2001  
DEFINITION Sequence 70 from Patent WO0127267.  
ACCESSION AX113023  
VERSION AX113023.1 GI:13939458  
KEYWORDS  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.  
TITLE Genes differentially expressed in trl cells and their use in the  
manufacture of immunoregulatory compositions  
JOURNAL Patent: WO 0127267-A 70 19-APR-2001;  
ISIS INNOVATION LIMITED (GB)

FEATURES  
source  
1. .10  
Location/Qualifiers  
/organism="Mus sp."  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10095"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
| | | | | | | |  
Db 2 TGGTGAAGG 10

RESULT 111  
AX152364 10 bp DNA linear PAT 22-JUN-2001

LOCUS AX152364 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 279 from Patent WO0138577.  
ACCESSION AX152364  
VERSION AX152364.1 GI:14534015  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE 1  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 279 31-MAY-2001;  
The Johns Hopkins University (US)

FEATURES  
source  
1. .10  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13  
| | | | | | | |  
Db 2 GGGCTGTGG 10

RESULT 112  
AX152365 10 bp DNA linear PAT 22-JUN-2001

LOCUS AX152365 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 280 from Patent WO0138577.  
ACCESSION AX152365  
VERSION AX152365.1 GI:14534016  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 280 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GCGCTGTGG 13
      | | | | | | | |
Db      2 GGGCTGTGG 10

RESULT 113
AX152532/c
LOCUS      AX152532      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 447 from Patent WO0138577.
ACCESSION  AX152532
VERSION     AX152532.1 GI:14534183
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 447 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGC 14
      | | | | | | | |
Db      9 CGCTGGGGC 1

RESULT 114
AX152671/c
LOCUS      AX152671      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 586 from Patent WO0138577.
ACCESSION  AX152671
VERSION     AX152671.1 GI:14534322
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 586 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGC 14
      | | | | | | | |
Db      9 CGCTGGGGC 1

RESULT 115
AX152819/c
LOCUS      AX152819      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 734 from Patent WO0138577.
ACCESSION  AX152819
VERSION     AX152819.1 GI:14534470
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 734 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGC 14
      | | | | | | | |
Db      10 CGCAGTGGC 2

RESULT 116
AX153110
LOCUS      AX153110      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1025 from Patent WO0138577.
ACCESSION  AX153110
VERSION     AX153110.1 GI:14534761
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1025 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 TGGCGAAGG 19
      | | | | | | | |
Db      10 TGGAGAAGG 2

RESULT 117
AX153110
LOCUS      AX153110      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1025 from Patent WO0138577.
ACCESSION  AX153110
VERSION     AX153110.1 GI:14534761
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1025 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCG 15
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Db      7 GCTGTGGCG 15
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGC 14
      | | | | | | | |
Db      10 CGCAGTGGC 2

RESULT 115
AX152819/c
LOCUS      AX152819      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 734 from Patent WO0138577.
ACCESSION  AX152819
VERSION     AX152819.1 GI:14534470
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 734 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 TGGCGAAGG 19
      | | | | | | | |
Db      10 TGGAGAAGG 2

RESULT 116
AX153110
LOCUS      AX153110      10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 1025 from Patent WO0138577.
ACCESSION  AX153110
VERSION     AX153110.1 GI:14534761
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE    1
AUTHORS      Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE        Human transcriptomes
JOURNAL      Patent: WO 0138577-A 1025 31-MAY-2001;
              The Johns Hopkins University (US)
FEATURES
  source      Location/Qualifiers
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCG 15
      | | | | | | | |
Db      7 GCTGTGGCG 15
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Db 1 GCTGTTGCG 9  
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RESULT 117  
AX153149  
LOCUS AX153149 10 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 1064 from Patent WO0138577.  
ACCESSION AX153149  
VERSION AX153149.1 GI:14534800  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Human transcriptomes  
JOURNAL Patent: WO 0138577-A 1064 31-MAY-2001;  
The Johns Hopkins University (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 11 TGGCGAAGG 19  
|||||  
Db 2 TGGTGAAGG 10  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 11 TGGCGAAGG 19  
|||||  
Db 2 TGGTGAAGG 10  
RESULT 118  
AX207895/c  
LOCUS AX207895 10 bp DNA linear PAT 31-AUG-2001  
DEFINITION Sequence 12 from Patent WO0157067.  
ACCESSION AX207895  
VERSION AX207895.1 GI:15422493  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.  
TITLE Ligand for vascular endothelial growth factor receptor  
JOURNAL Patent: WO 0157067-A 12 09-AUG-2001;  
SUPRATEK PHARMA INC. (CA)  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="chemical synthesis"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCT 9  
|||||  
Db 10 GGTGGCGCT 2  
RESULT 119  
AX301491/c  
LOCUS AX301491 10 bp DNA linear PAT 30-NOV-2001  
DEFINITION Sequence 205 from Patent WO0185941.  
ACCESSION AX301491  
VERSION AX301491.1 GI:17382574

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Versteeg,R. and Caron,H.N.  
TITLE Myc targets  
JOURNAL Patent: WO 0185941-A 205 15-NOV-2001;  
Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCT 9  
|||||  
Db 10 GGTCCCGCT 2  
RESULT 120  
AX328381/c  
LOCUS AX328381 10 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 9 from Patent WO0190139.  
ACCESSION AX328381  
VERSION AX328381.1 GI:18098355  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Tchistiakova,L., Li,S., Pietrzynski,G. and Alakhov,V.  
TITLE A ligand for enhancing oral and cns delivery of biological agents  
JOURNAL Patent: WO 0190139-A 9 29-NOV-2001;  
SUPRATEK PHARMA, INC. (CA)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="nucleotide"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCT 9  
|||||  
Db 10 GGTGGCGCT 2  
RESULT 121  
AX354798/c  
LOCUS AX354798 10 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 1 from Patent WO0186293.  
ACCESSION AX354798  
VERSION AX354798.1 GI:18619529  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Popkov,M., Mandeville,R., Romar,O. and Alakhov,V.  
TITLE Designing and screening random libraries of compounds  
JOURNAL Patent: WO 0186293-A 1 15-NOV-2001;  
SUPRATEK PHARMA, INC. (CA)  
FEATURES  
source Location/Qualifiers

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source      1. .10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="nucleotides isolated by chemical synthesis and
biosynthesis using E. coli"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCGGCGCT 9
      ||| |||||
Db      10 GGTGGCGCT 2

RESULT 122
AX958217/c
LOCUS      AX958217      10 bp      DNA      linear      PAT 08-JAN-2004
DEFINITION      Sequence 20 from Patent WO03046156.
ACCESSION      AX958217
VERSION      AX958217.1 GI:40785870
KEYWORDS      .
SOURCE      unidentified
ORGANISM      unidentified
unclassified sequences.
REFERENCE      1
AUTHORS      Claude,P.P.
TITLE      Novel bacterial biomasses, method for obtaining same and uses
thereof for bacterization of soils and crop residues
JOURNAL      Patent: WO 03046156-A 20 05-JUN-2003;
Valbios (FR)

FEATURES
source      Location/Qualifiers
      1. .10
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Azobacter"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CGCGCTGTG 12
      ||||| |
Db      10 CGCGCTGGG 2

RESULT 123
BD007752
LOCUS      BD007752      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      LPS activated human monocyte expressing genes.
ACCESSION      BD007752
VERSION      BD007752.1 GI:18636125
KEYWORDS      JP 2001069993-A/28.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 28 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/28
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,

REFERENCE      1
AUTHORS      Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE      LPS activated human monocyte expressing genes
JOURNAL      Patent: JP 2001069993-A 28 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
KEYWORDS      JP 2001069993-A/28.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 119 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/119
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,

FEATURES
source      Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCG 15
      ||| |||||
Db      10 GCTTGGCG 2

RESULT 125
BD007925
LOCUS      BD007925      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      LPS activated human monocyte expressing genes.
ACCESSION      BD007925
VERSION      BD007925.1 GI:18636298
KEYWORDS      JP 2001069993-A/201.
SOURCE      Homo sapiens (human)
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PC      A61P31/00,C12P21/08,C12N15/00
CC
FH      Key      Location/Qualifiers
FT      source      1. .10
FT      Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source      Location/Qualifiers
      1. .10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 TGGCGAAGG 19
      ||| |||||
Db      2 TGGTGAAGG 10

RESULT 124
BD007843/c
LOCUS      BD007843      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      LPS activated human monocyte expressing genes.
ACCESSION      BD007843
VERSION      BD007843.1 GI:18636216
KEYWORDS      JP 2001069993-A/119.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S. and Suzuki,T.
LPS activated human monocyte expressing genes
Patent: JP 2001069993-A 119 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2001069993-A/119
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,

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source      Location/Qualifiers
      1. .10
/organism="Homo sapiens"
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Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 57;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCG 15
      ||| |||||
Db      10 GCTTGGCG 2

RESULT 125
BD007925
LOCUS      BD007925      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      LPS activated human monocyte expressing genes.
ACCESSION      BD007925
VERSION      BD007925.1 GI:18636298
KEYWORDS      JP 2001069993-A/201.
SOURCE      Homo sapiens (human)
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.  
TITLE LPS activated human monocyte expressing genes  
JOURNAL Patent: JP 2001069993-A 201 21-MAR-2001;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2001069993-A/201  
PD 21-MAR-2001  
PF 28-APR-2000 JP 2000131079  
PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC  
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC  
A61P29/00,  
PC A61P31/00,C12P21/08,C12N15/00  
CC  
FH Key Location/Qualifiers  
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FT /organism='Homo sapiens (human)'.  
FEATURES  
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/db\_xref="taxon:9606"  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 57;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GCTGTGGCG 15  
Db |||||  
1 GCTGTGGCG 9  
RESULT 126  
AR002177/c  
LOCUS Sequence 31 from patent US 5741490. linear PAT 04-DEC-1998  
DEFINITION AR002177  
ACCESSION AR002177  
VERSION AR002177.1 GI:3963731  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Reyes,G.R., Bradley,D.W., Twu,J.-S., Purdy,M.A., Tam,A.W.,  
Krawczynski,K.Z. and Yarbrough,P.D.  
TITLE Hepatitis E virus vaccine and method  
JOURNAL Patent: US 5741490-A 31 21-APR-1998;  
FEATURES Location/Qualifiers  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 TGGCGAA 17  
Db |||||  
7 TGGCGAA 1  
RESULT 127  
AR071782/c  
LOCUS AR071782 10 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 11 from patent US 5912147.  
ACCESSION AR071782  
VERSION AR071782.1 GI:7222670  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Stoler,D., Basik,M. and Anderson,G.  
TITLE Rapid means of quantitating genomic instability  
JOURNAL Patent: US 5912147-A 11 15-JUN-1999;  
FEATURES Location/Qualifiers  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GTCGCGC 8  
Db |||||  
10 GTCGCGC 4  
RESULT 128  
AR092694  
LOCUS AR092694 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 6 from patent US 5998193.  
ACCESSION AR092694  
VERSION AR092694.1 GI:10019446  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 5998193-A 6 07-DEC-1999;  
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Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CTGTGGC 14  
Db |||||  
4 CTGTGGC 10  
RESULT 129  
AR106678  
LOCUS AR106678 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 6 from patent US 6107078.  
ACCESSION AR106678  
VERSION AR106678.1 GI:12821208  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 6 22-AUG-2000;  
source Location/Qualifiers  
1..10  
/organism="unknown"  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14  
Db 4 CTGTGGC 10

RESULT 130  
AR107802  
LOCUS AR107802 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 48 from patent US 6110667.  
ACCESSION AR107802  
VERSION AR107802.1 GI:12823289  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.  
TITLE Processes, apparatus and compositions for characterizing nucleotide sequences based on K-tuple analysis  
JOURNAL Patent: US 6110667-A 48 29-AUG-2000;  
FEATURES Location/Qualifiers  
source 1. .10  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13  
Db 4 GCTGTGG 10

RESULT 131  
AR174035/c  
LOCUS AR174035 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 25 from patent US 6306624.  
ACCESSION AR174035  
VERSION AR174035.1 GI:17914355  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.  
TITLE Retinoid metabolizing protein  
JOURNAL Patent: US 6306624-A 25 23-OCT-2001;  
FEATURES Location/Qualifiers  
source 1. .10  
/organism="unknown"  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
Db 9 TGGCGAA 3

RESULT 132  
BD065207  
LOCUS BD065207 10 bp DNA linear PAT 27-AUG-2002  
DEFINITION Characterization of the yeast transcriptome.  
ACCESSION BD065207  
VERSION BD065207.1 GI:22610810  
KEYWORDS JP 2001509017-A/143.  
SOURCE Saccharomyces cerevisiae (baker's yeast)  
ORGANISM Saccharomyces cerevisiae  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
1 (bases 1 to 10)  
Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.  
TITLE Characterization of the yeast transcriptome  
JOURNAL Patent: JP 2001509017-A 143 10-JUL-2001;  
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
COMMENT OS Saccharomyces cerevisiae (yeast)  
PN JP 2001509017-A/143  
PD 10-JUL-2001  
PF 22-JAN-1998 JP 1998532117  
PR 23-JAN-1997 US 60/035917  
PI VICTOR E VELCULESCU,BERT VOGELSTEIN,KENNETH W KINZLER PC  
C12N15/10,C12N15/31,C07K14/395,C12Q1/68,C12Q1/02 CC  
Characterization of the yeast transcriptome  
FH Key Location/Qualifiers  
FT source 1. .10  
FT /organism='Saccharomyces cerevisiae (yeast)'.  
FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:4932"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12  
Db 4 CGCTGTG 10

RESULT 133  
BD161475/c  
LOCUS BD161475 10 bp DNA linear PAT 17-JAN-2003  
DEFINITION Human activated Th1 and Th2 cell expression genes.  
ACCESSION BD161475  
VERSION BD161475.1 GI:27867233  
KEYWORDS JP 2002186482-A/297.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.  
TITLE Human activated Th1 and Th2 cell expression genes  
JOURNAL Patent: JP 2002186482-A 297 02-JUL-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002186482-A/297  
PD 02-JUL-2002  
PF 19-DEC-2000 JP 2000385816  
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC  
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human  
activated Th1 and Th2 cell expression genes FH Key  
FEATURES Location/Qualifiers  
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FT /organism='Homo sapiens (human)'.  
FEATURES Location/Qualifiers  
source 1. .10  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13  
Db 7 GCTGTGG 1

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RESULT 134
BD166636/c
LOCUS      BD166636
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166636
VERSION    BD166636.1 GI:27872448
KEYWORDS   JP 2002209591-A/181.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 181 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002209591-A/181
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
CC C12N15/00
CC Human liver disease-expressing genes
FH Key
FT source
FT Location/Qualifiers
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            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCGCTGT 11
    |||||
Db 7 GCGCTGT 1

RESULT 135
BD167128/c
LOCUS      BD167128
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167128
VERSION    BD167128.1 GI:27872940
KEYWORDS   JP 2002209591-A/673.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 673 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002209591-A/673
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
CC C12N15/00
CC Human liver disease-expressing genes
FH Key
FT source
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCGCTGT 11
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Db 7 GCGCTGT 1

RESULT 137
BD167128/c
LOCUS      BD167128
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD167128
VERSION    BD167128.1 GI:27872940
KEYWORDS   JP 2002209591-A/673.
SOURCE     unidentified
ORGANISM   unidentified
            unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 673 30-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
            PN JP 2002209591-A/673
            PD 30-JUL-2002
            PF 19-JAN-2001 JP 2001012328
            PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
            YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
CC C12N15/00
CC Human liver disease-expressing genes
FH Key
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Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TGTGGCG 15
    |||||
Db 7 TGTGGCG 1

RESULT 136
BD225345/c
LOCUS      BD225345
DEFINITION Compositions and methods for the identification of lung tumor
            cells.
ACCESSION  BD225345
VERSION    BD225345.1 GI:33035115
KEYWORDS   JP 2002509707-A/27.
SOURCE     synthetic construct
ORGANISM   synthetic construct
            other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE      Compositions and methods for the identification of lung tumor cells
JOURNAL    Patent: JP 2002509707-A 27 02-APR-2002;
            GENZYME CORP
COMMENT    OS Artificial Sequence
            PN JP 2002509707-A/27
            PD 02-APR-2002
            PF 30-MAR-1999 JP 2000541180
            PR 31-MAR-1998 US 60/080037
            PI GARY A BEAUDRY,STEPHEN L MADDEN,ARTHUR H BERTELSEN PC
            C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
            G01N33/566//
            PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
            Compositions and methods for the identification of lung tumor
            cells
            FH Key
            FT source
            FT Location/Qualifiers
            1..10
            /organism="Artificial Sequence".

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGGC 14
    |||||
Db 9 CTGTGGC 3

RESULT 137
BD238881
LOCUS      BD238881
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD238881
VERSION    BD238881.1 GI:33048651
KEYWORDS   JP 2002534056-A/299.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
```



PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
G01N37/00,  
PC C12N15/00,C12N5/00,C12N15/00  
CC Preparation and use of superior vaccines  
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FT /organism='Homo sapiens (human)'.  
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GCTGTGG 13  
|||||  
Db 9 GCTGTGG 3  
RESULT 140  
BD240601  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD240601  
VERSION BD240601.1 GI:33050371  
KEYWORDS JP 2002534056-A/2019.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 2019 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/2019  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR  
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR  
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR  
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR  
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR  
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR  
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR  
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR  
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR  
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR  
08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
C12N1/19,  
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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PC C12N15/00,C12N5/00,C12N15/00  
CC Preparation and use of superior vaccines  
FH Key Location/Qualifiers  
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FT /organism='Homo sapiens (human)'.  
FEATURES  
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Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GCTGTGG 13  
|||||  
Db 1 GCTGTGG 7  
RESULT 141  
BD249594/C  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Pi-ta gene imparting disease resistance to plants.  
ACCESSION BD249594  
VERSION BD249594.1 GI:33059364  
KEYWORDS JP 2002525033-A/9.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Valent,B.S. and Bryan,G.T.  
TITLE Pi-ta gene imparting disease resistance to plants  
JOURNAL Patent: JP 2002525033-A 9 13-AUG-2002;  
EI DU PONT DE NEMOURS AND CO  
COMMENT OS Artificial Sequence  
PN JP 2002525033-A/9  
PD 13-AUG-2002  
PF 03-AUG-1999 JP 2000563786  
PR 04-AUG-1998 US 60/095229,21-JUN-1999 US 09/336946 PI  
BARBARA SUE VALENT,GREGORY T BRYAN  
PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC  
Description of Artificial Sequence:Synthetic oligonucleotide FH  
Key Location/Qualifiers  
FT source 1..10  
FT /organism='Artificial Sequence'.  
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1..10  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 GCGCTGT 11  
|||||  
Db 7 GCGCTGT 1  
RESULT 142  
BD251793  
LOCUS 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Endo-selection in orthogenesis.  
ACCESSION BD251793  
VERSION BD251793.1 GI:33061563  
KEYWORDS JP 2002537836-A/3.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Short,J.M. and Frey,G.J.  
TITLE Endo-selection in orthogenesis  
JOURNAL Patent: JP 2002537836-A 3 12-NOV-2002;  
DIVERSA CORP  
COMMENT OS Artificial Sequence  
PN JP 2002537836-A/3  
PD 12-NOV-2002  
PF 09-MAR-2000 JP 2000603365



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PR      09-MAR-1999 US      09/267118,26-MAR-1999 US      09/276860 PR
14-JUN-1999 US      09/332835
PI      JAY M SHORT,GERHARD JOHANN FREY
PC      C12N15/09,C12N9/96,C12N15/00
CC      BspG I restriction site
FH      Key      Location/Qualifiers
FT      source      1..10
FT      Location/Qualifiers
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          /organism='Artificial Sequence'.

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    /mol_type="genomic DNA"
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGCGCTG 10
      |||||||
Db      1 CGCGCTG 7

RESULT 143
E54722/c
LOCUS      E54722      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION      Human normal liver cell expression genes.
ACCESSION      E54722
VERSION      E54722.1 GI:22556205
KEYWORDS      JP 2001211883-A/74.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 10)
Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
Human normal liver cell expression genes
Patent: JP 2001211883-A 74 07-AUG-2001;
SCIENCE & TECH AGENCY
OS      Homo sapiens (human)
PN      JP 2001211883-A/74
PD      07-AUG-2001
PF      31-JAN-2000 JP 2000023170
PI      KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC      C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC

FH      Key      Location/Qualifiers.
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          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"

FEATURES
    source
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    /organism="Homo sapiens"
    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      9 TGTGGCG 15
      |||||||
Db      7 TGTGGCG 1

RESULT 144
E64716/c
LOCUS      E64716      10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION      Method for distinguishing rice variety.
ACCESSION      E64716
VERSION      E64716.1 GI:18623011
KEYWORDS      JP 2000287691-A/2.
SOURCE      unidentified
ORGANISM      unidentified
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unclassified.
1 (bases 1 to 10)
Otsubo,K., Nakamura,S., Teshima,H., Okatome,H. and Kawasaki,S.
Method for distinguishing rice variety
Patent: JP 2000287691-A 2 17-OCT-2000;
NATL FOOD RES INST,KENICHI OTSUBO,HIDECHIKA TESHIMA,HIROSHI OKATOME
OS      Oryza sativa L. (rice)
PN      JP 2000287691-A/2
PD      17-OCT-2000
PF      09-APR-1999 JP 1999102709
PR
PI      KENICHI OTSUBO,SUMIKO NAKAMURA,HIDECHIKA TESHIMA, PI HIROSHI
OKATOME,
PI      SHINJI KAWASAKI
PC      C12N15/09,C12Q1/68,G01N33/10,C12N15/00
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    /mol_type="genomic DNA"
    /db_xref="taxon:32644"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GCTGTGG 13
      |||||||
Db      7 GCTGTGG 1

RESULT 145
AR202187
LOCUS      AR202187      10 bp      DNA      linear      PAT 20-APR-2002
DEFINITION      Sequence 6 from patent US 6361974.
ACCESSION      AR202187
VERSION      AR202187.1 GI:20256726
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
1 (bases 1 to 10)
Short,J.M., Djavakhishvili,T.David. and Frey,G.Johann.
Exonuclease-mediated nucleic acid reassembly in directed evolution
Patent: US 6361974-A 6 26-MAR-2002;
JOURNAL
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGCGCTG 10
      |||||||
Db      1 CGCGCTG 7

RESULT 146
AR254267/c
LOCUS      AR254267      10 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION      Sequence 13 from patent US 6479731.
ACCESSION      AR254267
VERSION      AR254267.1 GI:27303040
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
Unclassified.
1 (bases 1 to 10)
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AUTHORS Valent,B.S. and Bryan,G.T.  
TITLE Pi-ta gene conferring fungal disease resistance to plants  
JOURNAL Patent: US 6479731-A 13 12-NOV-2002;  
E. I. du Pont de Nemours and Company; Wilmington, DE

FEATURES  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGT 11  
Db 7 GCGCTGT 1

RESULT 147  
AR303347/c  
LOCUS AR303347 10 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 72 from patent US 6544736.  
ACCESSION AR303347  
VERSION AR303347.1 GI:31692123  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.  
TITLE Method for synthesizing cDNA from mRNA sample  
JOURNAL Patent: US 6544736-A 72 08-APR-2003;  
Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

FEATURES  
source  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13  
Db 10 GCTGTGG 4

RESULT 148  
AR303679  
LOCUS AR303679 10 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 404 from patent US 6544736.  
ACCESSION AR303679  
VERSION AR303679.1 GI:31692455  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.  
TITLE Method for synthesizing cDNA from mRNA sample  
JOURNAL Patent: US 6544736-A 404 08-APR-2003;  
Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

FEATURES  
source  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12  
Db 4 CGCTGTG 10

RESULT 149  
AR306871/c  
LOCUS AR306871 10 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 23 from patent US 6551476.  
ACCESSION AR306871  
VERSION AR306871.1 GI:31697271  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Scherba,E.S.  
TITLE Noble-metal coated inert anode for aluminum production  
JOURNAL Patent: US 6551476-A 23 22-APR-2003;  
FEATURES Location/Qualifiers  
1. .10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13  
Db 7 GCTGTGG 1

RESULT 150  
AR351634  
LOCUS AR351634 10 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 92 from patent US 6588746.  
ACCESSION AR351634  
VERSION AR351634.1 GI:33753430  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Dobrindt,D. and Fischer,U.  
TITLE Device for generating an offset of transported flexible sheet material  
JOURNAL Patent: US 6588746-A 92 08-JUL-2003;  
NexPress Solutions LLC; Rochester, NY; DEX;

FEATURES  
source  
Location/Qualifiers  
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/organism="unknown"  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCGAAG 18  
Db 4 GGCGAAG 10

RESULT 151  
AR351635  
LOCUS AR351635 10 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 93 from patent US 6588746.  
ACCESSION AR351635

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VERSION      AR351635.1  GI:33753431
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Dobrindt,D. and Fischer,U.
TITLE        Device for generating an offset of transported flexible sheet
JOURNAL      Patent: US 6588746-A 93 08-JUL-2003;
              NexPress Solutions LLC; Rochester, NY;
              DEX;
FEATURES     Location/Qualifiers
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGCGAAG 18
        |||||||
Db      4 GGCGAAG 10

RESULT 152
AR351736
LOCUS      AR351736          10 bp      DNA          linear          PAT 17-AUG-2003
DEFINITION Sequence 1278 from patent US 6588746.
ACCESSION AR351736
VERSION   AR351736.1  GI:33753532
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS   Dobrindt,D. and Fischer,U.
TITLE     Device for generating an offset of transported flexible sheet
JOURNAL   Patent: US 6588746-A 1278 08-JUL-2003;
          NexPress Solutions LLC; Rochester, NY;
          DEX;
FEATURES  Location/Qualifiers
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
        |||||||
Db      4 GCTGTGG 10

RESULT 153
AR351844
LOCUS      AR351844          10 bp      DNA          linear          PAT 17-AUG-2003
DEFINITION Sequence 1653 from patent US 6588746.
ACCESSION AR351844
VERSION   AR351844.1  GI:33753640
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS   Dobrindt,D. and Fischer,U.
TITLE     Device for generating an offset of transported flexible sheet
JOURNAL   Patent: US 6588746-A 1653 08-JUL-2003;
          NexPress Solutions LLC; Rochester, NY;
          DEX;
FEATURES  Location/Qualifiers
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          /mol_type="genomic DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
        |||||||
Db      4 GCTGTGG 10

RESULT 154
AR351845
LOCUS      AR351845          10 bp      DNA          linear          PAT 17-AUG-2003
DEFINITION Sequence 1654 from patent US 6588746.
ACCESSION AR351845
VERSION   AR351845.1  GI:33753641
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS   Dobrindt,D. and Fischer,U.
TITLE     Device for generating an offset of transported flexible sheet
JOURNAL   Patent: US 6588746-A 1654 08-JUL-2003;
          NexPress Solutions LLC; Rochester, NY;
          DEX;
FEATURES  Location/Qualifiers
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
        |||||||
Db      3 GGTCGCG 9

RESULT 155
AR351858
LOCUS      AR351858          10 bp      DNA          linear          PAT 17-AUG-2003
DEFINITION Sequence 1667 from patent US 6588746.
ACCESSION AR351858
VERSION   AR351858.1  GI:33753654
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS   Dobrindt,D. and Fischer,U.
TITLE     Device for generating an offset of transported flexible sheet
JOURNAL   Patent: US 6588746-A 1667 08-JUL-2003;
          NexPress Solutions LLC; Rochester, NY;
          DEX;
FEATURES  Location/Qualifiers
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
        |||||||
Db      3 GGTCGCG 9

RESULT 156
AR351859
LOCUS      AR351859          10 bp      DNA          linear          PAT 17-AUG-2003
DEFINITION Sequence 1668 from patent US 6588746.
ACCESSION AR351859
VERSION   AR351859.1  GI:33753655
KEYWORDS  .
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS   Dobrindt,D. and Fischer,U.
TITLE     Device for generating an offset of transported flexible sheet
JOURNAL   Patent: US 6588746-A 1668 08-JUL-2003;
          NexPress Solutions LLC; Rochester, NY;
          DEX;
FEATURES  Location/Qualifiers
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          /mol_type="genomic DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
        |||||||
Db      3 GGTCGCG 9
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Db 3 GGTGCG 9  
|||||  
RESULT 156  
AR410161  
LOCUS AR410161 10 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 6 from patent US 6635449.  
ACCESSION AR410161  
VERSION AR410161.1 GI:40161386  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Short,J.M.  
TITLE Exonuclease-mediated nucleic acid reassembly in directed evolution  
JOURNAL Patent: US 6635449-A 6 21-OCT-2003;  
Diversa Corporation; San Diego, CA  
FEATURES  
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/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CGCGCTG 10  
|||||  
Db 1 CGCGCTG 7  
RESULT 157  
AR477264  
LOCUS AR477264 10 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 5 from patent US 6696275.  
ACCESSION AR477264  
VERSION AR477264.1 GI:47234597  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Short,J.M. and Frey,G.J.  
TITLE End selection in directed evolution  
JOURNAL Patent: US 6696275-A 5 24-FEB-2004;  
Diversa Corporation; San Diego, CA  
FEATURES  
source 1..10  
/organism="unknown"  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CGCGCTG 10  
|||||  
Db 1 CGCGCTG 7  
RESULT 158  
AR489166  
LOCUS AR489166 10 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 6 from patent US 6709841.  
ACCESSION AR489166  
VERSION AR489166.1 GI:47256094  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)

AUTHORS Short,J.M.  
TITLE Exonuclease-mediated gene assembly in directed evolution  
JOURNAL Patent: US 6709841-A 6 23-MAR-2004;  
Diversa Corporation; San Diego, CA  
FEATURES  
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/organism="unknown"  
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Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CGCGCTG 10  
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Db 1 CGCGCTG 7  
RESULT 159  
AR490750  
LOCUS AR490750 10 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 10 from patent US 6713279.  
ACCESSION AR490750  
VERSION AR490750.1 GI:47258162  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Short,J.M.  
TITLE Non-stochastic generation of genetic vaccines and enzymes  
JOURNAL Patent: US 6713279-A 10 30-MAR-2004;  
Diversa Corporation; San Diego, CA  
FEATURES  
source 1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 CGCGCTG 10  
|||||  
Db 1 CGCGCTG 7  
RESULT 160  
AR561751  
LOCUS AR561751 10 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 15 from patent US 6759195.  
ACCESSION AR561751  
VERSION AR561751.1 GI:53975402  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Bentley,W.E. and Gill,R.  
TITLE Method of differential display of prokaryotic messenger RNA by  
JOURNAL RT-PCR  
Patent: US 6759195-A 15 06-JUL-2004;  
University of Maryland Biotechnology Institute; Baltimore, MD  
FEATURES  
source 1..10  
/organism="unknown"  
/mol\_type="genomic DNA"  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 TGGCGAA 17

Db

|||||  
4 TGGCGAA 10

RESULT 161  
AR568611  
LOCUS AR568611 10 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 6 from patent US 6740506.  
ACCESSION AR568611  
VERSION AR568611.1 GI:56568059  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Short,J.M. and Frey,G.J.  
TITLE End selection in directed evolution  
JOURNAL Patent: US 6740506-A 6 25-MAY-2004;  
Diversa Corporation; San Diego, CA  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10  
Db 1 CGCGCTG 7

RESULT 162  
AR630146/c  
LOCUS AR630146 10 bp DNA linear PAT 14-FEB-2005  
DEFINITION Sequence 200 from patent US 6838556.  
ACCESSION AR630146  
VERSION AR630146.1 GI:59762471  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,  
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,  
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.  
TITLE Promoters for regulated gene expression  
JOURNAL Patent: US 6838556-A 200 04-JAN-2005;  
Genelabs Technologies, Inc.; Redwood City, CA  
FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10  
Db 8 CGCGCTG 2

RESULT 163  
AR641621/c  
LOCUS AR641621 10 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 25 from patent US 6861238.  
ACCESSION AR641621  
VERSION AR641621.1 GI:62777326  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
1 (bases 1 to 10)  
Petrovich,P.M., White,J.A., Beckett,B.R. and Jones,G.  
TITLE Retinoid metabolizing protein  
JOURNAL Patent: US 6861238-A 25 01-MAR-2005;  
Queen's University at Kingston; Kingston;  
WOX;  
FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
Db 9 TGGCGAA 3

RESULT 164  
AR642558/c  
LOCUS AR642558 10 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 31 from patent US 6864052.  
ACCESSION AR642558  
VERSION AR642558.1 GI:62779712  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.  
TITLE Enhanced sequencing by hybridization using pools of probes  
JOURNAL Patent: US 6864052-A 31 08-MAR-2005;  
Callida Genomics, Inc.; Sunnyvale, CA  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14  
Db 8 CTGTGGC 2

RESULT 165  
AR642559/c  
LOCUS AR642559 10 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 32 from patent US 6864052.  
ACCESSION AR642559  
VERSION AR642559.1 GI:62779713  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.  
TITLE Enhanced sequencing by hybridization using pools of probes  
JOURNAL Patent: US 6864052-A 32 08-MAR-2005;  
Callida Genomics, Inc.; Sunnyvale, CA  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14  
Db 8 CTGTGGC 2

RESULT 166  
AR642559/c  
LOCUS AR642559 10 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 32 from patent US 6864052.  
ACCESSION AR642559  
VERSION AR642559.1 GI:62779713  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Drmanac,R., Drmanac,S., Kita,D., Cooke,C. and Xu,C.  
TITLE Enhanced sequencing by hybridization using pools of probes  
JOURNAL Patent: US 6864052-A 32 08-MAR-2005;  
Callida Genomics, Inc.; Sunnyvale, CA  
FEATURES  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY      8 CTGTGGC 14
Db      7 CTGTGGC 1

RESULT 166
AX152609
LOCUS      AX152609          10 bp      DNA      linear      PAT 22-JUN-2001
DEFINITION Sequence 524 from Patent WO0138577.
ACCESSION  AX152609
VERSION    AX152609.1  GI:14534260
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1
AUTHORS    Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE      Human transcriptomes
JOURNAL    Patent: WO 0138577-A 524 31-MAY-2001;
            The Johns Hopkins University (US)
FEATURES   source
            1..10
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
Db      4 CTGTGGC 10

RESULT 167
AX666643
LOCUS      AX666643          10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 92 from Patent WO0242459.
ACCESSION  AX666643
VERSION    AX666643.1  GI:29291111
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Liu,Q.
TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL    Patent: WO 0242459-A 92 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES   source
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGCGAAG 18
Db      4 GGCGAAG 10

RESULT 168
AX666644
LOCUS      AX666644          10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 1653 from Patent WO0242459.
ACCESSION  AX668204
VERSION    AX668204.1  GI:29291483
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Liu,Q.
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DEFINITION Sequence 93 from Patent WO0242459.
ACCESSION  AX666644
VERSION    AX666644.1  GI:29291112
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Liu,Q.
TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL    Patent: WO 0242459-A 93 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES   source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGCGAAG 18
Db      4 GGCGAAG 10

RESULT 169
AX667829
LOCUS      AX667829          10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 1278 from Patent WO0242459.
ACCESSION  AX667829
VERSION    AX667829.1  GI:29291366
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Liu,Q.
TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
            fingers
JOURNAL    Patent: WO 0242459-A 1278 30-MAY-2002;
            Sangamo Biosciences Inc. (US)
FEATURES   source
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            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="example target DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
Db      4 GCTGTGG 10

RESULT 170
AX668204
LOCUS      AX668204          10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 1653 from Patent WO0242459.
ACCESSION  AX668204
VERSION    AX668204.1  GI:29291483
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Liu,Q.
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TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
           fingers
JOURNAL    Patent: WO 0242459-A 1653 30-MAY-2002;
           Sangamo Biosciences Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
       |||||
Db      3 GGTCGCG 9

RESULT 171
AX668205
LOCUS      AX668205      10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 1654 from Patent WO0242459.
ACCESSION  AX668205
VERSION     AX668205.1 GI:29291484
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Liu,Q.
TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
           fingers
JOURNAL    Patent: WO 0242459-A 1654 30-MAY-2002;
           Sangamo Biosciences Inc. (US)
FEATURES   Location/Qualifiers
           1..10
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="example target DNA"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
       |||||
Db      3 GGTCGCG 9

RESULT 172
AX668218
LOCUS      AX668218      10 bp      DNA      linear      PAT 26-MAR-2003
DEFINITION Sequence 1667 from Patent WO0242459.
ACCESSION  AX668218
VERSION     AX668218.1 GI:29291497
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Liu,Q.
TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
           fingers
JOURNAL    Patent: WO 0242459-A 1667 30-MAY-2002;
           Sangamo Biosciences Inc. (US)
FEATURES   Location/Qualifiers
           1..10
           /organism="synthetic construct"
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           /db_xref="taxon:32630"

TITLE      Position dependent recognition of gnn nucleotide triplets by zinc
           fingers
JOURNAL    Patent: WO 0242459-A 1653 30-MAY-2002;
           Sangamo Biosciences Inc. (US)
FEATURES   Location/Qualifiers
           1..10
           /organism="synthetic construct"
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
       |||||
Db      3 GGTCGCG 9

RESULT 173
AX753482/c
LOCUS      AX753482      10 bp      DNA      linear      PAT 23-JUN-2003
DEFINITION Sequence 27 from Patent EP1310556.
ACCESSION  AX753482
VERSION     AX753482.1 GI:32166242
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE      Composition and methods for the identification of lung tumor cells
           Patent: EP 1310556-A 27 14-MAY-2003;
           GENZYME CORPORATION (US)
FEATURES   Location/Qualifiers
           1..10
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
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Db      9 CTGTGGC 3

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Job time : 0.001 secs
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
       |||||
Db      3 GGTCGCG 9

RESULT 173
AX753482/c
LOCUS      AX753482      10 bp      DNA      linear      PAT 23-JUN-2003
DEFINITION Sequence 27 from Patent EP1310556.
ACCESSION  AX753482
VERSION     AX753482.1 GI:32166242
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE      Composition and methods for the identification of lung tumor cells
           Patent: EP 1310556-A 27 14-MAY-2003;
           GENZYME CORPORATION (US)
FEATURES   Location/Qualifiers
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
       |||||
Db      9 CTGTGGC 3

Search completed: May 9, 2006, 15:46:51
Job time : 0.001 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:48:19 ; Search time 0.001 Seconds  
(without alignments)  
22.382 Million cell updates/sec

Title: US-09-904-968A-19-COPY  
Perfect score: 19  
Sequence: 1 ggtcgcgctgtgccaagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 57 seqs, 589 residues

Total number of hits satisfying chosen parameters: 114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 57 summaries

Database : issdb19.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	10.4	54.7	14	1	US-09-874-601-115
2	10.4	54.7	14	1	5427929-4
3	9.8	51.6	14	1	US-09-647-344A-33
C 4	9	47.4	10	1	US-08-826-246-18
C 5	9	47.4	10	1	US-08-944-495-18
C 6	9	47.4	10	1	US-09-126-640-18
C 7	9	47.4	10	1	US-08-925-588-18
C 8	9	47.4	10	1	US-09-288-292A-18
C 9	9	47.4	10	1	US-09-372-044-18
C 10	9	47.4	10	1	US-08-825-486-18
C 11	9	47.4	10	1	US-08-826-248-18
C 12	9	47.4	10	1	US-09-706-228-11
13	8.4	44.2	11	1	US-09-249-155A-305
14	8.4	44.2	12	1	US-09-494-102A-2
C 15	8.4	44.2	12	1	US-09-949-041A-50
16	7.8	41.1	11	1	US-09-314-847A-8
17	7.8	41.1	11	1	US-10-037-677A-10
C 18	7.4	38.9	10	1	US-08-171-718-30
C 19	7.4	38.9	10	1	US-08-171-718-36
C 20	7.4	38.9	10	1	US-08-388-353-259
C 21	7.4	38.9	10	1	US-08-388-353-260
C 22	7.4	38.9	10	1	US-08-488-551B-259
C 23	7.4	38.9	10	1	US-08-488-551B-260
C 24	7.4	38.9	10	1	US-08-478-087-30
C 25	7.4	38.9	10	1	US-08-478-087-36
26	7.4	38.9	10	1	US-09-398-499-52
C 27	7.4	38.9	10	1	US-08-899-241-240
C 28	7.4	38.9	10	1	US-09-848-537A-9
C 29	7.4	38.9	10	1	US-09-775-743C-12
30	7.4	38.9	10	1	US-09-875-453B-199
C 31	7.4	38.9	10	1	US-09-479-608A-29
C 32	7.4	38.9	10	1	US-09-479-608A-30
C 33	7.4	38.9	10	1	US-08-956-518A-92

C 34	7	36.8	10	1	US-08-259-148A-31	Sequence 31, Appl
C 35	7	36.8	10	1	US-07-876-941A-47	Sequence 47, Appl
C 36	7	36.8	10	1	US-08-734-973-11	Sequence 11, Appl
C 37	7	36.8	10	1	US-08-265-484B-6	Sequence 6, Appli
C 38	7	36.8	10	1	US-08-724-466B-25	Sequence 25, Appl
C 39	7	36.8	10	1	US-08-765-257A-6	Sequence 6, Appli
C 40	7	36.8	10	1	US-08-522-384-48	Sequence 48, Appl
C 41	7	36.8	10	1	US-08-882-164D-25	Sequence 25, Appl
C 42	7	36.8	10	1	US-09-535-754-6	Sequence 6, Appli
C 43	7	36.8	10	1	US-09-336-946B-13	Sequence 13, Appl
C 44	7	36.8	10	1	US-09-508-753B-72	Sequence 72, Appl
C 45	7	36.8	10	1	US-09-508-753B-404	Sequence 404, App
C 46	7	36.8	10	1	US-10-042-111-23	Sequence 23, Appl
C 47	7	36.8	10	1	US-10-108-077-6	Sequence 6, Appli
C 48	7	36.8	10	1	US-09-867-262-5	Sequence 5, Appli
C 49	7	36.8	10	1	US-10-087-426-6	Sequence 6, Appli
C 50	7	36.8	10	1	US-09-498-557-10	Sequence 10, Appl
C 51	7	36.8	10	1	US-09-885-551A-6	Sequence 6, Appli
C 52	7	36.8	10	1	US-09-534-366A-15	Sequence 15, Appl
C 53	7	36.8	10	1	US-09-875-453B-200	Sequence 200, App
C 54	7	36.8	10	1	US-09-668-482-25	Sequence 25, Appl
C 55	7	36.8	10	1	US-09-479-608A-31	Sequence 31, Appl
C 56	7	36.8	10	1	US-09-479-608A-32	Sequence 32, Appl
C 57	7	36.8	10	1	US-10-029-221C-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-874-601-115  
; Sequence 115, Application US/09874601  
; Patent No. 6632057  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.  
; APPLICANT: SHAW, LYNN C.  
; APPLICANT: GRANT, MARIA B.  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS  
; FILE REFERENCE: 4300.014100  
; CURRENT APPLICATION NUMBER: US/09/874,601  
; CURRENT FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: 09/063,667  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/046,147  
; PRIOR FILING DATE: 1997-05-09  
; PRIOR APPLICATION NUMBER: 60/044,492  
; PRIOR FILING DATE: 1997-04-21  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 115  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: ()..()  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
US-09-874-601-115

Query Match 54.7%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 2.8;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGAAGG 19

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Db 1 CUGUGGAGAAGG 12

RESULT 2

5427929-4

; Patent No. 5427929

; APPLICANT: RICHARDS, RODNEY M.; JONES, THEODORE; SNITMAN, DAVID

```
;L.;BROWN, GREGORY S.
; TITLE OF INVENTION: METHOD FOR REDUCING CARRYOVER CONTAMINATION
;IN AN AMPLIFICATION PROCEDURE
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/57,192
; FILING DATE: 3-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 686,478
; FILING DATE: 19-APR-1991
; APPLICATION NUMBER: 517,631
; FILING DATE: 01-MAY-1990
;SEQ ID NO:4:
; LENGTH: 14
5427929-4

Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 2.8;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGAAG 18
Db 1 GCTGTGGCGCAAG 12

RESULT 3
US-09-647-344A-33
; Sequence 33, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.PCT.US
; CURRENT APPLICATION NUMBER: US/09/647,344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-09-647-344A-33

Query Match 51.6%; Score 9.8; DB 1; Length 14;
Best Local Similarity 69.2%; Pred. No. 3.9;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCGCGCTGTGGC 14
Db 2 GUGGCGCUGGGC 14

RESULT 4
US-08-826-246-18/c
; Sequence 18, Application US/08826246
; Patent No. 6048709
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

; L.;BROWN, GREGORY S.
; TITLE OF INVENTION: METHOD FOR REDUCING CARRYOVER CONTAMINATION
;IN AN AMPLIFICATION PROCEDURE
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/57,192
; FILING DATE: 3-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 686,478
; FILING DATE: 19-APR-1991
; APPLICATION NUMBER: 517,631
; FILING DATE: 01-MAY-1990
;SEQ ID NO:4:
; LENGTH: 14
5427929-4

Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 2.8;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGAAG 18
Db 1 GCTGTGGCGCAAG 12

RESULT 3
US-09-647-344A-33
; Sequence 33, Application US/09647344A
; Patent No. 6586180
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.PCT.US
; CURRENT APPLICATION NUMBER: US/09/647,344A
; CURRENT FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-09-647-344A-33

Query Match 51.6%; Score 9.8; DB 1; Length 14;
Best Local Similarity 69.2%; Pred. No. 3.9;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTCGCGCTGTGGC 14
Db 2 GUGGCGCUGGGC 14

RESULT 4
US-08-826-246-18/c
; Sequence 18, Application US/08826246
; Patent No. 6048709
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,246
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE: 13-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/011,787
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-078-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)7909090
; TELEFAX: (212)8699741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
US-08-826-246-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18
Db 10 GTGGCGAAG 2

RESULT 5
US-08-944-495-18/c
; Sequence 18, Application US/08944495
; Patent No. 6087477
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,495
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/799,910
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-067-999
```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
US-08-944-495-18

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
|||||  
Db 10 GTGGCGAAG 2

RESULT 6  
US-09-126-640-18/c  
Sequence 18, Application US/09126640A  
Patent No. 6099823  
GENERAL INFORMATION:  
APPLICANT: FALB, Dean A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
FILE REFERENCE: 7853-126  
CURRENT APPLICATION NUMBER: US/09/126,640A  
CURRENT FILING DATE: 1998-07-30  
EARLIER APPLICATION NUMBER: 08/870,434  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 08/799,910  
EARLIER FILING DATE: 1997-02-13  
EARLIER APPLICATION NUMBER: 60/011,787  
EARLIER FILING DATE: 1996-02-16  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Primer  
US-09-126-640-18

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
|||||  
Db 10 GTGGCGAAG 2

RESULT 7  
US-08-925-588-18/c  
Sequence 18, Application US/08925588  
Patent No. 6221628  
GENERAL INFORMATION:  
APPLICANT: Falb, Dean  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
THE TREATMENT AND DIAGNOSIS OF  
CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY

COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/925,588  
FILING DATE: 08-Sep-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/799,910  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-067-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)7909090  
TELEFAX: (212)8699741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-08-925-588-18

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
|||||  
Db 10 GTGGCGAAG 2

RESULT 8  
US-09-288-292A-18/c  
Sequence 18, Application US/09288292A  
Patent No. 6359194  
GENERAL INFORMATION:  
APPLICANT: Dean A. Falb  
APPLICANT: Katherine Galvin  
APPLICANT: Michael Donovan  
APPLICANT: Dennis Huszar  
APPLICANT: Michael A. Gimbrone, Jr.  
TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of  
Cardiovascular Disease  
FILE REFERENCE: 7853-140-999  
CURRENT APPLICATION NUMBER: US/09/288,292A  
CURRENT FILING DATE: 1999-04-08  
PRIOR APPLICATION NUMBER: 08/870,434  
PRIOR FILING DATE: 1997-06-06  
PRIOR APPLICATION NUMBER: 08/799,910  
PRIOR FILING DATE: 1997-02-13  
PRIOR APPLICATION NUMBER: 60/011,787  
PRIOR FILING DATE: 1996-02-16  
PRIOR APPLICATION NUMBER: 08/485,573  
PRIOR FILING DATE: 1995-06-07  
PRIOR APPLICATION NUMBER: 08/386,844  
PRIOR FILING DATE: 1995-02-10  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 10  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-288-292A-18



Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 9

US-09-372-044-18/c  
; Sequence 18, Application US/09372044A  
; Patent No. 6492126  
; GENERAL INFORMATION:  
; APPLICANT: Dean FALB et al.  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease  
; FILE REFERENCE: 7853-152  
; CURRENT APPLICATION NUMBER: US/09/372,044A  
; CURRENT FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-372-044-18

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 10

US-08-825-486-18/c  
; Sequence 18, Application US/08825486  
; Patent No. 6534641  
; GENERAL INFORMATION:  
; APPLICANT: Falb, Dean  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/825,486  
; FILING DATE: 28-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/799,910  
; FILING DATE: 13-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-077-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)7909090

; TELEFAX: (212)8699741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
US-08-825-486-18

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 11

US-08-826-248-18/c  
; Sequence 18, Application US/08826248  
; Patent No. 6759210  
; GENERAL INFORMATION:  
; APPLICANT: Falb, Dean  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/826,248  
; FILING DATE: 28-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/799,910  
; FILING DATE: 13-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/011,787  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-079-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)7909090  
; TELEFAX: (212)8699741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
US-08-826-248-18

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
| | | | | | | |  
Db 10 GTGGCGAAG 2

RESULT 12  
US-09-706-228-11/c  
; Sequence 11, Application US/09706228  
; Patent No. 6803215  
; GENERAL INFORMATION:  
; APPLICANT: Shaw, Pang-Chui  
; APPLICANT: Wang, Jun  
; APPLICANT: But, Paul Pui-Hay  
; APPLICANT: Ha, Wai-Yan  
; APPLICANT: Yau, Forrest C.F.  
; APPLICANT: The Chinese University of Hong Kong  
; TITLE OF INVENTION: Sequence Characterization Amplified Region (SCAR) Test  
; Patent No. 6803215  
; TITLE OF INVENTION: for the Authentication of Traditional Chinese Medicinal  
; FILE OF INVENTION: Materials  
; FILE REFERENCE: 016285-001500US  
; CURRENT APPLICATION NUMBER: US/09/706,228  
; CURRENT FILING DATE: 2000-11-03  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:primer OPC-20  
US-09-706-228-11

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
| | | | | | | |  
Db 10 GTGGCGAAG 2

RESULT 13  
US-09-249-155A-305  
; Sequence 305, Application US/09249155A  
; Patent No. 6538173  
; GENERAL INFORMATION:  
; APPLICANT: Heber-Katz, Ellen  
; TITLE OF INVENTION: Compositions and Methods for Wound  
; TITLE OF INVENTION: Healing  
; FILE REFERENCE: 00486.78503  
; CURRENT APPLICATION NUMBER: US/09/249,155A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,737  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/097,937  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/102,051  
; PRIOR FILING DATE: 1998-09-28  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 305  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-249-155A-305

Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 11;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCGA 16  
| | | | | | | |

Db 1 GCTGTGGCCA 10

RESULT 14  
US-09-494-102A-2  
; Sequence 2, Application US/09494102A  
; Patent No. 6303293  
; GENERAL INFORMATION:  
; APPLICANT: Patterson, David  
; APPLICANT: Puskas, John  
; APPLICANT: Song, Keming  
; APPLICANT: Linnen, KemingJeffrey  
; TITLE OF INVENTION: OLIGONUCLEOTIDE REVERSE TRANSCRIPTION PRIMERS FOR EFFICIENT DE  
; TITLE OF INVENTION: HIV-1 AND HIV-2 AND METHODS OF USE THEREOF  
; FILE REFERENCE: 2094/1E284-US1  
; CURRENT APPLICATION NUMBER: US/09/494,102A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/118,417  
; PRIOR FILING DATE: 1999-02-02  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Oligonucleotide primer  
US-09-494-102A-2

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 10;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15  
| | | | | | | |  
Db 1 CCCTGTGGCG 10

RESULT 15  
US-09-949-041A-50/c  
; Sequence 50, Application US/09949041A  
; Patent No. 6902894  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Meng  
; APPLICANT: Woo, Hok  
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Ri  
; TITLE OF INVENTION: Resistance  
; FILE REFERENCE: fp4637  
; CURRENT APPLICATION NUMBER: US/09/949,041A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 50  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-949-041A-50

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 10;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14  
| | | | | | | |  
Db 11 GCGCTGGGCG 2

RESULT 16  
US-09-314-847A-8  
; Sequence 8, Application US/09314847A

Patent No. 6365410  
; GENERAL INFORMATION:  
; APPLICANT: Schellenberger, Volker  
; APPLICANT: Liu, Amy D.  
; APPLICANT: Selifonova, Olga V.  
; TITLE OF INVENTION: Directed Evolution of Microorganisms  
; FILE REFERENCE: GC560  
; CURRENT APPLICATION NUMBER: US/09/314,847A  
; CURRENT FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pos102 mutD mutated gene  
US-09-314-847A-8

Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 16;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGCGGCTGTG 12  
|| |||||  
Db 1 GTGCCGCTGTG 11

RESULT 17  
US-10-037-677A-10  
; Sequence 10, Application US/10037677A  
; Patent No. 6706503  
; GENERAL INFORMATION:  
; APPLICANT: Schellenberger, Volker  
; APPLICANT: Liu, Amy D.  
; APPLICANT: Selifonova, Olga V.  
; TITLE OF INVENTION: Directed Evolution of Microorganisms  
; FILE REFERENCE: GC560-D1  
; CURRENT APPLICATION NUMBER: US/10/037,677A  
; CURRENT FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 09/314,847  
; PRIOR FILING DATE: 1999-05-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: pos102 mutD mutated gene  
US-10-037-677A-10

Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 16;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGCGGCTGTG 12  
|| |||||  
Db 1 GTGCCGCTGTG 11

RESULT 18  
US-08-171-718-30/c  
; Sequence 30, Application US/08171718  
; Patent No. 5707863  
; GENERAL INFORMATION:  
; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,718  
FILING DATE: 22-DEC-1993  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/108,808  
FILING DATE: 19-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/022,034  
FILING DATE: 25-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/026,063  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Anne  
REGISTRATION NUMBER: 36,463  
REFERENCE/DOCKET NUMBER: 0609.3850003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-171-718-30  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 CTGTGGCGGA 16  
|| ||||| ||  
Db 10 CTGTGGGGA 2  
RESULT 19  
US-08-171-718-36/c  
; Sequence 36, Application US/08171718  
; Patent No. 5707863  
; GENERAL INFORMATION:  
; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/171,718

;  
; FILING DATE: 22-DEC-1993  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/108,808  
; FILING DATE: 19-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,034  
; FILING DATE: 25-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/026,063  
; FILING DATE: 04-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Anne  
; REGISTRATION NUMBER: 36,463  
; REFERENCE/DOCKET NUMBER: 0609.3850003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-171-718-36

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 16  
Db 10 CTGTGGCCA 2

RESULT 20  
US-08-388-353-259/c  
; Sequence 259, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 259:  
; SEQUENCE CHARACTERISTICS:

;  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-388-353-259

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 10 GTGGCTAAG 2

RESULT 21  
US-08-388-353-260/c  
; Sequence 260, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 260:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-388-353-260

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
Db 9 GTGGCTAAG 1

RESULT 22  
US-08-488-551B-259/c  
; Sequence 259, Application US/08488551B

```
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 259:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-259

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18
Db 10 GTGGCTAAG 2

RESULT 23
US-08-488-551B-260/c
; Sequence 260, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
```

```
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-260

Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18
Db 9 GTGGCTAAG 1

RESULT 24
US-08-478-087-30/c
; Sequence 30, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
```



/ FILING DATE: 22-DEC-1993  
 / APPLICATION NUMBER: US 08/108,808  
 / FILING DATE: 19-AUG-1993  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 08/022,034  
 / FILING DATE: 25-FEB-1993  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 08/026,063  
 / FILING DATE: 04-MAR-1993  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Brown, Anne  
 / REGISTRATION NUMBER: 36,463  
 / REFERENCE/DOCKET NUMBER: 0609.3850003  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (202) 371-2600  
 / TELEFAX: (202) 371-2540  
 / INFORMATION FOR SEQ ID NO: 30:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 10 base pairs  
 / TYPE: nucleic acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / US-08-478-087-30

```
Query Match      38.9%;      Score 7.4;  DB 1;  Length 10;
Best Local Similarity 88.5%;      Pred. No. 22;
Matches 8;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;
```

Qy 8 CTGTGGCGA 16  
|||  
Db 10 CTGTGGGGA 2

**RESULT 25**

```

US-08-478-087-36/c
; Sequence 36, Application US/08478087
; Patent No. 6077685
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,087
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,718
; FILING DATE: 22-DEC-1993
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne

```

; REGISTRATION NUMBER: 36,463  
 ; REFERENCE/DOCKET NUMBER: 0609.3850003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 371-2600  
 ; TELEFAX: (202) 371-2540  
 ; INFORMATION FOR SEQ ID NO: 36:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-478-087-36

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%;  
Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 16  
| | | | |  
Db 10 CTGTGGCGCA 2

## RESULT 26

```

US-09-398-499-52
; Sequence 52, Application US/09398499
; Patent No. 6284466
; GENERAL INFORMATION:
; APPLICANT: Benson, Andrew K.
; TITLE OF INVENTION: HIGH RESOLUTION GENOME SCANNING
; FILE REFERENCE: UNL 2963
; CURRENT APPLICATION NUMBER: US/09/398,499
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/101,011
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-398-499-52

```

```
Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 9 TGTGGCGAA 17  
| | | | |  
Db 2 TCTGGCGAA 10

## RESULT 27

```

US-08-899-241-240/c
; Sequence 240, Application US/08899241A
; Patent No. 6322995
; GENERAL INFORMATION:
; APPLICANT: Hohmann, Hans-Peter
; APPLICANT: Huembelin, Markus
; APPLICANT: van Loon, Adolphus
; APPLICANT: Schurter, Walter
; TITLE OF INVENTION: Improved Riboflavin Production
; FILE REFERENCE: Improved Riboflavin Prod
; CURRENT APPLICATION NUMBER: US/08/899,241A
; CURRENT FILING DATE: 1997-07-23
; EARLIER APPLICATION NUMBER: 96111905.4
; EARLIER FILING DATE: 1996-07-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA

```

```
; ORGANISM: Ac# J01749
US-08-899-241-240

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CGCGCTGCTG 12
      |||||
Db      9 CGCGCTGGG 1

RESULT 28
US-09-848-537A-9/c
; Sequence 9, Application US/09848537A
; Patent No. 6696274
; GENERAL INFORMATION:
; APPLICANT: Tchistiakova, Liudmila
; APPLICANT: Li, Shengmin
; APPLICANT: Pietrzynski, Grzegorz
; APPLICANT: Alakhov, Valery
; TITLE OF INVENTION: Ligand For Enhancing Oral And CNS Delivery of
; TITLE OF INVENTION: Biological Agents
; FILE REFERENCE: 082181-36910
; CURRENT APPLICATION NUMBER: US/09/848,537A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
US-09-848-537A-9

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCGCGCT 9
      |||
Db      10 GGTCGCGCT 2

RESULT 29
US-09-775-743C-12/c
; Sequence 12, Application US/09775743C
; Patent No. 6733755
; GENERAL INFORMATION:
; APPLICANT: Supratek Pharmaceuticals, Inc.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 082181-36154
; CURRENT APPLICATION NUMBER: US/09/775,743C
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/180,568
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-775-743C-12

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCGCGCT 9
      |||
Db      10 GGTCGCGCT 2

; ORGANISM: Ac# J01749
US-08-899-241-240

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CGCGCTGCTG 12
      |||||
Db      9 CGCGCTGGG 1

RESULT 30
US-09-875-453B-199
; Sequence 199, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mutated sequence
US-09-875-453B-199

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GTGCGGCTG 10
      |
Db      1 GGCGGCGTG 9

RESULT 31
US-09-479-608A-29/c
; Sequence 29, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-29

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 22;
```

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16  
| | | | | | | |  
Db 10 CTGTGGCAA 2

RESULT 32  
US-09-479-608A-30/c  
; Sequence 30, Application US/09479608A  
; Patent No. 6864052  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, R.  
; APPLICANT: Drmanac, S.  
; APPLICANT: Kita, D.  
; APPLICANT: Cooke, C.  
; APPLICANT: Xu, C.  
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES  
; FILE REFERENCE: 30311/35918  
; CURRENT APPLICATION NUMBER: US/09/479,608A  
; CURRENT FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: US 60/115,284  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 30  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hypothetical sequence  
US-09-479-608A-30

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16  
| | | | | | | |  
Db 9 CTGTGGCAA 1

RESULT 33  
US-08-956-518A-92/c  
; Sequence 92, Application US/08956518A  
; Patent No. 6875606  
; GENERAL INFORMATION:  
; APPLICANT: Leonard, Sherry  
; APPLICANT: Freedman, Robert  
; TITLE OF INVENTION: ALPHA-7 NICOTINIC RECEPTOR  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,518A  
; FILING DATE: 23-OCT-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: UTC-03042  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-705-8410

; TELEFAX: 415-397-8338  
; INFORMATION FOR SEQ ID NO: 92:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-08-956-518A-92

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16  
| | | | | | | |  
Db 10 CTGTGGAGA 2

RESULT 34  
US-08-259-148A-31/c  
; Sequence 31, Application US/08259148A  
; Patent No. 5741490  
; GENERAL INFORMATION:  
; APPLICANT: Reyes, Gregory R.  
; APPLICANT: Bradley, Daniel W.  
; APPLICANT: Twu, Jr-Shin  
; APPLICANT: Purdy, Michael A.  
; APPLICANT: Tam, Albert W.  
; APPLICANT: Krawczynski, Krzysztof Z.  
; APPLICANT: Yarbough, Patrice D.  
; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/259,148A  
; FILING DATE: 13-JUN-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 822,335  
; FILING DATE: 17-JAN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 505,888  
; FILING DATE: 05-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 420,921  
; FILING DATE: 13-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 367,486  
; FILING DATE: 16-JUN-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 336,672  
; FILING DATE: 11-APR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 208,997  
; FILING DATE: 17-JUN-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sholtz, Charles K.  
; REGISTRATION NUMBER: 38,615  
; REFERENCE/DOCKET NUMBER: 4600-0093.20  
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-08-259-148A-31

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCGAA 17
Db 7 TGGCGAA 1

RESULT 35
US-07-876-941A-47/c
; Sequence 47, Application US/07876941A
; Patent No. 5885768
; GENERAL INFORMATION:
; APPLICANT: Reyes, Gregory R.
; APPLICANT: Bradley, Daniel W.
; APPLICANT: Tam, Albert W.
; APPLICANT: Mitchell, Carl
; TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,941A
; FILING DATE: 01-MAY-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 822,335
; FILING DATE: 17-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 505,888
; FILING DATE: 05-APRIL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 420,921
; FILING DATE: 13-OCTOBER-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 367,486
; FILING DATE: 16-JUNE-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 336,672
; FILING DATE: 11-APRIL-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 208,997
; FILING DATE: 17-JUNE-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
```

```

; REFERENCE/DOCKET NUMBER: 4600-0093.33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-07-876-941A-47

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCGAA 17
Db 7 TGGCGAA 1

RESULT 36
US-08-734-973-11/c
; Sequence 11, Application US/08734973
; Patent No. 5912147
; GENERAL INFORMATION:
; APPLICANT: Stoler, Daniel L.
; APPLICANT: Basik, Mark
; APPLICANT: Anderson, Garth R.
; TITLE OF INVENTION: A Rapid Means For Quantitating
; TITLE OF INVENTION: Genomic Instability
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/ Microsoft Windows
; SOFTWARE: Wordperfect for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/734,973
; FILING DATE: October 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551.0021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 11 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: No
US-08-734-973-11

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 2 GTCGCGC 8  
Db 10 GTCGCGC 4

## RESULT 37

US-08-265-484B-6  
; Sequence 6, Application US/08265484B  
; Patent No. 5998193  
; GENERAL INFORMATION:  
; APPLICANT: Keese, Paul  
; APPLICANT: Stapper, Marianne  
; APPLICANT: Perriman, Rhonda  
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
; TITLE OF INVENTION: Ribozymes and Compositions Thereof  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/265,484B  
; FILING DATE: 24-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 45284  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other Nucleic Acid  
US-08-265-484B-6

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14  
Db 4 CUGUGGC 10

## RESULT 38

US-08-724-466B-25/c  
; Sequence 25, Application US/08724466B  
; Patent No. 6063606  
; GENERAL INFORMATION:  
; APPLICANT: Petkovich, P. Martin, White, Jay A.,  
; APPLICANT: Beckett, Barbara R., Jones, Glenville  
; TITLE OF INVENTION: Retinoid Metabolizing Protein  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blake, Cassels & Graydon  
; STREET: Box 25, Commerce Court West  
; CITY: Toronto  
; ZIP: M5L 1A9  
; COUNTRY: Canada

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
; COMPUTER: COMPAQ, IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 5.1  
; SOFTWARE: WORD PERFECT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,466B  
; FILING DATE: October 1, 1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/667,546  
; FILING DATE: June 21, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunt, John C.  
; REGISTRATION NUMBER: 36,424  
; REFERENCE/DOCKET NUMBER: 50767/00004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 863-4344  
; TELEFAX: (416) 863-2653  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-724-466B-25

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
Db 9 TGGCGAA 3

## RESULT 39

US-08-765-257A-6  
; Sequence 6, Application US/08765257A  
; Patent No. 6107078  
; GENERAL INFORMATION:  
; APPLICANT: Keese, Paul  
; APPLICANT: Stapper, Marianne  
; APPLICANT: Perriman, Rhonda  
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,  
; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes  
; TITLE OF INVENTION: and Compositions Thereof  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH, 1.44Mb  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.24  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/765,257A  
; FILING DATE: June 24, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 45284  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 977 9550  
; TELEFAX: 212 977 9809  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs



```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-765-257A-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      8 CTGTGGC 14
      |:|:|
Db      4 CUGUGGC 10

RESULT 40
US-08-522-384-48
; Sequence 48, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-48

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GCTGTGG 13
      |||||
Db      4 GCTGTGG 10

RESULT 41
US-08-882-164D-25/c
; Sequence 25, Application US/08882164D
; Patent No. 6306624
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; APPLICANT: Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,164D
; FILING DATE: June 25, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
```

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;
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-164D-25

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 TGGCGAA 17
      |||||
Db      9 TGGCGAA 3

RESULT 42
US-09-535-754-6
; Sequence 6, Application US/09535754
; Patent No. 6361974
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTIC
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/535,754
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-535-754-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGCGCTG 10
      |||||
Db      1 CGCGCTG 7

RESULT 43
US-09-336-946B-13/c
; Sequence 13, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A pi-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
```

; PRIOR FILING DATE: 1998-08-04  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 13  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide  
US-09-336-946B-13

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGT 11  
| | | | |  
Db 7 GCGCTGT 1

RESULT 44  
US-09-508-753B-72/c  
; Sequence 72, Application US/09508753B  
; Patent No. 6544736  
; GENERAL INFORMATION:  
; APPLICANT: Akira SHIMAMOTO  
; APPLICANT: Yasuhiro FURUICHI  
; APPLICANT: Yuko SHIBATA  
; APPLICANT: Hiroko FUNAKI  
; APPLICANT: Ei-ji OHARA  
; APPLICANT: Masanori WATAHIKI  
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample  
; FILE REFERENCE: 00162/HG  
; CURRENT APPLICATION NUMBER: US/09/508,753B  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: JP 9/270324  
; PRIOR FILING DATE: 1997-09-18  
; NUMBER OF SEQ ID NOS: 472  
; SEQ ID NO 72  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-508-753B-72

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13  
| | | | |  
Db 10 GCTGTGG 4

RESULT 45  
US-09-508-753B-404  
; Sequence 404, Application US/09508753B  
; Patent No. 6544736  
; GENERAL INFORMATION:  
; APPLICANT: Akira SHIMAMOTO  
; APPLICANT: Yasuhiro FURUICHI  
; APPLICANT: Yuko SHIBATA  
; APPLICANT: Hiroko FUNAKI  
; APPLICANT: Ei-ji OHARA  
; APPLICANT: Masanori WATAHIKI  
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample  
; FILE REFERENCE: 00162/HG  
; CURRENT APPLICATION NUMBER: US/09/508,753B  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: JP 9/270324  
; PRIOR FILING DATE: 1997-09-18  
; NUMBER OF SEQ ID NOS: 472

; SEQ ID NO 404  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-09-508-753B-404

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12  
| | | | |  
Db 4 CGCTGTG 10

RESULT 46  
US-10-042-111-23/c  
; Sequence 23, Application US/10042111  
; Patent No. 6551476  
; GENERAL INFORMATION:  
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES  
; APPLICANT: CHEN, Jinqing  
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS  
; FILE REFERENCE: ref.  
; CURRENT APPLICATION NUMBER: US/10/042,111  
; CURRENT FILING DATE: 2002-05-08  
; PRIOR APPLICATION NUMBER: CN 99124511.3  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 23  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: primer  
US-10-042-111-23

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13  
| | | | |  
Db 7 GCTGTGG 1

RESULT 47  
US-10-108-077-6  
; Sequence 6, Application US/10108077  
; Patent No. 6635449  
; GENERAL INFORMATION:  
; APPLICANT: DIVERSA CORPORATION  
; APPLICANT: SHORT, Jay  
; APPLICANT: DJAVAKHISHVILI, Tsotne  
; APPLICANT: FREY, Gerhard  
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUT  
; FILE REFERENCE: DIVER1460-14  
; CURRENT APPLICATION NUMBER: US/10/108,077  
; CURRENT FILING DATE: 2002-03-26  
; PRIOR APPLICATION NUMBER: US/09/535,754  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 09/522,289  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial sequence

```
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-108-077-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGCGCTG 10
      |||||
Db      1 CGCGCTG 7

RESULT 48
US-09-867-262-5
; Sequence 5, Application US/09867262
; Patent No. 6696275
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-867-262-5

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGCGCTG 10
      |||||
Db      1 CGCGCTG 7

RESULT 49
US-10-087-426-6
; Sequence 6, Application US/10087426
; Patent No. 6709841
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
```

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; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-087-426-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGCGCTG 10
      |||||
Db      1 CGCGCTG 7

RESULT 50
US-09-498-557-10
; Sequence 10, Application US/09498557
; Patent No. 6713279
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES AND ENZYMES
; FILE REFERENCE: DIVER1460-12
; CURRENT APPLICATION NUMBER: US/09/498,557
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/332,835
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-498-557-10

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4 CGCGCTG 10  
| | | | |  
Db 1 CGCGCTG 7

RESULT 51  
US-09-885-551A-6  
; Sequence 6, Application US/09885551A  
; Patent No. 6740506  
; GENERAL INFORMATION:  
; APPLICANT: DIVERSA CORPORATION  
; APPLICANT: SHORT, Jay  
; APPLICANT: DJAVAKHISHVILI, Tsotne  
; APPLICANT: FREY, Gerhard  
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN  
; TITLE OF INVENTION: DIRECTED EVOLUTION  
; FILE REFERENCE: DIVER1460-14  
; CURRENT APPLICATION NUMBER: US/09/885,551A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US/09/535,754  
; PRIOR FILING DATE: 2000-03-27  
; PRIOR APPLICATION NUMBER: US 09/522,289  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: BspG I restriction site  
US-09-885-551A-6

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10  
| | | | |  
Db 1 CGCGCTG 7

RESULT 52  
US-09-534-366A-15  
; Sequence 15, Application US/09534366A  
; Patent No. 6759195  
; GENERAL INFORMATION:  
; APPLICANT: Bentley, William E.  
; APPLICANT: Gill, Ryan T.  
; TITLE OF INVENTION: Method of Differential Display of Prokaryotic Messenger  
; TITLE OF INVENTION: RNA by RTPCR  
; FILE REFERENCE: Bentley et al., Method of . . .  
; CURRENT APPLICATION NUMBER: US/09/534,366A  
; CURRENT FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PROV 60/126,038  
; PRIOR FILING DATE: 1999-03-25  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthesized  
US-09-534-366A-15

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
| | | | |

Db 4 TGGCGAA 10

RESULT 53  
US-09-875-453B-200/c  
; Sequence 200, Application US/09875453B  
; Patent No. 6838556  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jungshuh P.  
; APPLICANT: Starr, Douglas B.  
; APPLICANT: Tam, Albert W.  
; APPLICANT: Laurance, Megan E.  
; APPLICANT: Michelotti, Emil F.  
; APPLICANT: Velligan, Mark D.  
; APPLICANT: Latour, Derek R.  
; APPLICANT: Thomas, Rita L.  
; APPLICANT: Kongpachith, Ana  
; APPLICANT: Sheppard, Liana T.  
; APPLICANT: Lim, Moon Young  
; APPLICANT: Bruice, Thomas W.  
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION  
; FILE REFERENCE: 54600-8135.US00  
; CURRENT APPLICATION NUMBER: US/09/875,453B  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/209,549  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 246  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 200  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutated sequence  
US-09-875-453B-200

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10  
| | | | |  
Db 8 CGCGCTG 2

RESULT 54  
US-09-668-482-25/c  
; Sequence 25, Application US/09668482  
; Patent No. 6861238  
; GENERAL INFORMATION:  
; APPLICANT: Petkovich, P. Martin, White, Jay A.,  
; Beckett, Barbara R., Jones, Glenville  
; TITLE OF INVENTION: Retinoid Metabolizing Protein  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blake, Cassels & Graydon  
; STREET: Box 25, Commerce Court West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5L 1A9  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
; COMPUTER: COMPAQ, IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 5.1  
; SOFTWARE: WORD PERFECT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/668,482  
; FILING DATE: 25-Sep-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/882,164  
; FILING DATE: June 25, 1997  
; APPLICATION NUMBER: 08/667,546

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;
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 25
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25
US-09-668-482-25

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGAA 17
      |||||
Db      9 TGGCGAA 3

RESULT 55
US-09-479-608A-31/c
; Sequence 31, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-31

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
      |||||
Db      8 CTGTGGC 2

RESULT 56
US-09-479-608A-32/c
; Sequence 32, Application US/09479608A
; Patent No. 6864052
; GENERAL INFORMATION:
; APPLICANT: Drmanac, R.
; APPLICANT: Drmanac, S.
; APPLICANT: Kita, D.
; APPLICANT: Cooke, C.
; APPLICANT: Xu, C.
```

```
;
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES
; FILE REFERENCE: 30311/35918
; CURRENT APPLICATION NUMBER: US/09/479,608A
; CURRENT FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: US 60/115,284
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hypothetical sequence
US-09-479-608A-32
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      8 CTGTGGC 14
      |||||
Db      7 CTGTGGC 1
```

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RESULT 57
US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Patent No. 6939689
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-029-221C-5
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Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      4 CGCGCTG 10
      |||||
Db      1 CGCGCTG 7
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Search completed: May 9, 2006, 15:48:19
Job time : 0.001 secs
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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:49:45 ; Search time 0.001 Seconds  
(without alignments)  
167.086 Million cell updates/sec

Title: US-09-904-968A-19-COPY  
Perfect score: 19  
Sequence: 1 ggtcgcgtgtggtggaagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 414 seqs, 4397 residues

Total number of hits satisfying chosen parameters: 828

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 414 summaries

*N-Geneseq*

Database : ngsdb19.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	AAD30245	Human PKD1 gene mu
2	11	57.9	13	ABF16246	Oligonucleotide SE
C 3	11	57.9	13	ABF16247	Oligonucleotide SE
4	10.4	54.7	14	AAQ15000	Amplification prob
5	10.4	54.7	14	ABZ72886	Rod opsin hairpin
C 6	10	52.6	12	ADZ85151	MODY 3 diabetes-as
C 7	10	52.6	13	ABC20757	Oligonucleotide SE
8	10	52.6	13	ABC20756	Oligonucleotide SE
9	9.8	51.6	13	ABC23004	Oligonucleotide SE
C 10	9.8	51.6	13	ABC88957	Oligonucleotide SE
C 11	9.8	51.6	13	ABF17107	Oligonucleotide SE
C 12	9.8	51.6	13	ABC88973	Oligonucleotide SE
C 13	9.8	51.6	13	ABC23005	Oligonucleotide SE
14	9.8	51.6	13	ABC88956	Oligonucleotide SE
15	9.8	51.6	13	ABC88972	Oligonucleotide SE
16	9.8	51.6	13	ABF17106	Oligonucleotide SE
17	9.8	51.6	14	AAZ23797	HSV RNA fragment 1
C 18	9.4	49.5	12	ABH84869	Oligonucleotide pr
C 19	9.4	49.5	12	ABH90694	Oligonucleotide pr
C 20	9.4	49.5	12	ABI50257	Oligonucleotide pr
21	9.4	49.5	12	ADF57536	PCR primer used in
22	9.4	49.5	12	ADG28788	Bacterial strain i
23	9.4	49.5	12	ADR05232	Wilting bacterial-
24	9.4	49.5	12	ADZ39909	Primer used in bac
25	9.4	49.5	13	ABH32686	Oligonucleotide SE
C 26	9.4	49.5	13	ABC86975	Oligonucleotide SE
27	9.4	49.5	13	ABC63144	Oligonucleotide SE
C 28	9.4	49.5	13	ABH65141	Oligonucleotide SE
C 29	9.4	49.5	13	ABC53131	Oligonucleotide SE
30	9.4	49.5	13	ABF03962	Oligonucleotide SE
31	9.4	49.5	13	ABF16244	Oligonucleotide SE
32	9.4	49.5	13	ABC53130	Oligonucleotide SE
C 33	9.4	49.5	13	ABF04975	Oligonucleotide SE

34	9.4	49.5	13	1	ABH19540	Oligonucleotide SE
C 35	9.4	49.5	13	1	ABH19543	Oligonucleotide SE
C 36	9.4	49.5	13	1	ABF16163	Oligonucleotide SE
37	9.4	49.5	13	1	ABH19542	Oligonucleotide SE
38	9.4	49.5	13	1	ABF04974	Oligonucleotide SE
C 39	9.4	49.5	13	1	ABC63145	Oligonucleotide SE
40	9.4	49.5	13	1	ABF16162	Oligonucleotide SE
C 41	9.4	49.5	13	1	ABF16245	Oligonucleotide SE
C 42	9.4	49.5	13	1	ABC76993	Oligonucleotide SE
43	9.4	49.5	13	1	ABC76992	Oligonucleotide SE
44	9.4	49.5	13	1	ABC86974	Oligonucleotide SE
C 45	9.4	49.5	13	1	ABH19541	Oligonucleotide SE
C 46	9.4	49.5	13	1	ABF03963	Oligonucleotide SE
47	9.4	49.5	13	1	ABH65140	Oligonucleotide SE
C 48	9.4	49.5	13	1	ABH32687	Oligonucleotide SE
49	9.4	49.5	13	1	ADZ85140	MODY 3 diabetes-as
C 50	9	47.4	10	1	AAT94476	Human Fchd540 gene
C 51	9	47.4	10	1	AAV34958	Synthetic Agaricus
C 52	9	47.4	10	1	AAZ58826	Human MUC11 gene a
C 53	9	47.4	10	1	AAZ50718	Reverse primer for
C 54	9	47.4	10	1	ABL60664	Parax species geno
55	9	47.4	11	1	ABV69628	Human skin EST 741
C 56	9	47.4	12	1	ABI04019	Oligonucleotide pr
C 57	8.8	46.3	12	1	AAV65455	Primer pBS800-23J
C 58	8.8	46.3	12	1	ABI59311	Oligonucleotide pr
59	8.8	46.3	12	1	ABI24865	Oligonucleotide pr
C 60	8.8	46.3	12	1	ABH89194	Oligonucleotide pr
61	8.8	46.3	12	1	ABX10162	Human TIGR/Myocili
62	8.8	46.3	12	1	ADW86997	Protein labelling
C 63	8.4	44.2	10	1	AAZ77822	Human dendritic ce
64	8.4	44.2	10	1	AAZ77845	Human dendritic ce
65	8.4	44.2	10	1	AAZ84021	Metastatic breast
C 66	8.4	44.2	10	1	AAZ85539	Metastatic breast
C 67	8.4	44.2	10	1	AAZ84999	Metastatic breast
68	8.4	44.2	10	1	AAZ85922	Metastatic breast
69	8.4	44.2	10	1	AAZ81487	Metastatic breast
C 70	8.4	44.2	10	1	AAZ84108	Metastatic breast
C 71	8.4	44.2	10	1	AAH64063	Human ubiquitously
72	8.4	44.2	10	1	AAF42948	Yeast NORF gene SA
73	8.4	44.2	10	1	AAF41527	Yeast NORF gene SA
C 74	8.4	44.2	10	1	ABL88334	Human CHRNE gene p
75	8.4	44.2	10	1	ABN87962	Human GSR preferre
C 76	8.4	44.2	10	1	ABV78444	Human Th1 cell pre
C 77	8.4	44.2	10	1	AAS97347	Human CRYBB1 gene
78	8.4	44.2	10	1	ABL45886	Human EDG6 gene al
C 79	8.4	44.2	10	1	ABI99149	Human PCDH2 ASO PC
80	8.4	44.2	10	1	AAD52054	Human CES2 gene po
81	8.4	44.2	10	1	ACA94569	DNA tag from human
82	8.4	44.2	10	1	ADK13021	Human glioma endot
C 83	8.4	44.2	11	1	AAN20067	DNA primer for HLA
84	8.4	44.2	11	1	AAZ18995	Murine MRL SAGE ta
85	8.4	44.2	11	1	ABQ86261	Human skin stress/
C 86	8.4	44.2	11	1	ABQ87168	Human skin stress/
87	8.4	44.2	11	1	ABV65931	Human skin EST 371
88	8.4	44.2	11	1	ABV69764	Human skin EST 755
89	8.4	44.2	11	1	ABV70774	Human skin EST 856
C 90	8.4	44.2	11	1	ABV69072	Human skin EST 685
C 91	8.4	44.2	11	1	ABV69619	Human skin EST 740
92	8.4	44.2	11	1	ABV71417	Human skin EST 920
93	8.4	44.2	11	1	ABV63353	Human skin EST 113
C 94	8.4	44.2	11	1	ABV66009	Human skin EST 379
95	8.4	44.2	11	1	ABV67796	Human skin EST 558
96	8.4	44.2	11	1	ABV68820	Human skin EST 660
97	8.4	44.2	11	1	ABV63996	Human skin EST 178
98	8.4	44.2	11	1	ABV62343	Human skin EST 129
C 99	8.4	44.2	11	1	ADQ35656	Human hair-bearing
100	8.4	44.2	11	1	ADQ36012	Human hair-bearing
101	8.4	44.2	11	1	ADQ35381	Human hair-bearing
C 102	8.4	44.2	11	1	ADQ32141	Human facial skin-
103	8.4	44.2	11	1	ADQ34986	Human facial skin-
104	8.4	44.2	11	1	ADQ35029	Human facial skin-
C 105	8.4	44.2	11	1	ADQ34095	Human facial skin-
106	8.4	44.2	12	1	AAV65451	Primer pBS800-23E

107	8.4	44.2	12	1	AAV65548	Forward primer 18
108	8.4	44.2	12	1	AAV65547	Forward primer 17
109	8.4	44.2	12	1	AAV65546	Forward primer 16
110	8.4	44.2	12	1	AAA74607	HIV-specific rever
111	8.4	44.2	12	1	ABI23621	Oligonucleotide pr
112	8.4	44.2	12	1	ABI12916	Oligonucleotide pr
c 113	8.4	44.2	12	1	ABI06621	Oligonucleotide pr
c 114	8.4	44.2	12	1	ABI64116	Oligonucleotide pr
c 115	8.4	44.2	12	1	ABH90350	Oligonucleotide pr
116	8.4	44.2	12	1	ABH95969	Oligonucleotide pr
117	8.4	44.2	12	1	ABH73785	Oligonucleotide pr
118	8.4	44.2	12	1	ABH90189	Oligonucleotide pr
119	8.4	44.2	12	1	ABH72007	Oligonucleotide pr
120	8.4	44.2	12	1	ABI25686	Oligonucleotide pr
121	8.4	44.2	12	1	ABI26828	Oligonucleotide pr
c 122	8.4	44.2	12	1	ABH90031	Oligonucleotide pr
c 123	8.4	44.2	12	1	ABI29748	Oligonucleotide pr
124	8.4	44.2	12	1	ABI12040	Oligonucleotide pr
125	8.4	44.2	12	1	ABI117107	Oligonucleotide pr
126	8.4	44.2	12	1	ABI50801	Oligonucleotide pr
127	8.4	44.2	12	1	ABH95967	Oligonucleotide pr
c 128	8.4	44.2	12	1	ABH90353	Oligonucleotide pr
c 129	8.4	44.2	12	1	ADC33639	M. tuberculosis PC
c 130	8.4	44.2	12	1	ADZ45204	Parallel stranded
131	8	42.1	10	1	AAZ79106	Human dendritic ce
132	8	42.1	10	1	AAZ81742	Metastatic breast
133	8	42.1	10	1	AAZ85240	Metastatic breast
c 134	8	42.1	10	1	AAZ85260	Metastatic breast
135	8	42.1	10	1	AAZ84921	Metastatic breast
136	8	42.1	10	1	AAZ84042	Metastatic breast
137	8	42.1	10	1	AAZ79746	Human colon prefer
138	8	42.1	10	1	AAH63878	Human ubiquitously
139	8	42.1	10	1	AAH32681	LPS activated huma
140	8	42.1	10	1	ABA06193	Human normal hepat
141	8	42.1	10	1	ABA83148	Claudin 2 ovarian
142	8	42.1	10	1	AAF43250	Yeast NORF gene SA
143	8	42.1	10	1	ABL42674	Human maturation/a
144	8	42.1	10	1	ABL42776	Human maturation/a
145	8	42.1	10	1	ABK96054	Human LIPE gene po
146	8	42.1	10	1	AAL48073	Human CSF3 gene al
147	8	42.1	10	1	ABK23699	Transcript tag DNA
148	8	42.1	10	1	ACA94662	DNA tag from human
149	8	42.1	10	1	ACA94515	DNA tag from human
150	8	42.1	10	1	ADS76513	Breast cancer dete
151	8	42.1	10	1	ADS78031	Breast cancer dete
152	8	42.1	10	1	ADS76514	Breast cancer dete
153	8	42.1	10	1	ADU19803	Hypoxia-related tu
c 154	8	42.1	11	1	ABV69823	Human skin EST 760
c 155	8	42.1	11	1	ABV62402	Human skin EST 188
c 156	8	42.1	11	1	ABV67604	Human skin EST 539
157	7.8	41.1	11	1	AAC85261	mutD promoter sequ
158	7.8	41.1	11	1	ABQ87267	Human skin stress/
c 159	7.8	41.1	11	1	ABQ87096	Human skin stress/
c 160	7.8	41.1	11	1	ABQ87230	Human skin stress/
c 161	7.8	41.1	11	1	ABV68460	Human skin EST 624
162	7.8	41.1	11	1	ABV69665	Human skin EST 745
163	7.8	41.1	11	1	ABV65281	Human skin EST 306
c 164	7.8	41.1	11	1	ABV67742	Human skin EST 552
c 165	7.8	41.1	11	1	ABV70868	Human skin EST 865
c 166	7.8	41.1	11	1	ABV63447	Human skin EST 123
c 167	7.8	41.1	11	1	ABV72108	Human skin EST 989
168	7.8	41.1	11	1	ABV66734	Human skin EST 452
169	7.8	41.1	11	1	ABV62244	Human skin EST 30.
170	7.8	41.1	11	1	ADQ36355	Human hair-bearing
171	7.8	41.1	11	1	ADQ35677	Human hair-bearing
c 172	7.8	41.1	11	1	ADQ34103	Human facial skin-
173	7.8	41.1	11	1	ADT79188	Oligonucleotide #1
c 174	7.8	41.1	11	1	ADZ24827	Human SNP detectio
c 175	7.4	38.9	10	1	AAQ71089	Merlin exon 7 spli
c 176	7.4	38.9	10	1	AAQ71095	Merlin exon 10 spl
c 177	7.4	38.9	10	1	AAQ96664	HIV-1 NL4-3 nef ge
c 178	7.4	38.9	10	1	AAQ96663	HIV-1 NL4-3 nef ge
179	7.4	38.9	10	1	AAX18633	p53 serial analysi

c 180	7.4	38.9	10	1	AAZ79074	Human dendritic ce
181	7.4	38.9	10	1	AAZ79675	Human dendritic ce
182	7.4	38.9	10	1	AAZ79480	Human dendritic ce
c 183	7.4	38.9	10	1	AAZ78781	Human dendritic ce
c 184	7.4	38.9	10	1	AAZ82348	Metastatic breast
c 185	7.4	38.9	10	1	AAZ81963	Metastatic breast
c 186	7.4	38.9	10	1	AAZ85441	Metastatic breast
187	7.4	38.9	10	1	AAZ83525	Metastatic breast
188	7.4	38.9	10	1	AAZ82033	Metastatic breast
189	7.4	38.9	10	1	AAZ84603	Metastatic breast
c 190	7.4	38.9	10	1	AAZ81044	Metastatic breast
191	7.4	38.9	10	1	AAZ81349	Metastatic breast
c 192	7.4	38.9	10	1	AAZ82759	Metastatic breast
c 193	7.4	38.9	10	1	AAZ81572	Metastatic breast
c 194	7.4	38.9	10	1	AAZ81415	Metastatic breast
c 195	7.4	38.9	10	1	AAZ82829	Metastatic breast
c 196	7.4	38.9	10	1	AAZ84942	Metastatic breast
c 197	7.4	38.9	10	1	AAZ80867	Metastatic breast
198	7.4	38.9	10	1	AAZ74122	Human monocyte and
199	7.4	38.9	10	1	AAZ73917	Human dendritic ce
c 200	7.4	38.9	10	1	AAZ74079	Human dendritic ce
201	7.4	38.9	10	1	AAA56244	Human macrophage g
202	7.4	38.9	10	1	AAA56333	Human macrophage g
203	7.4	38.9	10	1	AAA56136	Human monocyte gen
204	7.4	38.9	10	1	AAA14154	E. coli K-12 leadi
c 205	7.4	38.9	10	1	AAA73645	Probe #14 for sequ
c 206	7.4	38.9	10	1	AAA73646	Probe #15 for sequ
207	7.4	38.9	10	1	AAI70450	Oligonucleotide us
208	7.4	38.9	10	1	AAH19999	Mouse Treg immunor
209	7.4	38.9	10	1	AAI67372	Human FKBP8 gene p
c 210	7.4	38.9	10	1	AAS09210	Oligonucleotide ON
c 211	7.4	38.9	10	1	AAH63607	Human ubiquitously
c 212	7.4	38.9	10	1	AAH63746	Human ubiquitously
213	7.4	38.9	10	1	AAH64224	Human ubiquitously
214	7.4	38.9	10	1	AAH63440	Human ubiquitously
215	7.4	38.9	10	1	AAH63439	Human ubiquitously
216	7.4	38.9	10	1	AAH64185	Human ubiquitously
c 217	7.4	38.9	10	1	AAH63894	Human ubiquitously
c 218	7.4	38.9	10	1	AAD20721	Primer #13 used to
219	7.4	38.9	10	1	AAH32655	LPS activated huma
220	7.4	38.9	10	1	AAH32828	LPS activated huma
c 221	7.4	38.9	10	1	AAH32746	Human phospholipid
c 222	7.4	38.9	10	1	ABA81653	Human normal hepat
223	7.4	38.9	10	1	ABA06025	Human normal hepat
224	7.4	38.9	10	1	ABA06218	Human normal hepat
225	7.4	38.9	10	1	AAA91471	Human CHRM5 gene,
c 226	7.4	38.9	10	1	AAF36041	Yeast NORF gene SA
227	7.4	38.9	10	1	AAF43354	Yeast NORF gene SA
c 228	7.4	38.9	10	1	AAF39191	Yeast NORF gene SA
229	7.4	38.9	10	1	AAF34571	Yeast NORF gene SA
230	7.4	38.9	10	1	AAF35628	Yeast NORF gene SA
231	7.4	38.9	10	1	AAF37416	Yeast NORF gene SA
c 232	7.4	38.9	10	1	AAF36771	Yeast NORF gene SA
c 233	7.4	38.9	10	1	AAF37531	Yeast NORF gene SA
c 234	7.4	38.9	10	1	AAF43175	Yeast NORF gene SA
235	7.4	38.9	10	1	AAF43253	Yeast NORF gene SA
236	7.4	38.9	10	1	AAF43167	Yeast NORF gene SA
237	7.4	38.9	10	1	AAS19671	Primer-extension o
c 238	7.4	38.9	10	1	ABL01179	Human AKR1B1 gene
c 239	7.4	38.9	10	1	AAS98835	Colony stimulating
240	7.4	38.9	10	1	ABL42636	Human maturation/a
c 241	7.4	38.9	10	1	AAD25385	Human primer #2 to
242	7.4	38.9	10	1	ABN81464	Human HTATIP PCR p
243	7.4	38.9	10	1	ABK96027	Human LIPE gene po
244	7.4	38.9	10	1	AAI48067	Human CSF3 gene al
c 245	7.4	38.9	10	1	AAI48068	Human CSF3 gene al
c 246	7.4	38.9	10	1	AAD27409	Oligo #2, to const
247	7.4	38.9	10	1	ABL39499	Human ETVB primer-
248	7.4	38.9	10	1	ABT05346	Human NAGA-alpha g
c 249	7.4	38.9	10	1	ABT05344	Human NAGA-alpha g
c 250	7.4	38.9	10	1	AAS99201	UDP glycosyltransf
251	7.4	38.9	10	1	ABV84886	Human thymosin bet
252	7.4	38.9	10	1	ABV84695	Chronic hepatitis

253	7.4	38.9	10	1	ABV84505	Human apolipoprote
254	7.4	38.9	10	1	ABV84523	Human HCC underexp
255	7.4	38.9	10	1	ABV84710	Human apolipoprote
256	7.4	38.9	10	1	ABV84764	Chronic hepatitis
257	7.4	38.9	10	1	ABV84791	Human apolipoprote
258	7.4	38.9	10	1	ABV84741	Chronic hepatitis
259	7.4	38.9	10	1	ABV84919	Human apolipoprote
260	7.4	38.9	10	1	ABV84967	Human thymosin bet
C 261	7.4	38.9	10	1	ABK23578	Transcript tag DNA
C 262	7.4	38.9	10	1	ABA96213	Half-site oligonuc
C 263	7.4	38.9	10	1	AAS19821	Oligonucleotide #1
264	7.4	38.9	10	1	ABA93366	Human ACAA1 gene p
C 265	7.4	38.9	10	1	AAS19954	Primer-extension o
C 266	7.4	38.9	10	1	ABL45924	Human EDG6 gene al
C 267	7.4	38.9	10	1	ABK81557	Human CASP5 gene a
C 268	7.4	38.9	10	1	ABK96167	Human CYP1A2 allel
C 269	7.4	38.9	10	1	AAS94665	Human PLTP gene al
C 270	7.4	38.9	10	1	AAD25031	Human AANAT gene p
271	7.4	38.9	10	1	ABK30052	Vancomycin-resista
272	7.4	38.9	10	1	ABL36392	Human lysosomal ac
273	7.4	38.9	10	1	AAL48136	Human neuropeptide
C 274	7.4	38.9	10	1	AAS95999	Human CALM1 gene a
C 275	7.4	38.9	10	1	AAS96001	Human CALM1 gene a
276	7.4	38.9	10	1	ABK81811	Human CHRM5 gene p
C 277	7.4	38.9	10	1	ACA94410	DNA tag from human
C 278	7.4	38.9	10	1	ACA94519	DNA tag from human
279	7.4	38.9	10	1	ACA94580	DNA tag from human
C 280	7.4	38.9	10	1	ADC15526	Biological molecu
C 281	7.4	38.9	10	1	ADJ93954	Azotobacter bacter
C 282	7.4	38.9	10	1	ADG65513	UCP2 primer extens
C 283	7.4	38.9	10	1	ADN89094	Hyperlipidemia tre
284	7.4	38.9	10	1	ADN89098	Hyperlipidemia tre
C 285	7.4	38.9	10	1	ADQ82166	Human Short statur
C 286	7.4	38.9	10	1	ADR27907	Human VE-statin ex
C 287	7.4	38.9	10	1	ADR27977	Murine VE-statin i
C 288	7.4	38.9	10	1	ADR88561	Alpha 7 nicotinic
C 289	7.4	38.9	10	1	ADS76954	Breast cancer dete
C 290	7.4	38.9	10	1	ADS77992	Breast cancer dete
C 291	7.4	38.9	10	1	ADS77023	Breast cancer dete
292	7.4	38.9	10	1	ADS76564	Breast cancer dete
C 293	7.4	38.9	10	1	ADS76953	Breast cancer dete
294	7.4	38.9	10	1	ADS77055	Breast cancer dete
C 295	7.4	38.9	10	1	ADS78162	Breast cancer dete
296	7.4	38.9	10	1	ADS76565	Breast cancer dete
C 297	7.4	38.9	10	1	ADS77022	Breast cancer dete
C 298	7.4	38.9	10	1	ADU19103	Breast cancer dete
299	7.4	38.9	10	1	ADU18946	Hypoxia-related tu
300	7.4	38.9	10	1	ADU18864	Hypoxia-related tu
301	7.4	38.9	10	1	ADZ24419	Hypoxia-related tu
302	7.4	38.9	10	1	ADZ24430	Human SNP detectio
303	7.4	38.9	10	1	AEA37223	Human SNP detectio
C 304	7	36.8	10	1	AAT29313	MoMLV derived vect
C 305	7	36.8	10	1	AAV09238	5'-primer for mamm
C 306	7	36.8	10	1	AAV12230	Degenerate RT-PCR
307	7	36.8	10	1	AAV34959	Differential displ
308	7	36.8	10	1	AAV50187	Synthetic Agaricus
309	7	36.8	10	1	AAV35966	Yeast tag for addi
C 310	7	36.8	10	1	AAV77467	Primer used in RAP
C 311	7	36.8	10	1	AAZ28347	US5912147 primer 1
C 312	7	36.8	10	1	AAZ61441	Lung cancer indica
313	7	36.8	10	1	AAZ79591	Primer SP4A5 for g
314	7	36.8	10	1	AAZ77871	Human dendritic ce
C 315	7	36.8	10	1	AAZ79427	Human dendritic ce
C 316	7	36.8	10	1	AAZ78099	Human dendritic ce
317	7	36.8	10	1	AAZ82030	Metastatic breast
C 318	7	36.8	10	1	AAZ83360	Metastatic breast
C 319	7	36.8	10	1	AAZ84570	Metastatic breast
320	7	36.8	10	1	AAZ82784	Metastatic breast
321	7	36.8	10	1	AAZ84917	Metastatic breast
C 322	7	36.8	10	1	AAZ86247	Metastatic breast
323	7	36.8	10	1	AAZ81792	Metastatic breast
324	7	36.8	10	1	AAZ81334	Metastatic breast
325	7	36.8	10	1	AAZ85903	Metastatic breast

326	7	36.8	10	1	AAZ82560	Metastatic breast
C 327	7	36.8	10	1	AAZ82992	Metastatic breast
328	7	36.8	10	1	AAA99863	Prokaryote RT-PCR
C 329	7	36.8	10	1	AAA73648	Probe #17 for sequ
C 330	7	36.8	10	1	AAA73647	Probe #16 for sequ
C 331	7	36.8	10	1	AAA70761	PCR primer #7 for
C 332	7	36.8	10	1	AAS04437	Human DAXX DNA pri
333	7	36.8	10	1	AAH63684	Human ubiquitously
334	7	36.8	10	1	AAS57302	Human CHRN2 allel
335	7	36.8	10	1	AAF31259	GC-rich template c
C 336	7	36.8	10	1	AAH41713	Anti-PEP gene cons
C 337	7	36.8	10	1	ABA06097	Human normal hepat
C 338	7	36.8	10	1	AAF36769	Yeast NORF gene SA
339	7	36.8	10	1	AAF37041	Yeast NORF gene SA
340	7	36.8	10	1	AAF33704	Yeast NORF gene SA
C 341	7	36.8	10	1	AAF36509	Yeast NORF gene SA
C 342	7	36.8	10	1	AAF43348	Yeast NORF gene SA
343	7	36.8	10	1	AAF33404	Yeast NORF gene SA
C 344	7	36.8	10	1	AAF40064	Yeast NORF gene SA
345	7	36.8	10	1	AAF40212	Yeast NORF gene SA
C 346	7	36.8	10	1	AAF34364	Yeast NORF gene SA
347	7	36.8	10	1	AAF36295	Yeast NORF gene SA
C 348	7	36.8	10	1	AAF42137	Yeast NORF gene SA
C 349	7	36.8	10	1	AAF37397	Yeast NORF gene SA
350	7	36.8	10	1	AAF433249	Yeast NORF gene SA
351	7	36.8	10	1	AAF40108	Yeast NORF gene SA
352	7	36.8	10	1	AAF43351	Yeast NORF gene SA
353	7	36.8	10	1	AAF33705	Yeast NORF gene SA
C 354	7	36.8	10	1	AAF41416	Yeast NORF gene SA
355	7	36.8	10	1	AAF41494	Yeast NORF gene SA
356	7	36.8	10	1	AAF37535	Yeast NORF gene SA
357	7	36.8	10	1	AAF33686	Yeast NORF gene SA
358	7	36.8	10	1	AAF36000	Yeast NORF gene SA
C 359	7	36.8	10	1	AAF42020	Yeast NORF gene SA
C 360	7	36.8	10	1	AAS95650	Human NPY1R gene a
C 361	7	36.8	10	1	AAD25081	Primer #8 used to
362	7	36.8	10	1	AAD26712	Human GPR31 gene p
363	7	36.8	10	1	AAS98814	Colony stimulating
364	7	36.8	10	1	ABQ71544	Zinc finger protei
365	7	36.8	10	1	ABQ71291	Zinc finger protei
366	7	36.8	10	1	ABQ71292	Zinc finger protei
367	7	36.8	10	1	ABQ71662	Zinc finger protei
368	7	36.8	10	1	ABQ71675	Zinc finger protei
369	7	36.8	10	1	ABQ71661	Zinc finger protei
370	7	36.8	10	1	ABQ88698	Human CFL1 primer
371	7	36.8	10	1	ABA03980	Human STK11 gene p
C 372	7	36.8	10	1	ABN80659	Human P450(cytochr
C 373	7	36.8	10	1	ABV78586	Human Th2 cell pre
C 374	7	36.8	10	1	ABV84371	Human MHC class II
C 375	7	36.8	10	1	ABV84863	Human 3,4-catechol
C 376	7	36.8	10	1	ABL52041	Human SLC18A2 pref
C 377	7	36.8	10	1	AAS97348	Human CRYBB1 gene
C 378	7	36.8	10	1	AAD24500	Retinoid-regulated
C 379	7	36.8	10	1	ABK30053	Vancomycin-resista
C 380	7	36.8	10	1	AAS95992	Human CALM1 gene a
C 381	7	36.8	10	1	ADH22188	Primer extension D
382	7	36.8	10	1	ACC41737	Zinc finger protei
C 383	7	36.8	10	1	ABT14391	Nucleic acid PCR a
384	7	36.8	10	1	ADA62122	Zinc finger target
385	7	36.8	10	1	ADA63307	Zinc finger target
386	7	36.8	10	1	ADA63696	Zinc finger target
387	7	36.8	10	1	ADA63683	Zinc finger target
388	7	36.8	10	1	ADA62121	Zinc finger target
389	7	36.8	10	1	ADA63682	Zinc finger target
390	7	36.8	10	1	ADB81067	LINE retro-positio
C 391	7	36.8	10	1	ADE14136	Optineurin promote
392	7	36.8	10	1	ADM22181	Synthetic zinc fin
393	7	36.8	10	1	ADM22194	Synthetic zinc fin
394	7	36.8	10	1	ADM20326	Synthetic zinc fin
395	7	36.8	10	1	ADM20325	Synthetic zinc fin
396	7	36.8	10	1	ADM21511	Synthetic zinc fin
397	7	36.8	10	1	ADM22180	Synthetic zinc fin
C 398	7	36.8	10	1	ADH57701	Extendable oligo E

399 Extracellular tumo  
c 400 Enhancer sequence  
c 401 West Nile virus de  
402 Loquat crown-gall  
c 403 Murine VE-statin e  
c 404 Hypoxia-related tu  
405 Hypoxia-related tu  
c 406 Hypoxia-related tu  
c 407 zP450RAI gene isol  
c 408 Degenerate primer,  
c 409 Zebrafish P450RAI  
c 410 Oligonucleotide re  
411 Oligonucleotide re  
c 412 Oligonucleotide re  
413 Oligonucleotide re  
c 414 Oligonucleotide re

ALIGNMENTS

RESULT 1  
AAD30245  
ID AAD30245 standard; DNA; 19 BP.  
XX  
AC AAD30245;  
XX  
DT 17-MAY-2002 (first entry)  
XX  
DE Human PKD1 gene mutation detecting nested PCR primer, 1F1.  
XX  
KW Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;  
KW acquired cystic disease; transgenic animal; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200206529-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 13-JUL-2001; 2001WO-US022035.  
XX  
PR 13-JUL-2000; 2000US-0218261P.  
PR 13-APR-2001; 2001US-0283691P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Germino GG, Watnick TJ, Phakdeekitcharoen B;  
XX WPI; 2002-179805/23.  
DR  
XX  
CC The present invention relates to compositions and methods useful for the  
CC identification and detection of polycystic kidney disease (PKD1) gene  
CC mutations. The invention also relates to primers comprising a 5' region  
CC having a sequence that selectively hybridizes to a PKD1 gene sequence and  
CC optionally, to a PKD1 homologue sequence and an adjacent 3' region having  
CC a sequence that selectively hybridizes to a PKD1 gene sequence and not to  
CC a PKD1 homologue sequence. Primer pairs of the invention are useful for  
CC detecting the presence or absence of a mutation in a PKD1 polynucleotide  
CC in a sample, for identifying a subject at risk for a PKD1-associated  
CC disorder such as autosomal dominant polycystic kidney disease ( ADPKD) or  
CC acquired cystic disease and for diagnosing a PKD1- associated disorder in  
CC a subject. They are useful for selectively amplifying a region of a PKD1  
CC gene. PKD1 DNA fragments are useful detecting the presence of a mutant  
CC PKD1 polynucleotide in a sample, as a probe for an amplification  
CC reaction, in hybridisation or amplification assays of biological samples  
CC to detect abnormalities of PKD1 expression and for engineering transgenic

CC animals. The present sequence is a PCR primer used to detect mutation in  
CC human PKD1 gene  
XX  
SQ Sequence 19 BP; 2 A; 4 C; 10 G; 3 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTGCGGCTGTGGCGAAGG 19  
Db 1 GGTGCGGCTGTGGCGAAGG 19  
RESULT 2  
ABF16246  
ID ABF16246 standard; DNA; 13 BP.  
XX  
AC ABF16246;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 116243 for detecting SNP TSC0029111.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 116243; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 1 Other;  
Query Match 57.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 TGTGGCGAAGG 19  
Db 2 TGTGGCGAAGG 12



```
RESULT 3
ABF16247/c
ID ABF16247 standard; DNA; 13 BP.
XX
XX AC ABF16247;
XX
XX DT 21-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 116244 for detecting SNP TSC0029111.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX DR WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 116244; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 2 A; 6 C; 1 G; 3 T; 0 U; 1 Other;

Query Match 57.9%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGTGGCGAAGG 2

RESULT 4
AAQ15000
ID AAQ15000 standard; DNA; 14 BP.
XX
XX AC AAQ15000;
XX
XX DT 17-FEB-1992 (first entry)
XX
XX DE Amplification probe AP2 with single base mismatch to target sequence.
XX KW ligase chain reaction; LCR; carryover contamination; ss.
XX
XX
```

```
OS Synthetic.
XX
XX PN WO9117270-A.
XX
XX PD 14-NOV-1991.
XX
XX PF 01-MAY-1990; 90US-00517631.
XX
XX PR 01-MAY-1990; 90US-00517631.
XX PR 19-APR-1991; 91US-00686478.
XX
XX PA (AMGE-) AMGEN.
XX
XX PI Richards RM, Jones T, Snitman DL;
XX
XX DR WPI; 1991-353789/48.
XX
XX PT Redn. of amplification prod. contamination - in amplification procedure
XX PT and kits for use in polymerase or ligase chain reaction procedures.
XX
XX PS Example 1 and 2; Fig 11B; 134pp; English.
XX
XX CC Restriction enzyme modification sites are introduced into amplification
XX CC sequence AS1 (see AAQ14998) during LCR using amplification probes AP1,
XX CC AP2 and AP3 (see AAQ14999 and AAQ15001 for the other two APs).
XX CC Amplification sequence AS1 contains the corresponding preferred pseudo
XX CC restriction sites
XX
XX SQ Sequence 14 BP; 3 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 54.7%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCGAAG 18
Db 1 GCTGTGGCGAAG 12

RESULT 5
ABZ72886
ID ABZ72886 standard; RNA; 14 BP.
XX
XX AC ABZ72886;
XX
XX DT 09-APR-2003 (first entry)
XX
XX DE Rod opsin hairpin ribozyme oligonucleotide.
XX
XX KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
XX KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
XX KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX PN WO200288320-A2.
XX
XX PD 07-NOV-2002.
XX
XX PF 01-MAY-2002; 2002WO-US013679.
XX
XX PR 01-MAY-2001; 2001US-00847601.
XX
XX PA (UYFL ) UNIV FLORIDA.
XX
XX PI Lewin AS, Shaw LC, Grant MB;
XX
XX DR WPI; 2003-111880/10.
XX
XX PT A recombinant adeno-associated virus-vectored ribozyme composition,
XX PT useful for treating a disease or dysfunction of the mammalian eye e.g.
```



PT retinal disease, e.g. diabetic retinopathy or age-related macular  
PT degeneration.  
XX  
PS Example 5; Page 62; 115pp; English.  
XX  
CC The present invention describes a recombinant adeno-associated virus  
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a  
CC first ribozyme that specifically cleaves an mRNA encoding a protein,  
CC polypeptide, or peptide selected from the group of rod opsin, iNOS,  
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin  
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a  
CC vector comprising a polynucleotide encoding the ribozyme, where the  
CC polynucleotide operably positioned downstream of at least a first  
CC promoter that directs expression of the polynucleotide in a selected  
CC mammalian cell transformed with the vector; (c) a viral particle  
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector  
CC comprising the ribozyme or the polynucleotide; or (e) a host cell  
CC comprising the ribozyme or the polynucleotide. Also described is a method  
CC for decreasing the amount of mRNA encoding a selected polypeptide in a  
CC retinal cell of a mammalian eye, comprising providing to the eye the  
CC composition described above, and for a time effective to specifically  
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can  
CC be used in gene therapy. (I) can be used for treating a disease or  
CC dysfunction of the mammalian eye, such as a retinal disease or retinal  
CC dysfunction, (diabetic) retinopathy, or (age-related) macular  
CC degeneration. (I) is also useful for manufacturing a medicament for  
CC treating the diseases mentioned above, including autosomal dominant  
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful  
CC for treating, decreasing the severity, or ameliorating the symptoms of a  
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,  
CC blindness, a reduction in central or peripheral vision, or a reduction in  
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 14 BP; 5 A; 1 C; 6 G; 0 T; 2 U; 0 Other;  
  
Query Match 54.7%; Score 10.4; DB 1; Length 14;  
Best Local Similarity 75.0%; Pred. No. 24;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGAAGG 19  
|:|:| |  
Db 1 CUGUGGAGAAGG 12  
  
RESULT 6  
ADZ85151/c  
ID ADZ85151 standard; DNA; 12 BP.  
XX  
AC ADZ85151;  
XX  
DT 28-JUL-2005 (first entry)  
XX  
DE MODY 3 diabetes-associated probe, SEQ ID 27.  
XX  
KW Analyte detection; microarray; probe; ss; diabetes.  
XX  
OS Unidentified.  
XX  
PN US2005112677-A1.  
XX  
PD 26-MAY-2005.  
XX  
PF 22-NOV-2004; 2004US-00994626.  
XX  
PR 22-NOV-2003; 2003KR-00083356.  
XX  
PA (SHIM/) SHIM J.  
XX  
PI Shim J;  
XX  
DR WPI; 2005-403357/41.  
XX

PT Substrate for use in optically detecting target materials, comprises an  
PT oxide layer having thickness that may vary to wavelength of excitation  
PT light used.  
XX  
PS Example 1; SEQ ID NO 27; 20pp; English.  
XX  
CC The present invention relates to a novel substrate having an oxide layer,  
CC which is useful in optically detecting a target material. The thickness  
CC of the oxide layer may vary to the wavelength of excitation light used.  
CC Also claimed is a method for detecting a target material, comprising  
CC immobilizing a probe material on a substrate, reacting the immobilized  
CC probe material and the target material, illuminating a reaction product  
CC with excitation light, and measuring light emitted from the reaction  
CC product by the excitation light. In an example from the invention,  
CC microarrays were fabricated by forming fused silica (SiO2) layers on  
CC silicon wafers, followed by linkage with a coupling agent and  
CC immobilization of oligonucleotide probes. The microarrays were then  
CC incubated with labeled oligonucleotides and exposed to excitation light,  
CC and light emitted from the target oligonucleotides was measured, to  
CC evaluate the intensity of detected signals with respect to the thickness  
CC of the SiO2 layers. ADZ85128-ADZ85203, MODY 3 diabetes-associated probes  
CC used with the target sequence of human glyceraldehyde-3-phosphate  
CC dehydrogenase (GAPDH), were used to show that when a target  
CC oligonucleotide is detected using a microarray including a substrate with  
CC an oxide layer a good signal is obtained compared to that with no oxide  
CC layers.  
XX  
SQ Sequence 12 BP; 2 A; 6 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 52.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 TGTGCGGAAG 18  
| | | | | | | | | |  
Db 10 TGTGCGGAAG 1  
  
RESULT 7  
ABC20757/c  
ID ABC20757 standard; DNA; 13 BP.  
XX  
AC ABC20757;  
XX  
DT 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 20774 for detecting SNP TSC0004222.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 20774; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 52.6%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
|||||

Db 13 TGTGGCGAAG 4

RESULT 8

ABC20756

ID ABC20756 standard; DNA; 13 BP.

AC ABC20756;

XX 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 20773 for detecting SNP TSC0004222.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

PD 18-OCT-2001.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

PS Claim 1; SEQ ID NO 20773; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 1 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 52.6%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
|||||

Db 1 TGTGGCGAAG 10

RESULT 9

ABC23004

ID ABC23004 standard; DNA; 13 BP.

XX ABC23004;

XX 20-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 23021 for detecting SNP TSC0004520.

KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB0000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

PS Claim 1; SEQ ID NO 23021; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 0 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 37;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCGCTGTGG 13  
|||||

Db 1 GGTGCGTGTGG 13

RESULT 10

ABC88957/c  
ID ABC88957 standard; DNA; 13 BP.  
XX  
AC ABC88957;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 88974 for detecting SNP TSC0022356.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 88974; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 5 C; 3 G; 0 T; 0 U; 0 Other;  
XX  
Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 37;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 3 TCGCGCTGTGCG 15  
Db 13 TCGCGTTGTGCG 1  
RESULT 11  
ABF17107/c  
ID ABF17107 standard; DNA; 13 BP.  
XX  
AC ABF17107;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 117104 for detecting SNP TSC0029306.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX

OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 117104; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 37;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 7 GCTGTGGCGAAGG 19  
Db 13 GTTGTGGTGAAGG 1  
RESULT 12  
ABC88973/c  
ID ABC88973 standard; DNA; 13 BP.  
XX  
AC ABC88973;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 88990 for detecting SNP TSC0022356.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 88990; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 6 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. NO. 37;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 TCGCGCTGTGGC 15  
Db 13 TCGCGCGTTGCG 1  
  
RESULT 13  
ABC23005/c  
ID ABC23005 standard; DNA; 13 BP.  
XX  
AC ABC23005;  
XX  
XX 20-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 23022 for detecting SNP TSC0004520.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 23022; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 8 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. NO. 37;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCTGTGG 13  
Db 13 GGTCGCGTTGCG 1  
  
RESULT 14  
ABC88956  
ID ABC88956 standard; DNA; 13 BP.  
XX  
AC ABC88956;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 88973 for detecting SNP TSC0022356.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 88973; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 0 A; 3 C; 5 G; 5 T; 0 U; 0 Other;  
  
Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. NO. 37;



Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15  
||||| ||| |||

Db 1 TCGCGTTGTGGC 13

RESULT 15  
ABC88972  
ID ABC88972 standard; DNA; 13 BP.  
XX  
AC ABC88972;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 88989 for detecting SNP TSC0022356.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 88989; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 0 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 37;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15  
||||| ||| |||

Db 1 TCGCGCGTTGCG 13

RESULT 16  
ABF17106  
ID ABF17106 standard; DNA; 13 BP.  
XX  
AC ABF17106;

DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 117103 for detecting SNP TSC0029306.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 117103; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 51.6%; Score 9.8; DB 1; Length 13;  
Best Local Similarity 84.6%; Pred. No. 37;  
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTGGCGAAGG 19  
||||| ||| |||

Db 1 GTTGTGTTGAAGG 13

RESULT 17  
AAZ23797  
ID AAZ23797 standard; RNA; 14 BP.  
XX  
AC AAZ23797;  
XX  
DT 14-JAN-2000 (first entry)  
XX  
DE HSV RNA fragment 15.  
XX  
KW Antisense; DNA library; identification; multiple cloning site; MCS;  
KW inhibition; ss.  
XX  
OS Herpes simplex virus unknown type.  
XX  
PN WO9950457-A1.  
XX  
PD 07-OCT-1999.



PF 28-MAR-1999; 99WO-US006742.  
XX  
PR 28-MAR-1998; 98US-0079792P.  
PR 06-NOV-1998; 98US-0107504P.  
XX  
PA (UTAH ) UNIV UTAH RES FOUND.  
XX  
PI Ruffner DE, Pierce ML, Chen Z;  
XX  
XX  
DR WPI; 1999-610866/52.  
XX  
PT Production of antisense libraries, used for identifying antisense agents  
PT and for identifying target sites for antisense-mediated inhibition of a  
PT selected gene.  
XX  
PS Example 4; Page 60; 63pp; English.  
XX  
CC This invention describes a novel method for generating an antisense  
CC library targeted to a selected RNA transcript. The methods can be used  
CC for identifying antisense agents and for identifying target sites for  
CC antisense-mediated inhibition of a selected gene. The use of a direct  
CC library for target site selection significantly simplifies the screening  
CC process, since only very small libraries need be prepared and assayed.  
CC AAZ23783-223798 represent RNA fragments derived from the Herpes simplex  
CC virus genome which are used to illustrate the method of the invention  
XX  
SQ Sequence 14 BP; 0 A; 4 C; 8 G; 0 T; 2 U; 0 Other;  
  
Query Match 51.6%; Score 9.8; DB 1; Length 14;  
Best Local Similarity 69.2%; Pred. NO. 34;  
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 GTCGCGCTGTGGC 14  
|: ||||: |||  
Db 2 GUGGCGCUGGGC 14  
  
RESULT 18  
ABH84869/C  
ID ABH84869 standard; DNA; 12 BP.  
XX  
AC ABH84869;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 284862 for detecting SNP TSC0012030.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 284862; 29pp + Sequence Listing; German.  
XX

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 8 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 49;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGGC 15  
| ||| |||||  
Db 11 GCGCGGTGGC 1  
  
RESULT 19  
ABH90694/C  
ID ABH90694 standard; DNA; 12 BP.  
XX  
AC ABH90694;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 290687 for detecting SNP TSC0014474.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 290687; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

```
SQ      Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

Query Match          49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TGTGGCGAAGG 19
Db      12 TGTGGGGAAGG 2

RESULT 20
ABI50257/c
ID      ABI50257 standard; DNA; 12 BP.
XX
AC      ABI50257;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 350230 for detecting SNP TSC0008276.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX
WPI; 2001-657177/75.
XX
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
XX
Claim 1; SEQ ID NO 350230; 29pp + Sequence Listing; German.
XX
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
XX
Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;

Query Match          49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TGTGGCGAAGG 19
Db      12 TGTGGGGAAGG 2

RESULT 21
ADF57536
```

```
ID      ADF57536 standard; DNA; 12 BP.
XX
AC      ADF57536;
XX
DT      12-FEB-2004 (first entry)
XX
DE      PCR primer used in method for detecting bacterial DNA in food, SEQ ID 37.
XX
KW      Food; bacterial; bacterium; Single Strain Counting-PCR; SSC-PCR; PCR;
KW      primer; ss.
XX
OS      Unidentified.
XX
PN      JP2003250541-A.
XX
PD      09-SEP-2003.
XX
PF      27-FEB-2002; 2002JP-00052215.
XX
PR      27-FEB-2002; 2002JP-00052215.
XX
PA      (SAOL ) SANYO ELECTRIC CO LTD.
XX
DR      WPI; 2003-883774/82.
XX
Foodstuff testing method involves amplifying DNA fragment of bacteria
extracted from foodstuff, by single strain counting polymerase chain
reaction method.
XX
Claim 6; SEQ ID NO 37; 27pp; Japanese.
XX
The present invention relates to a foodstuff testing method. The method
comprises extracting bacterial DNA fragment from foodstuff, amplifying
the DNA fragment by Single Strain Counting-PCR (SSC-PCR) method. The
amplified linear fragment is analyzed and the recycling method of
foodstuff is determined based on the analysis result. The present primer
was used to illustrate the method of the invention.
XX
Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

Query Match          49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 49;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCGCGCTGTGG 13
Db      1 TCGCGCTTGG 11

RESULT 22
ADG28788
ID      ADG28788 standard; DNA; 12 BP.
XX
AC      ADG28788;
XX
DT      26-FEB-2004 (first entry)
XX
DE      Bacterial strain identification-related PCR primer G44.
XX
KW      Escherichia coli; Bacillus; Shigella; bacterial strain identification;
KW      PCR; primer; ss.
XX
OS      Bacteria.
XX
PN      JP2003169686-A.
XX
PD      17-JUN-2003.
XX
PF      19-DEC-2001; 2001JP-00386731.
XX
PR      25-SEP-2001; 2001JP-00292674.
XX
PA      (SAOL ) SANYO ELECTRIC CO LTD.
```

XX WPI; 2003-783166/74.  
XX  
PT Identifying bacteria by amplifying DNA of bacteria by PCR,  
PT electrophoresing amplified DNA, obtaining electrophoretic image and  
PT identifying if bacteria is predetermined strain of Escherichia coli by  
PT DNA-fragment length.  
XX  
PS Example 1; SEQ ID NO 37; 114pp; Japanese.  
XX  
CC The invention relates to a novel method for identifying bacteria by  
CC amplifying DNA of the bacteria by PCR using a primer of specific  
CC sequence, electrophoresing the amplified DNA, obtaining an  
CC electrophoretic image and identifying whether the bacteria is a  
CC predetermined strain of Escherichia coli, Bacillus or Shigella by the  
CC appearance and position of DNA-fragment length within the electrophoretic  
CC image. The method of the invention may be useful for specifically  
CC identifying bacteria. The current sequence is that of the bacterial  
CC strain identification-related PCR primer of the invention.  
XX  
SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 49;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 TCGCGCTGTGG 13  
Db 1 TCGCGCTTTGG 11  
  
RESULT 23  
ADR05232  
ID ADR05232 standard; DNA; 12 BP.  
XX  
AC ADR05232;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Wilting bacterial-disease resistance carnation PCR primer, SEQ ID 2.  
XX  
KW Wilting bacterial-disease resistance; carnation; primer; PCR; ss.  
XX  
OS Unidentified.  
XX  
PN JP2004222532-A.  
XX  
PD 12-AUG-2004.  
XX  
PF 20-JAN-2003; 2003JP-00011119.  
XX  
PR 20-JAN-2003; 2003JP-00011119.  
XX  
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.  
XX  
XX WPI; 2004-585595/57.  
XX  
PT Novel oligonucleotide useful for identifying wilting bacterial-disease  
PT resistance carnation and for selecting wilting bacterial-disease  
PT resistance carnation.  
XX  
PS Claim 1; SEQ ID NO 2; 14pp; Japanese.  
XX  
CC The invention relates to a novel oligonucleotide for selecting a wilting  
CC bacterial-disease resistance carnation. The oligonucleotide for selecting  
CC a wilting bacterial-disease resistance carnation is selected from  
CC ADR05232, ADR05233, ADR05234, ADR05235, ADR05236 or ADR05237. The  
CC oligonucleotide is useful for identifying a wilting bacterial-disease  
CC resistance carnation, which involves extracting DNA from the carnation,  
CC using it as a template, performing amplification of the DNA by PCR using  
CC one or a combination of the oligonucleotides, and carrying out  
CC electrophoresis analysis of the obtained amplified product. This  
CC polynucleotide sequence represents a wilting bacterial-disease resistance

CC carnation primer oligo of the invention.  
XX  
SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 49;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 TCGCGCTGTGG 13  
Db 1 TCGCGCTTTGG 11  
  
RESULT 24  
ADZ39909  
ID ADZ39909 standard; DNA; 12 BP.  
XX  
AC ADZ39909;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Primer used in bacteria detection #8.  
XX  
KW bacteria; primer; ss.  
XX  
OS Unidentified.  
XX  
PN JP2003265198-A.  
XX  
PD 24-SEP-2003.  
XX  
PF 19-MAR-2002; 2002JP-00075994.  
XX  
PR 19-MAR-2002; 2002JP-00075994.  
XX  
PA (SAOL ) SANYO ELECTRIC CO LTD.  
XX  
DR WPI; 2004-084978/09.  
XX  
PT Identifying bacteria involves amplifying DNA fragment of bacteria by PCR  
PT using twelve kinds of primers specific sequence, subjecting amplified DNA  
PT to electrophoresis and identifying bacteria based on electrophoresis  
PT result.  
XX  
PS Claim 1; SEQ ID NO 8; 18pp; Japanese.  
XX  
CC The present invention relates to identifying bacteria by amplifying DNA  
CC fragments from bacteria by PCR using twelve kinds of primers, is new. The  
CC method and the associated apparatus are useful for identifying bacteria  
CC such as food poisoning bacteria. The detection and identification of  
CC bacteria is performed easily in short time. The present sequence  
CC represents a primer of the invention.  
XX  
SQ Sequence 12 BP; 1 A; 3 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 12;  
Best Local Similarity 90.9%; Pred. No. 49;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 TCGCGCTGTGG 13  
Db 1 TCGCGCTTTGG 11  
  
RESULT 25  
ABH32686  
ID ABH32686 standard; DNA; 13 BP.  
XX  
AC ABH32686;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 232663 for detecting SNP TSC0056734.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 232663; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 1 C; 8 G; 1 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 9 TGTGGCGAAGG 19  
Db 2 TGGGGCGAAGG 12  
  
RESULT 26  
ABC86975/c  
ID ABC86975 standard; DNA; 13 BP.  
XX  
AC ABC86975;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 86992 for detecting SNP TSC0021858.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX

PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
DR  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 86992; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 9 TGTGGCGAAGG 19  
Db 11 TGTGGCGAAGG 1  
  
RESULT 27  
ABC63144  
ID ABC63144 standard; DNA; 13 BP.  
XX  
AC ABC63144;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 63161 for detecting SNP TSC0016688.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 63161; 29pp + Sequence Listing; German.



XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 3 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19  
| | | | |  
Db 2 TTTGGCGAAGG 12

RESULT 28  
ABH65141/c  
ID ABH65141 standard; DNA; 13 BP.

AC ABH65141;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 265118 for detecting SNP TSC0064243.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB0000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

PS Claim 1; SEQ ID NO 265118; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 13 BP; 2 A; 6 C; 1 G; 4 T; 0 U; 0 Other;  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19  
| | | | |  
Db 12 TGTGACGAAGG 2

RESULT 29  
ABC53131/c  
ID ABC53131 standard; DNA; 13 BP.

XX ABC53131;

DT 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 53148 for detecting SNP TSC0014679.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB0000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

PS Claim 1; SEQ ID NO 53148; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

SQ Sequence 13 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 1 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19  
| | | | |  
Db 12 TGTGCGAAGG 2

RESULT 30



ABF03962  
ID ABF03962 standard; DNA; 13 BP.  
XX  
AC ABF03962;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 103959 for detecting SNP TSC0025999.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 103959; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 0 A; 2 C; 5 G; 5 T; 0 U; 1 Other;  
CC  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 0 A; 2 C; 5 G; 5 T; 0 U; 1 Other;  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGTGT 11  
Db 1 GGTCGCGTGT 11  
RESULT 31  
ABF16244  
ID ABF16244 standard; DNA; 13 BP.  
XX  
AC ABF16244;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 116241 for detecting SNP TSC0029111.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX

OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 116241; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 1 Other;  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 9 TGTGGCGAAGG 19  
Db 2 TGTGGTGAAGG 12  
RESULT 32  
ABC53130  
ID ABC53130 standard; DNA; 13 BP.  
XX  
AC ABC53130;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 53147 for detecting SNP TSC0014679.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 53147; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 1 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
Db 2 TGTGGCGAAGG 12  
  
RESULT 33  
ABF04975/c  
ID ABF04975 standard; DNA; 13 BP.  
XX  
AC ABF04975;  
XX  
XX 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 104972 for detecting SNP TSC0026284.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 104972; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
Db 13 TGTGGAGAAGG 3  
  
RESULT 34  
ABH19540  
ID ABH19540 standard; DNA; 13 BP.  
XX  
AC ABH19540;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 219517 for detecting SNP TSC0053391.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 219517; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19  
          ||||| |||||  
Db 2 TGTGGGGAAGG 12

RESULT 35  
ABH19543/c  
ID ABH19543 standard; DNA; 13 BP.  
XX  
AC ABH19543;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 219520 for detecting SNP TSC0053391.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 219520; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19  
          ||||| |||||  
Db 12 TGTGGAGAAGG 2

RESULT 36  
ABF16163/c  
ID ABF16163 standard; DNA; 13 BP.  
XX  
AC ABF16163;  
XX

DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 116160 for detecting SNP TSC0029108.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 116160; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 8 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19  
          ||||| |||||  
Db 12 TGTGGCGGAGG 2

RESULT 37  
ABH19542  
ID ABH19542 standard; DNA; 13 BP.  
XX  
AC ABH19542;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 219519 for detecting SNP TSC0053391.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB0000713.  
PF 07-APR-2000; 2000DE-01019173.  
PR (EPIG-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 219519; 29pp + Sequence Listing; German.  
PS This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 0 C; 6 G; 4 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
Db 2 TGTGGAGAAGG 12  
  
RESULT 38  
ABF04974  
ID ABF04974 standard; DNA; 13 BP.  
XX  
AC ABF04974;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 104971 for detecting SNP TSC0026284.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.  
XX Claim 1; SEQ ID NO 104971; 29pp + Sequence Listing; German.  
PS This invention describes novel oligonucleotide primers or peptide nucleic  
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
Db 1 TGTGGAGAAGG 11  
  
RESULT 39  
ABC63145/c  
ID ABC63145 standard; DNA; 13 BP.  
XX  
AC ABC63145;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 63162 for detecting SNP TSC0016688.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 63162; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX



CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 6 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 9 TGTGGCGAAGG 19  
Db 12 TTTGGCGAAGG 2  
  
RESULT 40  
ABF16162  
ID ABF16162 standard; DNA; 13 BP.  
XX  
AC ABF16162;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 116159 for detecting SNP TSC0029108.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
AC ABF16162;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 116159 for detecting SNP TSC0029108.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 116159; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 1 A; 1 C; 8 G; 3 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 9 TGTGGCGAAGG 19  
Db 2 TGTGGCGGAGG 12

RESULT 41  
ABF16245/c  
ID ABF16245 standard; DNA; 13 BP.  
XX  
AC ABF16245;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 116242 for detecting SNP TSC0029111.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 116242; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 9 TGTGGCGAAGG 19  
Db 12 TGTGCTGAAGG 2  
  
RESULT 42  
ABC76993/c  
ID ABC76993 standard; DNA; 13 BP.  
XX  
AC ABC76993;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 77010 for detecting SNP TSC0019655.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;



KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 77010; 29pp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 1 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GTCGCGCTGTG 12  
Db 12 GTCGCGTGTG 2  
  
RESULT 43  
ABC76992  
ID ABC76992 standard; DNA; 13 BP.  
XX  
AC ABC76992;  
XX  
XX 21-FEB-2002 (first entry)  
DT  
XX  
DE Oligonucleotide SEQ ID NO 77009 for detecting SNP TSC0019655.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX

PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 77009; 29pp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 1 A; 2 C; 5 G; 4 T; 0 U; 1 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GTCGCGCTGTG 12  
Db 2 GTCGCGTGTG 12  
  
RESULT 44  
ABC86974  
ID ABC86974 standard; DNA; 13 BP.  
XX  
AC ABC86974;  
XX  
XX 21-FEB-2002 (first entry)  
DT  
XX  
DE Oligonucleotide SEQ ID NO 86991 for detecting SNP TSC0021858.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX  
XX 18-OCT-2001.  
PD  
XX  
XX 06-APR-2001; 2001WO-IB0000713.  
PF  
XX  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
XX Claim 1; SEQ ID NO 86991; 29pp + Sequence Listing; German.  
PS  
XX  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 2 A; 0 C; 7 G; 4 T; 0 U; 0 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
Db 3 TGTGGGGAAGG 13  
||||| |||||  
  
RESULT 45  
ABH19541/c  
ID ABH19541 standard; DNA; 13 BP.  
XX  
AC ABH19541;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 219518 for detecting SNP TSC0053391.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 219518; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
Db 12 TGTGGGGAAGG 2  
||||| |||||  
  
RESULT 46  
ABF03963/c  
ID ABF03963 standard; DNA; 13 BP.  
XX  
AC ABF03963;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 103960 for detecting SNP TSC0025999.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 103960; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 5 C; 2 G; 0 T; 0 U; 1 Other;  
  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTGCGCTGT 11  
Db 13 GGTGCGGTTGT 3  
||||| |||||  
  
RESULT 47  
ABH65140  
ID ABH65140 standard; DNA; 13 BP.

XX ABH65140;  
AC  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 265117 for detecting SNP TSC0064243.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
XX WO200177384-A2.  
PN  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 265117; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
XX  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
||| |||||  
Db 2 TGTGACGAAGG 12  
  
RESULT 48  
ABH32687/c  
ID ABH32687 standard; DNA; 13 BP.  
XX  
AC ABH32687;  
XX  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 232664 for detecting SNP TSC0056734.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX

PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 232664; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 1 A; 8 C; 1 G; 3 T; 0 U; 0 Other;  
XX

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
||| |||||  
Db 12 TGGGCGAAGG 2  
  
RESULT 49  
ADZ85140  
ID ADZ85140 standard; DNA; 13 BP.  
XX  
AC ADZ85140;  
XX  
DT 28-JUL-2005 (first entry)  
XX  
DE MODY 3 diabetes-associated probe, SEQ ID 16.  
XX  
KW Analyte detection; microarray; probe; ss; diabetes.  
XX  
OS Unidentified.  
XX  
PN US2005112677-A1.  
XX  
PD 26-MAY-2005.  
XX  
PF 22-NOV-2004; 2004US-00994626.  
XX  
PR 22-NOV-2003; 2003KR-00083356.  
XX  
PA (SHIM/) SHIM J.  
XX  
PI Shim J;  
XX  
DR WPI; 2005-403357/41.  
XX  
PT Substrate for use in optically detecting target materials, comprises an

PT oxide layer having thickness that may vary to wavelength of excitation  
PT light used.  
XX  
PS Example 1; SEQ ID NO 16; 20pp; English.  
XX The present invention relates to a novel substrate having an oxide layer,  
CC which is useful in optically detecting a target material. The thickness  
CC of the oxide layer may vary to the wavelength of excitation light used.  
CC Also claimed is a method for detecting a target material, comprising  
CC immobilizing a probe material on a substrate, reacting the immobilized  
CC probe material and the target material, illuminating a reaction product  
CC with excitation light, and measuring light emitted from the reaction  
CC product by the excitation light. In an example from the invention,  
CC microarrays were fabricated by forming fused silica (SiO2) layers on  
CC silicon wafers, followed by linkage with a coupling agent and  
CC immobilization of oligonucleotide probes. The microarrays were then  
CC incubated with labeled oligonucleotides and exposed to excitation light,  
CC and light emitted from the target oligonucleotides was measured, to  
CC evaluate the intensity of detected signals with respect to the thickness  
CC of the SiO2 layers. ADZ85128-ADZ85203, MODY 3 diabetes-associated probes  
CC used with the target sequence of human glyceraldehyde-3-phosphate  
CC dehydrogenase (GAPDH), were used to show that when a target  
CC oligonucleotide is detected using a microarray including a substrate with  
CC an oxide layer a good signal is obtained compared to that with no oxide  
CC layers.  
XX  
SQ Sequence 13 BP; 0 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 46;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 3 TCGCGCTGTGG 13  
|| |||||  
Db 3 TCCCGCTGTGG 13  
RESULT 50  
AAT94476/c  
ID AAT94476 standard; DNA; 10 BP.  
XX  
AC AAT94476;  
XX  
DT 03-MAR-1998 (first entry)  
XX  
DE Human Fchd540 gene reverse PCR primer.  
XX  
KW Fchd540 gene; differential expression; endothelial cell; human;  
KW shear stress; cardiovascular disease; atherosclerosis; ischaemia;  
KW reperfusion; hypertension; restenosis; arterial inflammation; therapy;  
KW diagnosis; drug screening; marker; PCR; primer; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO9730065-A1.  
XX  
PD 21-AUG-1997.  
XX  
PF 14-FEB-1997; 97WO-US002291.  
XX  
PR 16-FEB-1996; 96US-0011787P.  
PR 13-FEB-1997; 97US-00799910.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Palb DA;  
XX  
DR WPI; 1997-424966/39.  
XX  
PT New genes differentially expressed in cardiovascular disease - used for  
PT diagnosis, drug screening and treatment of cardiovascular disease, e.g.  
PT atherosclerosis, restenosis, hypertension, etc.

XX Example 6.1.3; Page 120; 163pp; English.  
XX  
CC This oligonucleotide comprises a reverse primer specific to the novel  
CC human fchd540 gene (see AAT94468) that is up-regulated in endothelial  
CC cells subjected to shear stress. It was used with primer for-T11XC in a  
CC differential display paradigm used to detect genes that are  
CC differentially expressed in endothelial cells under fluid shear stress.  
CC Shear stress is thought to be responsible for the prevalence of  
CC atherosclerotic lesions in areas of unusual circulatory flow. The novel  
CC fchd540 gene can be used in the diagnosis and treatment of cardiovascular  
CC disease  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 GTGGCGAAG 18  
|||||  
Db 10 GTGGCGAAG 2  
RESULT 51  
AAV34958/c  
ID AAV34958 standard; DNA; 10 BP.  
XX  
AC AAV34958;  
XX  
DT 13-OCT-1998 (first entry)  
XX  
DE Synthetic Agaricus bisporus RAPD primer.  
XX  
KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.  
XX  
OS Synthetic.  
XX  
PN WO9821975-A1.  
XX  
PD 28-MAY-1998.  
XX  
PF 19-NOV-1996; 96WO-US018686.  
XX  
PR 19-NOV-1996; 96WO-US018686.  
XX  
PA (AMYC-) AMYCEL INC.  
XX  
PI Loftus MG, Lodder SC, Legg EJ;  
XX  
DR WPI; 1998-312054/27.  
XX  
PT New strains of Agaricus bisporus with improved cap whiteness - compared  
PT with the U1 strain but retaining other desirable features of this strain.  
XX  
PS Disclosure; Page 10; 26pp; English.  
XX  
CC The sequence is that of an RAPD (random amplified DNA) primer which was  
CC used in the isolation of an Agaricus bisporus mushroom strain which has  
CC whiter caps, less scaling than known strains, particularly for mushrooms  
CC produced in the first break, so it is more valuable (suitable for  
CC marketing fresh rather than canning). It also retains the desirable  
CC characteristics (good cap shape and shelf life, thick stem and veil) of  
CC the U1 strain  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 GTGGCGAAG 18  
|||||



Db 10 GTGGCGAAG 2

RESULT 52  
AAZ58826/c  
ID AAZ58826 standard; DNA; 10 BP.  
XX AC AAZ58826;  
XX DT 25-APR-2000 (first entry)  
XX DE Human MUC11 gene amplifying primer.  
XX KW Mucin; MUC11; MUC12; human; chromosome 7q22; epithelial inflammation;  
KW Crohn's disease; ulcerative colitis; asthma; chronic bronchitis;  
KW colorectal cancer; cystic fibrosis; inflammatory bowel disease;  
KW breast cancer; PCR primer; ss.  
XX OS Homo sapiens.  
XX PN WO200004142-A1.  
XX PD 27-JAN-2000.  
XX PF 16-JUL-1999; 99WO-AU000579.  
XX PR 16-JUL-1998; 98AU-00004708.  
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.  
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.  
XX PI Williams SJ, Antalis TM, McGuckin MA, Gotley DC;  
XX WPI; 2000-182416/16.  
XX DR Novel MUC nucleic acid corresponding to mucin gene, useful for treating  
PT associated disease conditions e.g. colorectal, breast cancer, cystic  
PT fibrosis and inflammatory bowel disease.  
XX Example 5; Page 38; 103pp; English.  
XX CC The invention provides mucin genes (MUC11 and MUC12) located on human  
CC chromosome 7q22. The mucin genes or its portion is used in detecting  
CC polymorphism, mutation, deletion, truncation and expansion in the gene or  
CC its gene transcript. Pharmaceutical compositions and gene therapy  
CC constructs comprising the mucin genes are used for treating disease  
CC conditions associated with aberrant Mucin expression, altered properties  
CC of mucus or epithelial inflammatory processes involving Mucins like  
CC Crohn's disease, ulcerative colitis, asthma, chronic bronchitis and  
CC colorectal cancer, cystic fibrosis, inflammatory bowel disease and breast  
CC cancer. The mucin genes and the polypeptides are used for determining  
CC these diseases or their predisposition. The MUC11 and MUC12 polypeptides  
CC are used for preparing antagonist and antibodies. The present sequence  
CC represents a primer for amplifying the human MUC11 gene  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 53  
AAZ50718/c  
ID AAZ50718 standard; DNA; 10 BP.  
XX AC AAZ50718;  
XX DT 31-MAY-2000 (first entry)

XX DE Reverse primer for differential display analysis of fchd540 gene.  
XX KW PCR primer; fingerprint gene; human; cardiovascular disease;  
KW oncogenic disorder; diabetic retinopathy; fibroproliferative disorder;  
KW arterosclerosis; TGF-beta signalling pathway; pancreatic cancer;  
KW angiogenesis; TGF; Transforming growth factor; inflammation; fibrosis;  
KW tumour growth; vascularisation; cytostatic; antidiabetic;  
KW ophthalmological; ss.  
XX OS Homo sapiens.  
XX PN WO200006206-A1.  
XX PD 10-FEB-2000.  
XX PF 30-JUL-1999; 99WO-US017394.  
XX PR 30-JUL-1998; 98US-00126640.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Falb DA;  
XX DR WPI; 2000-205414/18.  
XX PT Identifying substances for ameliorating symptoms of fibroproliferative  
PT diseases or oncogenic related disorders.  
XX PS Example; Page 126; 214pp; English.  
XX CC The patent discloses methods for the treatment and diagnosis of  
CC cardiovascular diseases by novel human genes (fingerprint genes) which  
CC are differentially expressed in different cardiovascular disease states.  
CC Compositions which can modify TGF-beta signalling pathway are identified  
CC by screening. These are used therapeutically to treat fibroproliferative  
CC and oncogenic disorders, especially TGF (Transforming growth factor) -  
CC beta related disorders, including diabetic retinopathy, inflammation,  
CC arterosclerosis, pancreatic cancer, angiogenesis, fibrosis, tumour  
CC growth and vascularisation. The present sequence is the reverse PCR  
CC primer used to study the differential display of fingerprint gene,  
CC fchd540. Differential display was performed on endothelial cells  
CC subjected to laminar shear stress compared with static control. fchd540  
CC was detected as up-regulated under shear stress  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2

RESULT 54  
ABL60664/c  
ID ABL60664 standard; DNA; 10 BP.  
XX AC ABL60664;  
XX DT 27-AUG-2002 (first entry)  
XX DE Panax species genomic DNA RAPD analysis primer OPC-20.  
XX KW Herbal; polymorphism; medicine; SCAR; rapid amplified polymorphic DNA;  
KW plant; RAPD; primer; ss.  
XX OS Panax sp.  
XX PN WO200236805-A2.  
XX



PD 10-MAY-2002.  
XX  
PF 17-OCT-2001; 2001WO-US032602.  
XX  
PR 03-NOV-2000; 2000US-00706228.  
XX  
PA (UYCH-) UNIV CHINESE HONG KONG.  
XX  
PI Shaw P, Wang J, But PP, Ha W, Yau FCF;  
XX WPI; 2002-471504/50.  
DR  
XX Determining if an herbal material is of a Mirabilis jalapa or a Panax  
PT species, e.g. P. ginseng, or P. quinquefolius, comprises amplifying a  
PT polymorphic region of an extracted nucleic acid sequence using several  
PT primers.  
XX  
PS Example 3; Page 19; 50pp; English.  
XX  
CC The invention relates to determining whether a given herbal material is  
CC that of Panax ginseng, P. quinquefolius, P. notoginseng (Burk), P.  
CC japonicus major, P. japonicus, P. trifolius, Mirabilis jalapa L. or P.  
CC acinosa Roxb. The method involves amplifying a polymorphic region of the  
CC extracted nucleic acid using at least 2 different oligonucleotide primers  
CC that flank the polymorphic region. The method is useful for identifying  
CC ingredients in traditional Chinese medicines, and distinguishing them  
CC from common adulterants or ersatz ingredients, and for identifying an  
CC unknown sample as one of several possible known species, each  
CC characterized by the presence of a SCAR (sequence characterised amplified  
CC regions) absent from the others. The present sequence represents a primer  
CC for amplifying Pinax species genomic DNA, used for identification of  
CC polymorphic regions by RAPD (rapid amplified polymorphic DNA)  
CC fingerprinting  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2  
|||||  
RESULT 55  
ABV69628  
ID ABV69628 standard; cDNA; 11 BP.  
XX  
AC ABV69628;  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX Human skin EST 7414.  
DE  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX

DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 232; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 47.4%; Score 9; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGG 13  
Db 3 GCGCTGTGG 11  
|||||  
RESULT 56  
ABI04019/c  
ID ABI04019 standard; DNA; 12 BP.  
XX  
AC ABI04019;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 303992 for detecting SNP TSC0020735.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 303992; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,

CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 12 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 47.4%; Score 9; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17  
|||||  
Db 10 TGTGGCGAA 2

RESULT 57  
AAV65455/C  
ID AAV65455 standard; DNA; 12 BP.

XX AAV65455;

DT 08-DEC-1998 (first entry)

XX Primer pBS800-23J used in the course of the invention.

DE Nucleic acid determination; hybridisation; probe; mismatch; SBH;  
XX sequencing by hybridisation; PCR primer; ss.

OS Synthetic.

XX JP10243785-A.

XX 14-SEP-1998.

PF 03-MAR-1997; 97JP-00047821.

PR 03-MAR-1997; 97JP-00047821.

XX (BUNS-) BUNSHI BIOTONICS KENKYUSHO KK.

XX WPI; 1998-549781/47.

XX Determination of nucleic acid base sequence - is sensitive and rapid  
PT without mismatch in hybridisation as in sequencing by hybridisation  
PT method.

XX Example; Page 9; 20pp; Japanese.

CC Sequences shown in AAV65401 to AAV65580 represent PCR primers used in the  
CC course of the invention which provides a method for determining a single  
CC stranded nucleic acid base sequence. The method comprises separation of  
CC 4k oligonucleotide probe as a primer from all combinations of k base  
CC sequences and hybridising the probe and the nucleic acid to be tested.  
CC The probe is elongated to make a primer using the nucleic acid to be  
CC tested as a template and the elongated primer is determined. The base  
CC sequence of the nucleic acid is determined based on the elongated amount.  
CC The method allows sensitive and rapid determination of nucleic acid base  
CC sequence without mismatch in hybridisation as in sequencing by  
CC hybridisation (SBH) method

XX Sequence 12 BP; 1 A; 4 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CGCTGTGGCGAA 17  
|||||  
Db 12 CGCTGGCGCGAA 1

RESULT 58  
ABI59311/c  
ID ABI59311 standard; DNA; 12 BP.

XX ABI59311;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 359284 for detecting SNP TSC0008283.

DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB0000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX Claim 1; SEQ ID NO 359284; 29pp + Sequence Listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 12 BP; 3 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGCG 15  
|||||  
Db 12 CGCGTGTGGAG 1

RESULT 59  
ABI24865/c  
ID ABI24865 standard; DNA; 12 BP.

XX ABI24865;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 324838 for detecting SNP TSC0032252.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
PT  
XX Claim 1; SEQ ID NO 324838; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 7 GCTGTGCGGAAG 18  
Db 12 GATGTGCGGAG 1  
  
RESULT 60  
ABH89194  
ID ABH89194 standard; DNA; 12 BP.  
XX  
AC ABH89194;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 289187 for detecting SNP TSC0013829.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX

PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 289187; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 0 Other;  
  
Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGCGGA 16  
Db 1 GGGTTGTGCGGA 12  
  
RESULT 61  
ABX10162  
ID ABX10162 standard; cDNA; 12 BP.  
XX  
AC ABX10162;  
XX  
DT 27-JAN-2003 (first entry)  
XX  
DE Human TIGR/Myocilin variant cDNA deletion 3' flank #5.  
XX  
KW Human; ss; TIGR; MYOC; Myocilin; Glaucoma; blindness;  
KW trabecular meshwork inducible glucocorticoid responsive protein;  
KW retinal degenerative disease; RDD; retinitis pigmentosa;  
KW macular degeneration; Usher syndrome; cardiovascular disease;  
KW congenital heart disease; myocardial ischaemia; stroke;  
KW acute endocarditis; hypertensive heart disease; arrhythmia;  
KW arteriosclerotic heart disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200282969-A2.  
XX  
PD 24-OCT-2002.  
XX  
PF 11-DEC-2001; 2001WO-US048622.  
XX  
PR 05-APR-2001; 2001US-0281442P.  
PR 23-JUL-2001; 2001US-0306889P.  
XX  
PA (KONG/) KONG T H.  
XX  
PI Kong TH;  
XX  
DR WPI; 2003-058597/05.  
XX  
PT Determining the presence or the risk of having glaucoma, retinal  
PT degenerative or cardiovascular diseases in a subject, comprises

PT generating transcriptional or translational profiles based on myocilin  
PT nucleic acids and proteins.  
XX  
PS Disclosure; Fig 4c; 55pp; English.  
XX  
CC The invention relates to determining whether a subject has or is at risk  
CC of developing glaucoma, retinal degenerative disease, or a cardiovascular  
CC disease, comprises generating a transcriptional or translational profile  
CC (i.e. 'fingerprint') in the subject or in a sample obtained from the  
CC subject, based on the expression of the different myocilin (MYOC, also  
CC known as trabecular meshwork inducible glucocorticoid responsive protein,  
CC TIGR) mRNA species or polypeptide forms, where a difference in the  
CC profile relative to that in a normal subject indicates that the subject  
CC has or is at risk of developing the above-mentioned diseases. Also  
CC included are: (1) a method for establishing MYOC genetic population  
CC profile in a population of individuals having glaucoma, retinal  
CC degenerative disease, or a cardiovascular disease; (2) a method for  
CC pharmacogenomically selecting a therapy to administer to an individual  
CC having glaucoma, retinal degenerative disease, or a cardiovascular  
CC disease, comprising determining MYOC genetic profile of an individual and  
CC comparing the individual's MYOC genetic profile to MYOC genetic  
CC population profile, to select a therapy for administration to the  
CC individual; and a kit for determining whether a subject has or is likely  
CC to develop glaucoma, retinal degenerative disease, or a cardiovascular  
CC disease, comprising a probe or primer which hybridises to the MYOC  
CC nucleic acid, or an antibody or peptide probe capable of specifically  
CC binding to the novel MYOC polypeptide(s), and instructions for use. The  
CC method is useful for the prognosis and/or diagnosis of glaucoma, retinal  
CC degenerative diseases (RDD) or cardiovascular diseases (e.g. blindness,  
CC retinitis pigmentosa, macular degeneration, Usher syndrome, congenital  
CC heart disease, myocardial ischaemia, stroke, acute endocarditis,  
CC hypertensive heart disease, arrhythmia and arteriosclerotic heart  
CC disease), and in screening assays for the identification of therapeutics  
CC and the evaluation of their effectiveness for treating the above-  
CC mentioned diseases in a subject. The present sequence represents the 3'  
CC flanking sequence surrounding the deletion present in a MYOC cDNA variant  
XX  
SQ Sequence 12 BP; 0 A; 4 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGCC 14  
||| ||||| |  
Db 1 TCGGGCTGTGCC 12

RESULT 62  
ADW86997  
ID ADW86997 standard; DNA; 12 BP.  
XX  
AC ADW86997;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE Protein labelling method sequence #199.  
XX  
KW DNA purification; protein engineering; diagnosis; ss.  
XX  
OS Unidentified.  
XX  
PN WO2004113530-A1.  
XX  
PD 29-DEC-2004.  
XX  
PF 18-JUN-2004; 2004WO-JP008953.  
XX  
PR 18-JUN-2003; 2003JP-00173634.  
XX  
PA (MITU ) MITSUBISHI CHEM CORP.  
XX  
PI Naka D, Nakano H, Shiratori M, Kobayashi T, Suzuki K;

PI Hashimoto H, Sasaki T;  
XX  
DR WPI; 2005-075248/08.  
XX  
PT Novel polynucleotide having ability to increase labeling efficiency of  
PT labeling compound, useful for synthesizing labeled protein in presence of  
XX labeling compound.  
PS Disclosure; Fig 20; 140pp; Japanese.  
XX  
CC The invention relates to a polynucleotide (I) for synthesizing labeled  
CC protein and having ability to increase labeling efficiency of labeling  
CC compound, where protein is produced by adding labeling compound to 3',  
CC terminal of sequence encoding target protein of gene template, where  
CC labeling compound has label portion and acceptor portion having compound  
CC capable of binding to C-terminus of label portion and translating gene  
CC template in presence of labeled compound. (I) is useful for producing a  
CC labeling protein, which involves preparing a gene template by adding (I)  
CC to the 3'-terminal of base sequence encoding the target protein,  
CC translating the gene template in the presence of the labeling compound  
CC containing acceptor portion and label portion, and obtaining protein  
CC synthesized in the translation system. The base sequence encoding the  
CC target protein either contains the termination codon or does not contain  
CC the termination codon. The labeling compound is added after the  
CC initiation of the translation. The labeled protein (Lp1) is useful in a  
CC performance-analysis of a protein, which involves contacting the test  
CC substance with (Lp1), and analyzing the interaction between the protein  
CC and the test substance. (I) has the ability to increase labeling  
CC efficiency of a labeling compound and thus effectively produces labeled  
CC protein. This sequence corresponds to a sequence used in the method of  
CC the invention.  
XX  
SQ Sequence 12 BP; 2 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 46.3%; Score 8.8; DB 1; Length 12;  
Best Local Similarity 83.3%; Pred. No. 68;  
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 GCTGTGCGGAAG 18  
||| ||||| |  
Db 1 GCGGCGGCGAAG 12

RESULT 63  
AAZ77822/c  
ID AAZ77822 standard; DNA; 10 BP.  
XX  
AC AAZ77822;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:250.

KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.



PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 71; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GGTCGCGCTG 10  
|| |||||  
Db 10 GGGCGGCTG 1  
  
RESULT 64  
AAZ77845  
ID AAZ77845 standard; DNA; 10 BP.  
XX  
AC AAZ77845;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:273.  
XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
(GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 72; 130pp; English.  
XX



CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15  
| | | | | | | |  
Db 1 CGCTGTGGGG 10

RESULT 65  
AAZ84021  
ID AAZ84021 standard; DNA; 10 BP.  
AC AAZ84021;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #3255.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 146; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoded by the transcripts for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19  
| | | | | | | |  
Db 1 GTGGCCAAGG 10

RESULT 66  
AAZ85539/C  
ID AAZ85539 standard; DNA; 10 BP.  
XX  
AC AAZ85539;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #4773.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA

```
XX      (GENZ ) GENZYME CORP.
PA      (ROBE/) ROBERTS B L.
PA      (SHAN/) SHANKARA S.
XX
XX      Roberts BL,  Shankara S;
XX
XX      WPI; 2000-106079/09.
XX
XX      Isolated polynucleotides differentially expressed between metastatic and
PT      non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT      treatment of cancer.
XX
XX      Claim 1; Page 186; 219pp; English.
XX
XX      AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC      that are preferentially transcribed in the metastatic breast tumour
CC      tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC      preferentially transcribed in the primary or non-metastatic breast tumour
CC      tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC      transcripts can be used for diagnosis, prognosis, monitoring and
CC      treatment of breast cancer, particularly where metastatic. Diagnosis is
CC      by standard immunoassays or hybridisation/amplification reactions.
CC      Compounds that modulate expression of the transcripts are potentially
CC      useful for treatment of (metastatic) breast cancer, while promoters from
CC      the transcripts are used to direct expression, in selected cell types, of
CC      e.g. therapeutic genes (also ribozymes or antisense sequences),
CC      particularly an antigen-encoding sequence for use in gene or cell-based
CC      vaccines. Polypeptides encoded by the transcripts are also useful in
CC      antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC      agents. Host cells that produce the polypeptides can be used to expand
CC      and isolate populations of educated, antigen-specific immune effector
CC      cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC      immunotherapy
XX
XX      Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
SQ
      Query Match      44.2%; Score 8.4; DB 1; Length 10;
      Best Local Similarity 90.0%; Pred. No. 1e+02;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GCGCTGTGGC 14
      ||||| |||
Db      10 GCGCTGAGGC 1

RESULT 67
AAZ84999/c
ID      AAZ84999 standard; DNA; 10 BP.
XX
XX      AAZ84999;
XX
XX      07-APR-2000 (first entry)
XX
XX      Metastatic breast tumour cell downregulated transcript tag #4233.
DE
XX      Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW      non-metastatic breast tumour tissue; gene therapy; anticancer;
KW      antimetastatic; vaccine; diagnosis; ss.
XX
XX      Homo sapiens.
OS
XX      WO9965928-A2.
PN
XX      23-DEC-1999.
PD
XX      18-JUN-1999; 99WO-US013647.
PF
XX      19-JUN-1998; 98US-0089853P.
PR
XX      19-JUN-1998; 98US-0089997P.
PR
XX      19-JUN-1998; 98US-0090039P.
PR
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PR      19-JUN-1998; 98US-0090040P.
PR      19-JUN-1998; 98US-0090041P.
XX
XX      (GENZ ) GENZYME CORP.
PA      (ROBE/) ROBERTS B L.
PA      (SHAN/) SHANKARA S.
XX
XX      Roberts BL,  Shankara S;
XX
XX      WPI; 2000-106079/09.
XX
XX      Isolated polynucleotides differentially expressed between metastatic and
PT      non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT      treatment of cancer.
XX
XX      Claim 1; Page 171; 219pp; English.
XX
XX      AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC      that are preferentially transcribed in the metastatic breast tumour
CC      tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC      preferentially transcribed in the primary or non-metastatic breast tumour
CC      tissue (i.e. are downregulated in the primary or non-metastatic breast tumour
CC      tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC      transcripts can be used for diagnosis, prognosis, monitoring and
CC      treatment of breast cancer, particularly where metastatic. Diagnosis is
CC      by standard immunoassays or hybridisation/amplification reactions.
CC      Compounds that modulate expression of the transcripts are potentially
CC      useful for treatment of (metastatic) breast cancer, while promoters from
CC      the transcripts are used to direct expression, in selected cell types, of
CC      e.g. therapeutic genes (also ribozymes or antisense sequences),
CC      particularly an antigen-encoding sequence for use in gene or cell-based
CC      vaccines. Polypeptides encoded by the transcripts are also useful in
CC      antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC      agents. Host cells that produce the polypeptides can be used to expand
CC      and isolate populations of educated, antigen-specific immune effector
CC      cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC      immunotherapy
XX
XX      Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
SQ
      Query Match      44.2%; Score 8.4; DB 1; Length 10;
      Best Local Similarity 90.0%; Pred. No. 1e+02;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GGTCGCGCTG 10
      || ||||| |
Db      10 GGGCGCGCTG 1

RESULT 68
AAZ85922
ID      AAZ85922 standard; DNA; 10 BP.
XX
XX      AAZ85922;
XX
XX      07-APR-2000 (first entry)
XX
XX      Metastatic breast tumour cell downregulated transcript tag #5156.
DE
XX      Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW      non-metastatic breast tumour tissue; gene therapy; anticancer;
KW      antimetastatic; vaccine; diagnosis; ss.
XX
XX      Homo sapiens.
OS
XX      WO9965928-A2.
PN
XX      23-DEC-1999.
PD
XX      18-JUN-1999; 99WO-US013647.
PF
XX      19-JUN-1998; 98US-0089853P.
PR
XX      19-JUN-1998; 98US-0089853P.
PR
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PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 195; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
Db 1 GTGGCGGAGG 10
|||||
|||||

RESULT 69
AAZ81487
ID AAZ81487 standard; DNA; 10 BP.
XX
AC AAZ81487;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #721.
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX WO9965928-A2.
PN
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
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XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 77; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15
Db 1 CGCTGTGGGG 10
|||||
|||||

RESULT 70
AAZ84108/C
ID AAZ84108 standard; DNA; 10 BP.
XX
AC AAZ84108;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3342.
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX Homo sapiens.
XX WO9965928-A2.
PN
XX
PD 23-DEC-1999.
```

XX 18-JUN-1999; 99WO-US013647.  
PF  
XX 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
XX WPI; 2000-106079/09.  
DR  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 148; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoded sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCTG 10  
Db ||| |||||  
10 GGTGGCGCTG 1  
  
RESULT 71  
AAH64063/c  
ID AAH64063 standard; cDNA; 10 BP.  
XX  
AC AAH64063;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 903.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX

PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX WPI; 2001-367706/38.  
DR  
XX New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 13; Page 59; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCTG 10  
Db ||| |||||  
10 GGGCGCGCTG 1  
  
RESULT 72  
AAF42948  
ID AAF42948 standard; DNA; 10 BP.  
XX  
AC AAF42948;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11087.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX



PS Example; Page 346; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

SQ

Query Match 44.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 TCGCGTGTG 12

DB 1 TCGTGTGTG 10

RESULT 73

AAAF41527

ID AAF41527 standard; DNA; 10 BP.

XX

AC AAF41527;

XX

DT 23-MAR-2001 (first entry)

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8266.

XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

PD 21-DEC-2000.

XX

PF 14-JUN-2000; 2000WO-US016223.

XX

XX

PR 16-JUN-1999; 99US-00335032.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Velculescu V, Vogelstein B, Kinzler K;

XX

DR WPI; 2001-061874/07.

XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 295; 419pp; English.

XX

CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

SQ

Query Match 44.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 8 CTGTGGCGAA 17

DB 1 CTGTGGTGAA 10

RESULT 74

ABL88334/c

ID ABL88334 standard; DNA; 10 BP.

XX

AC ABL88334;

XX

DT 20-MAY-2002 (first entry)

XX

DE Human CHRNE gene polymorphism detection primer, SEQ ID NO:68.

XX

KW Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNE;

KW chromosome 17p13-12; acetylcholine receptor; AChR;

KW neuromuscular junction; skeletal muscle; postnatal development;

KW congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;

KW genetic variant; single nucleotide polymorphism; SNP; gene therapy;

KW drug screening; primer extension; primer; ss.

XX

OS Homo sapiens.

XX

PN WO200198316-A2.

XX

PD 27-DEC-2001.

XX

PF 20-JUN-2001; 2001WO-US019835.

XX

PR 20-JUN-2000; 2000US-0212870P.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX



PI Amaro E, Bieglecki KM, Kliem SE, Koshy B, Tanguay DA;  
XX WPI; 2002-130787/17.  
DR  
XX Novel genetic variants of cholinergic receptor, nicotinic, epsilon  
PT polypeptide gene useful in studying expression and function of the  
PT protein, and for screening drugs to treat diseases e.g. congenital  
PT myasthenic syndrome.  
XX  
PS Claim 19; Page 15; 104pp; English.  
XX  
CC The invention relates to a method for haplotyping the cholinergic  
CC receptor, nicotinic, epsilon polypeptide (CHRNA) gene (AB08268) of an  
CC individual, and also describes 17 novel polymorphic sites within the  
CC human CHRNA gene. The CHRNA gene is located on chromosome 17p13-12 and  
CC contains 12 exons which encode a 493 amino acid protein (AB049112). The  
CC CHRNA protein is one of the 5 subunits of mammalian acetylcholine  
CC receptors (AChRs) found at neuromuscular junctions in juveniles and  
CC adults, and is essential for the normal postnatal development of skeletal  
CC muscle. Mutations in the CHRNA gene are associated with congenital  
CC myasthenic syndrome (CMS). CHRNA gene sequences can therefore be used in  
CC gene therapy. The CHRNA gene is also useful for studying the expression  
CC and function of CHRNA, and in expressing CHRNA protein for use in  
CC screening for candidate drugs to treat diseases related to CHRNA. The  
CC method of the invention is useful for haplotyping the CHRNA gene in an  
CC individual, and can also be used in pharmaceutical research to validate  
CC CHRNA as a candidate target for, and in design of clinical trials of  
CC candidate drugs for, treating a specific condition or disease  
CC predicted to be associated with CHRNA activity such as CMS. Polymorphisms  
CC in the target region may be determined by the use of allele-specific  
CC oligonucleotides (ASOs; AB08370-AB08320) as probes and primers, and by  
CC primer extension using oligonucleotide primers comprising sequences  
CC AB08371-AB08354. The CHRNA protein is useful for improving the  
CC efficiency and reliability of several steps in the discovery and  
CC development of drugs for treating diseases associated with CHRNA  
CC activity, and may be used to screen drugs which target CHRNA. Sequences  
CC AB08321-AB08354 represent sequences that are specifically claimed as  
CC components of primers used to detect polymorphisms in the CHRNA gene by  
CC primer extension  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAG 18  
Db 10 TGTGGCGAAG 1  
  
RESULT 75  
ABN87962  
ID ABN87962 standard; DNA; 10 BP.  
AC ABN87962;  
XX  
DT 12-AUG-2002 (first entry)  
XX  
DE Human GSR preferred oligonucleotide detection primer SEQ ID NO:81.  
XX  
KW Human; glutathione reductase; GSR; enzyme; haemolytic anaemia;  
KW gene therapy; antianaemic; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200242320-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 13-NOV-2001; 2001WO-US046473.  
XX  
PR 10-NOV-2000; 2000US-0247202P.

XX (GENA-) GENAISSANCE PHARM INC.  
PA Bieglecki KM, Sanchis A, Sausker EA, Sun X;  
XX WPI; 2002-471719/50.  
PI  
XX New genetic variants of Glutathione reductase isogenes, useful for  
PT improving efficiency and reliability in drug development for treating  
PT hemolytic anemia.  
XX  
PS Claim 16; Page 15; 137pp; English.  
XX  
CC The present invention describes genetic variants of the human glutathione  
CC reductase (GSR) gene (I). (I) has antianaemic activity and can be used in  
CC gene therapy. (I) can be used in screening for drugs targeting (I) that  
CC are useful for treating haemolytic anaemia. Methods from the present  
CC invention can be used: for improving the efficiency and reliability of  
CC several steps in the discovery and development of drugs for treating  
CC diseases associated with GSR activity; for haplotyping, which is also  
CC used by the pharmaceutical research scientist to validate GSR as a  
CC candidate target for treating a specific condition or disease predicted  
CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the  
CC design of clinical trials for treating a specific condition of disease  
CC associated with GSR activity; and for screening compounds targeting GSR.  
CC (I) is useful in studying the expression and function of GSR, and in  
CC expressing GSR protein for use in screening for candidate drugs to treat  
CC diseases related to GSR activity. (I) is also useful in studying the  
CC effect of the variation on the biological activity of GSR as well as on  
CC the binding affinity of candidate drugs targeting GSR for the treatment  
CC of haemolytic anaemia. The present sequence represents a preferred  
CC oligonucleotide detection primer for the human GSR gene, which is given  
CC in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGGC 14  
Db 1 GCGCTGTGGC 10  
  
RESULT 76  
ABV78444/c  
ID ABV78444 standard; cDNA; 10 BP.  
XX  
AC ABV78444;  
XX  
DT 29-NOV-2002 (first entry)  
XX  
DE Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:155.  
XX  
KW SAGE tag; serial analysis of gene expression; human; Th1 cell;  
KW activated T cell; T lymphocyte; immune response; expression pattern;  
KW preferential expression; immune disorder; EST; expressed sequence tag;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002186482-A.  
XX  
PD 02-JUL-2002.  
XX  
PF 19-DEC-2000; 2000JP-00385816.  
XX  
PR 19-DEC-2000; 2000JP-00385816.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-594261/64.

XX Human activated Th1 and Th2 cell expression gene group, useful for the  
PT diagnosis and treatment of Th1 and Th2-related diseases.  
XX  
PS Claim 19; Page 10; 60pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are expressed in activated human Th1  
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence  
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif  
CC lying nearest to the polyA region of cDNAs derived from a variety of  
CC genes. These tags serve to uniquely identify each transcript and can thus  
CC be used to analyse the pattern of gene expression in particular cell  
CC types. The invention also relates to proteins encoded by the genes  
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and  
CC inhibitors of the expression of groups of genes that are expressed in  
CC either or both the two cell types. Groups of genes expressed in Th1  
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1  
CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags  
CC representing 171 genes which are more highly expressed in Th1 cells  
CC compared with Th2 cells  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCTG 10  
Db 10 GGGCGCGCTG 1  
  
RESULT 77  
AAS97347/c  
ID AAS97347 standard; DNA; 10 BP.  
XX  
AC AAS97347;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human CRYBB1 gene ASO primer extension PCR primer 3' end #6.  
XX  
KW Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmological;  
KW cataract; allele specific oligonucleotide; ASO; ss; haplotype;  
KW genotyping; transgenic animal; PCR primer; primer extension.  
XX  
OS Homo sapiens.  
XX  
PN WO200185998-A1.  
XX  
PD 15-NOV-2001.  
XX  
PF 07-MAY-2001; 2001WO-US014715.  
XX  
PR 05-MAY-2000; 2000US-0202253P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Choi JY, Kazemi A, Kliem SE, Koshy B, Rounds E;  
XX WPI; 2002-062253/08.  
DR  
XX Novel polymorphic variants of crystallin, beta B1 useful in studying  
PT expression and function of the protein, useful for screening candidate  
PT drugs to treat diseases e.g. cataract.  
XX  
PS Claim 17; Page 13; 94pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising a sequence  
CC which is a polymorphic variant of a reference sequence for crystallin,  
CC beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment,  
CC where the polymorphic variant comprises a CRYBB1 isogene defined by a

CC haplotype from haplotypes 1-16 as given in the specification. Also  
CC included are a transgenic non-human animal transformed or transfected  
CC with the polymorphic variant, a computer system for storing and analysing  
CC polymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene  
CC which comprises the defined CRYBB1 isogenes, methods of determining an  
CC individuals haplotype or genotype as well as methods of determining the  
CC association of a particular haplotype with a disease or trait and a  
CC composition comprising at least one genotyping oligonucleotide  
CC (especially allele-specific oligonucleotides (ASO)) for detecting a  
CC polymorphism in the CRYBB1. The isogenes or haplotypes are useful for  
CC improving the efficiency and reliability of several steps in the  
CC discovery and development of drugs for treating diseases associated with  
CC CRYBB1 activity, e.g. cataract. and can also be used by the  
CC pharmaceutical research scientist to validate CRYBB1 as a candidate  
CC target for, and in design of clinical trials of candidate drugs for,  
CC treating a specific condition drugs or disease predicted to be associated  
CC with CRYBB1 activity. The ASOs are useful as probes and primers, and for  
CC assaying a polymorphism in the target region. The present sequence is the  
CC allele specific 3' end of a PCR primer used in primer extension  
CC experiment to detect polymorphisms in CRYBB1  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGGC 14  
Db 10 GCGCAGTGGC 1  
  
RESULT 78  
ABL45886  
ID ABL45886 standard; DNA; 10 BP.  
XX  
AC ABL45886;  
XX  
DT 26-APR-2002 (first entry)  
XX  
DE Human EDG6 gene allele specific primer extension oligo SEQ ID NO: 80.  
XX  
KW Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;  
KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;  
KW cytostatic; antiinflammatory; gene therapy; SNP;  
KW single nucleotide polymorphism; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200206446-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 17-JUL-2001; 2001WO-US022523.  
XX  
PR 17-JUL-2000; 2000US-0218727P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Kliem SE, Koshy B;  
XX WPI; 2002-171804/22.  
DR  
XX New genetic variants of endothelial differentiation, G-protein coupled  
PT receptor-6 gene for studying expression, function of the gene and  
PT expressing EDG6 protein for use in screening drugs to treat cancer,  
PT inflammation.  
XX  
PS Claim 18; Page 14; 111pp; English.  
XX  
CC The present invention provides the gene, protein and cDNA sequences of  
CC the human endothelial differentiation, G-protein coupled receptor 6  
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found

CC within the sequences. The sequences can be used in the identification of  
CC the haplotype of an individual, and in the treatment of cancer,  
CC angiogenesis and inflammation. The present sequence is an allele specific  
CC primer extension oligonucleotide for the EDG6 gene, which is found on  
CC chromosome 19p13.3  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGCTGTGGC 14  
|||  
Db 1 GCGCTGGGC 10

RESULT 79  
ABI99149/C  
ID ABI99149 standard; DNA; 10 BP.  
XX  
AC ABI99149;  
XX  
DT 27-FEB-2002 (first entry)  
XX  
DE Human PCDH2 ASO PCR primer SEQ ID NO 106.  
XX  
KW Human; PCDH2; protocadherin 2; haplotyping; polymorphic variant; SNP;  
KW single nucleotide polymorphism; cytostatic; cancer; chromosome 5q31;  
KW allele-specific oligonucleotide; ASO; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200194361-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 06-JUN-2001; 2001WO-US018321.  
XX  
PR 06-JUN-2000; 2000US-0209564P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Kliem SE, Koshy B, Tanguay DA;  
XX  
DR WPI; 2002-097928/13.  
XX

PT New protocadherin 2 (PCDH2) polymorphic variants and encoding genes,  
PT useful in expressing PCDH2 protein for screening candidate drugs to treat  
PT diseases related to PCDH2 activity.  
XX

PS Claim 18; Page 14; 127pp; English.  
XX  
CC The invention relates to haplotyping the protocadherin 2 (PCDH2) gene,  
CC comprising determining which of the haplotypes given in the specification  
CC defines one or both copies of the individual's PCDH2 gene. The  
CC polymorphisms are within a 30244 base pair sequence (ABA05413), fully  
CC defined in the specification. The polymorphic variants are useful in  
CC studying the expression and function of PCDH2, in expressing PCDH2  
CC protein for use in screening for candidate drugs to treat diseases such  
CC as cancer, related to PCDH2 activity, in studying the effect of the  
CC variation on the biological activity of PCDH2 and the binding affinity of  
CC candidate drugs targeting PCDH2. The haplotyping methods are useful in  
CC validating PCDH2 as a candidate target for treating a specific condition  
CC or disease predicted to be associated with PCDH2 activity or in the  
CC design of clinical trials of candidate drugs for treating a specific  
CC condition or disease associated with PCDH2 activity. The present sequence  
CC is that of a PCDH2 allele-specific oligonucleotide (ASO) PCR primer of  
CC the invention  
XX

SQ Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;  
Query Match 44.2%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 5 GCGCTGTGGC 14  
|||  
Db 10 GCGCTGTGGC 1

RESULT 80  
AAD52054  
ID AAD52054 standard; DNA; 10 BP.  
XX  
AC AAD52054;  
XX  
DT 02-MAY-2003 (first entry)  
XX  
DE Human CES2 gene polymorphism detecting primer #8.  
XX

KW Human; carboxylesterase 2; CES2; drug screening; antiaddictive; cancer;  
KW transgenic; gene therapy; polymorphism; cytostatic; primer; ss.  
XX

OS Homo sapiens.  
XX  
PN WO200290378-A2.  
XX  
PD 14-NOV-2002.  
XX

PF 09-MAY-2002; 2002WO-US014813.  
XX  
PR 09-MAY-2001; 2001US-0289886P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX

PI Gilson CR, Kazemi A, Russo DP;  
XX  
DR WPI; 2003-148336/14.  
XX

XX New genetic variants of human carboxylesterase 2 (CES2) gene having  
PT polymorphisms, useful for screening drugs for treating disorders  
PT associated with CES2 isogene activity e.g. cancer or substance  
PT abuse/addiction.  
XX

PS Claim 32; Page 15; 85pp; English.  
XX

CC The invention relates to genetic variants of human carboxylesterase 2  
CC (CES2) gene. Polymorphic variants of CES2 gene are useful in studying the  
CC expression and function of CES2, and in expressing CES2 proteins for use  
CC in screening candidate drugs to treat diseases associated with CES2  
CC activity, e.g. cancer or substance abuse/addiction. Establishing CES2  
CC haplotype or haplotype pair of an individual is useful for improving the  
CC efficiency and reliability of several steps in the discovery and  
CC development of drugs for treating diseases associated with CES2 activity.  
CC Haplotype information is useful in improving the efficiency and output of  
CC several steps in drug discovery and development process, including target  
CC validation, identifying lead compounds, and early phase clinical trials.  
CC The transgenic animals are useful for studying expression of the CES2  
CC isogenes in vivo, for in vivo screening and testing of drugs targeted  
CC against CES2 protein, and for testing the efficacy of the therapeutic  
CC agents and compounds. CES2 gene is used in gene therapy. The present  
CC sequence is a primer used for detecting human CES2 gene polymorphisms  
XX

SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CGCGCTGTGG 13  
|||  
Db 1 CGCGCTGGGG 10

RESULT 81

ACA94569  
ID ACA94569 standard; DNA; 10 BP.  
XX  
AC ACA94569;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DE DNA tag from human transcript repressed in adenomas/cancers #102.  
XX  
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;  
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;  
KW kidney proximal tubule.  
XX  
OS Homo sapiens.  
XX  
PN WO2003022863-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028518.  
XX  
PR 07-SEP-2001; 2001US-0317494P.  
PR 30-MAY-2002; 2002US-0383805P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Buckhaults P, Kinzler KW, Vogelstein B;  
XX  
XX WPI; 2003-313220/30.  
DR  
XX  
PT Detecting colorectal cancer in a subject, involves detecting macrophage  
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood  
PT of the subject.  
XX  
PS Disclosure; Page 29; 59pp; English.  
XX  
CC The invention relates to detecting CC (colorectal cancer e.g. colorectal  
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)  
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing  
CC amount of MIC or RDP detected to that in normal subjects, where an  
CC elevated amount of MIC or RDP in the subject is an indicator of CC in  
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting  
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP  
CC mRNA detected to that in normal subjects, where an elevated amount of MIC  
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)  
CC isolating epithelial cells from blood of a subject, isolating an mRNA  
CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP  
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in  
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where  
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicator  
CC of CC in the subject; (d) contacting blood or faeces of a subject, with  
CC an RDP substrate, detecting activity of RDP in the blood or faeces by  
CC detection of increased reaction product or decreased RDP substrate, and  
CC comparing the amount of activity of RDP in blood or faeces of the subject  
CC to that in normal subjects, where an elevated amount of activity of RDP  
CC in the blood or faeces of the subject is an indicator of CC in the  
CC subject; (e) administering to a subject an antibody which specifically  
CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is  
CC labeled with a moiety which is detectable from outside of the subject and  
CC detecting the moiety in the subject from outside of the subject, where an  
CC area of localisation of the moiety within the subject but outside the  
CC proximal tubules of the kidney identifies CC; or (f) administering to a  
CC subject a substrate for RDP, the substrate being labeled with a  
CC detectable moiety, isolating faeces or blood from the subject, and  
CC detecting in the faeces or blood RDP reaction product or RDP substrate  
CC with the detectable moiety, where increased product or decreased  
CC substrate in the faeces or blood indicates CC in the subject. The methods  
CC are useful for detecting colorectal cancer in a subject. The present  
CC sequence is a DNA tag derived from a human transcript whose expression is  
CC repressed in colorectal cancer or colorectal adenoma  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. NO. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 6 CGCTGTGGCG 15  
Db 1 CGCTGTGGG 10  
RESULT 82  
ADK13021  
ID ADK13021 standard; DNA; 10 BP.  
XX  
AC ADK13021;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human glioma endothelial marker (GEM) standard tag SEQ ID NO:199.  
XX  
KW glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;  
KW anticancer; antiglioma; immune response; cytostatic;  
KW multi-drug sensitive glioma; human; standard tag; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2004016758-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 15-AUG-2003; 2003WO-US025614.  
XX  
PR 15-AUG-2002; 2002US-0403390P.  
PR 01-APR-2003; 2003US-0458978P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Madden SI, Wang CJ, Cook BP, Lattera J, Walter K;  
XX  
XX WPI; 2004-247973/23.  
DR  
XX  
PT Diagnosing glioma by detecting expression product of any one of 255  
PT genes, glioma endothelial markers, in brain tissue sample suspected of  
PT being neoplastic, and comparing the expression with expression in normal  
PT brain tissue sample.  
XX  
PS Example 2; SEQ ID NO 199; 114pp; English.  
XX  
CC The present invention describes a method (M1) for aiding in the diagnosis  
CC of glioma. (M1) involves detecting an expression product of at least one  
CC gene (I) in a first brain tissue sample (T) suspected of being  
CC neoplastic, where (I) is chosen from any one of 255 genes (glioma  
CC endothelial markers (GEMs)) as given in specification, and comparing the  
CC expression of (I) in (T) with expression of (I) in a second normal brain  
CC tissue sample (R), where increased expression of (I) in (T) relative to  
CC (R), identifies (T) as likely to be neoplastic. Also described: (1)  
CC treating (M2) glioma involves contacting cells of the glioma with an  
CC antibody that specifically binds to a extracellular epitope; (2)  
CC identifying (M3) a test compound as potential anticancer or antiglioma  
CC drug involves contacting a test compound with the cell which expresses  
CC (I), monitoring an expression product of the at least one gene and  
CC identifying test compound as a potential anticancer drug if it decreases  
CC the expression of at least one gene; (3) identifying (M4) a test compound  
CC as potential anticancer or antiglioma drug involves contacting a test  
CC compound with the cell which expresses mRNA of at least one gene  
CC identified by a tag as described above, monitoring mRNA of the gene, and  
CC identifying the test compound as a potential anticancer drug if it  
CC decreases the expression of at least one gene; and (4) inducing (M5) an  
CC immune response to glioma involves administering to a mammal, a protein  
CC or (I). (I) have cytostatic activities, and can be used to trigger immune  
CC destruction of glioma cells, and as immune response inducers. (M1) is  
CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi



CC -drug sensitive glioma in a human. (M5) is useful for inducing an immune  
CC response to a glioma in a mammal having glioma or in a mammal who has had  
CC a glioma surgically removed. The present sequence represents a human GEM  
CC standard tag oligonucleotide, which is used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 1e+02;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15  
| | | | | | | | | |  
Db 1 CGCTGTGGGG 10

RESULT 83  
AAN20067/c  
ID AAN20067 standard; DNA; 11 BP.

XX AC AAN20067;

XX DT 25-MAR-2003 (revised)  
DT 21-SEP-1992 (first entry)

XX DE DNA primer for HLA-B locus.

XX KW DNA primer; HLA-B; ss.

XX OS Homo sapiens.

XX PN W08202060-A.

XX PD 24-JUN-1982.

XX PF 18-DEC-1980; 80US-00217643.

XX PR 18-DEC-1980; 80US-00217643.

XX PR 13-JUL-1983; 83US-00513524.

XX PR 31-MAR-1986; 86US-00846481.

XX PA (UYYA ) UNIV YALE.

XX PI Weissman SM, Pereira D, Sood A;

DR WPI; 1982-54906E/26.

XX PT Isolating and identifying recombinant clones - contg. DNA derived from

PT one component of a messenger RNA mixt.

XX PS Claim 11; Page 33; 40pp; English.

XX CC The DNA primer is complementary to a region of target mRNA coding for a  
CC portion of the HLA-B antigen. (Updated on 25-MAR-2003 to correct PR  
CC field.) (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
| | | | | | | | | |  
Db 10 TGTGGAGAAG 1

RESULT 84  
AAZ18995  
ID AAZ18995 standard; DNA; 11 BP.  
XX AC AAZ18995;

XX DT 22-OCT-1999 (first entry)  
XX DE Murine MRL SAGE tag 2603602.  
XX KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;  
KW healing response; microsatellite marker; treatment; central nerve;  
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.  
XX OS Mus sp.  
XX PN W09941364-A2.  
XX PD 19-AUG-1999.  
XX PF 12-FEB-1999; 99WO-US002962.  
XX PR 13-FEB-1998; 98US-0074737P.  
XX PR 26-AUG-1998; 98US-0097937P.  
XX PR 28-SEP-1998; 98US-0102051P.

XX PA (WIST-) WISTAR INST.

XX PI Heber-Katz E;

XX DR WPI; 1999-494533/41.

XX PT New mammalian model for enhanced wound healing - useful for identifying

PT enhanced wound healing genes.

XX PS Claim 13; Page 74; 136pp; English.

XX CC This invention describes a novel non-MRL healer mouse (M) having at least

CC one quantitative trait locus selected from those given in the

CC specification, exhibiting an enhanced healing response to a wound

CC compared to mice (m) without the locus. The invention describes a novel

CC method of identifying a gene involved in enhanced wound healing by

CC identifying DNA microsatellite markers which can distinguish healer mice

CC from non-healer mice and identifying microsatellite markers which

CC segregate with enhanced wound healing in progeny of the mice, where a

CC chromosomal locus containing at least one enhanced wound healing gene is

CC identified. A method of treating a wound in a mammal is also disclosed.

CC The new methods are useful for treating wounds, especially central and

CC peripheral nerve wound. The methods of the invention are useful for

CC restoring function after nerve injury in a mammal. (M) is useful as a

CC mammalian model of enhanced wound healing, useful for identifying genes

CC and gene products involved in enhanced wound healing, and to provide

CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags

CC from C57BL/6 and MRL mice which are used to illustrate the method of the

CC invention  
XX  
SQ Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGCGCA 16  
| | | | | | | | | |

Db 1 GCTGTGCGCCA 10

RESULT 85  
ABQ86261  
ID ABQ86261 standard; cDNA; 11 BP.

XX AC ABQ86261;

XX DT 10-SEP-2002 (first entry)

XX DE Human skin stress/ageing related EST SEQ ID NO 16.

XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.



XX Homo sapiens.  
OS WO200253773-A2.  
XX  
PN  
XX  
XX  
PD 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-EP015178.  
XX  
XX 03-JAN-2001; 2001DE-01000121.  
PR  
XX (HENK ) HENKEL KGAA.  
XX  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-528865/56.  
XX  
PT Identifying genes involved in skin stress and aging, useful e.g. in  
PT screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
XX  
XX Claim 8; Page 36; 325pp; German.  
PS  
XX The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
PS  
XX Claim 8; Page 36; 325pp; German.  
XX  
XX The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
PS  
XX Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
Db |||||  
1 GTGGCGAATG 10  
RESULT 86  
ABQ87168/c  
ID ABQ87168 standard; cDNA; 11 BP.  
XX  
XX ABQ87168;  
XX  
XX 10-SEP-2002 (first entry)  
XX  
XX Human skin stress/ageing related EST SEQ ID NO 923.  
DE  
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200253773-A2.  
PN  
XX 11-JUL-2002.  
XX  
XX 20-DEC-2001; 2001WO-EP015178.  
PF  
XX  
XX 03-JAN-2001; 2001DE-01000121.  
PR  
XX (HENK ) HENKEL KGAA.  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-528865/56.  
XX  
DR

XX Identifying genes involved in skin stress and aging, useful e.g. in  
PT screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
XX  
XX Claim 8; Page 75; 325pp; German.  
PS  
XX The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
PS  
XX Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
Db |||||  
11 GTGGAGAAGG 2  
RESULT 87  
ABV65931  
ID ABV65931 standard; cDNA; 11 BP.  
XX  
XX ABV65931;  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX Human skin EST 3717.  
DE  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200253774-A2.  
PN  
XX 11-JUL-2002.  
PD  
XX 20-DEC-2001; 2001WO-EP015179.  
PF  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
PR  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
XX Disclosure; Page 128; 1345pp; German.  
PS  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 9 TGTGGCGAAG 18  
|||||  
Db 1 TGTGGCAAAG 10  
  
RESULT 88  
ABV69764  
ID ABV69764 standard; cDNA; 11 BP.  
XX  
AC ABV69764;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 7550.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 238; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 10 GTGGCGAAG 19

Db 1 GTGGCGAATG 10  
|||||  
RESULT 89  
ABV70774  
ID ABV70774 standard; cDNA; 11 BP.  
XX  
AC ABV70774;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 8560.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 274; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 10 GTGGCGAAG 19  
|||||  
Db 1 GTGGCGAATG 10  
  
RESULT 90  
ABV69072/c  
ID ABV69072 standard; cDNA; 11 BP.  
XX  
AC ABV69072;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 6858.

XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX Homo sapiens.  
OS  
XX WO200253774-A2.  
PN  
XX 11-JUL-2002.  
PD  
XX 20-DEC-2001; 2001WO-EP015179.  
PF  
XX 03-JAN-2001; 2001DE-01000127.  
PR  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT  
XX Disclosure; Page 216; 1345pp; German.  
PS  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAGG 19  
Db 11 GTGGAGAAGG 2  
  
RESULT 91  
ABV69619/c  
ID ABV69619 standard; cDNA; 11 BP.  
XX  
AC ABV69619;  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX Human skin EST 7405.  
DE  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX

PR 03-JAN-2001; 2001DE-01000127.  
XX (HENK ) HENKEL KGAA.  
PA  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT  
XX Disclosure; Page 232; 1345pp; German.  
PS  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCTG 10  
Db 10 GGGCGCGCTG 1  
  
RESULT 92  
ABV71417  
ID ABV71417 standard; cDNA; 11 BP.  
XX  
AC ABV71417;  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX Human skin EST 9203.  
DE  
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200253774-A2.  
PN  
XX 11-JUL-2002.  
PD  
XX 20-DEC-2001; 2001WO-EP015179.  
PF  
XX 03-JAN-2001; 2001DE-01000127.  
PR  
XX (HENK ) HENKEL KGAA.  
PA  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX WPI; 2002-590638/63.  
DR  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT  
XX Claim 24; Page 296; 1345pp; German.  
PS

XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 6 CGCTGTGGCG 15  
Db 2 CGATGTGGCG 11  
  
RESULT 93  
ABV63353  
ID ABV63353 standard; cDNA; 11 BP.  
XX  
AC ABV63353;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 1139.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 56; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention

XX  
SQ Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 10 GTGGCGAAGG 19  
Db 1 GTGGCGAATG 10  
  
RESULT 94  
ABV66009/c  
ID ABV66009 standard; cDNA; 11 BP.  
XX  
AC ABV66009;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 3795.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 130; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 3 G; 1 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 5 GCGCTGTGGC 14  
Db 11 GCGCAGTGGC 2  
  
RESULT 95

ABV67796  
ID ABV67796 standard; cDNA; 11 BP.  
XX  
AC ABV67796;  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX Human skin EST 5582.  
DE  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200253774-A2.  
PN  
XX  
XX 11-JUL-2002.  
PD  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
PF  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
PR  
XX  
XX (HENK ) HENKEL KGAA.  
PA  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX  
XX WPI; 2002-590638/63.  
DR  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT  
XX  
XX Disclosure; Page 179; 1345pp; German.  
PS  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGGC 14  
| | | | | | | |  
Db 2 GGGCTGTGGC 11  
  
RESULT 96  
ABV68820  
ID ABV68820 standard; cDNA; 11 BP.  
XX  
AC ABV68820;  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX Human skin EST 6606.  
DE  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX

OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
XX 11-JUL-2002.  
PD  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
PF  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
PR  
XX  
XX (HENK ) HENKEL KGAA.  
PA  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
PI  
XX  
XX WPI; 2002-590638/63.  
DR  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
PT  
XX  
XX Disclosure; Page 208; 1345pp; German.  
PS  
XX  
XX The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 0 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CGCTGTGGCG 15  
| | | | | | | |  
Db 1 CGCTGTGGGG 10  
  
RESULT 97  
ABV63996  
ID ABV63996 standard; cDNA; 11 BP.  
XX  
AC ABV63996;  
XX  
XX 21-OCT-2002 (first entry)  
DT  
XX Human skin EST 1782.  
DE  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200253774-A2.  
PN  
XX  
XX 11-JUL-2002.  
PD  
XX  
XX 20-DEC-2001; 2001WO-EP015179.  
PF  
XX  
XX 03-JAN-2001; 2001DE-01000127.  
PR  
XX  
XX (HENK ) HENKEL KGAA.  
PA  
XX  
XX Petersohn D, Conradt M, Hofmann K;  
PI



XX WPI; 2002-590638/63.

DR

XX

PT In vitro identification of skin-expressed genes, useful for determining

PT homeostasis and identifying cosmetic or pharmaceutical agents against

PT e.g. skin cancer.

XX

PS Disclosure; Page 74; 1345pp; German.

XX

CC The invention relates to in vitro identification (M1) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically

CC encoded factors from skin, to serial analysis of gene expression (SAGE)

CC so as to identify skin-expressed genes and quantify their expression.

CC (M1) is useful for identifying genes involved in skin homeostasis; to

CC determine skin homeostasis and to test agent (A) that maintains or

CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

CC skin. The present sequence is that of a human expressed sequence tag

CC (EST) of the invention

XX

SQ Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 93;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGCG 15

Db 2 CGATGTGGCG 11

RESULT 98

ABV62343

ID ABV62343 standard; cDNA; 11 BP.

XX

AC ABV62343;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human skin EST 129.

XX

KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;

KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;

KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

XX

OS Homo sapiens.

XX

PN WO200253774-A2.

XX

PD 11-JUL-2002.

XX

PF 20-DEC-2001; 2001WO-EP015179.

XX

PR 03-JAN-2001; 2001DE-01000127.

XX

PA (HENK ) HENKEL KGAA.

XX

PI Petersohn D, Conradt M, Hofmann K;

XX

DR WPI; 2002-590638/63.

XX

PT In vitro identification of skin-expressed genes, useful for determining

PT homeostasis and identifying cosmetic or pharmaceutical agents against

PT e.g. skin cancer.

XX

PS Disclosure; Page 29; 1345pp; German.

XX

CC The invention relates to in vitro identification (M1) of genes expressed

CC in the skin of humans or animals by subjecting a mixture of genetically

CC encoded factors from skin, to serial analysis of gene expression (SAGE)

CC so as to identify skin-expressed genes and quantify their expression.

CC (M1) is useful for identifying genes involved in skin homeostasis; to

CC determine skin homeostasis and to test agent (A) that maintains or

CC promotes skin homeostasis or that can be used for treating skin

CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;

CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

CC skin. The present sequence is that of a human expressed sequence tag

CC (EST) of the invention

XX

SQ Sequence 11 BP; 3 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 93;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19

Db 1 GTGGCGAATG 10

RESULT 99

ADQ35656/c

ID ADQ35656 standard; DNA; 11 BP.

XX

AC ADQ35656;

XX

DT 23-SEP-2004 (first entry)

XX

DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 473.

XX

KW hair-bearing skin; human; serial analysis of gene expression; SAGE;

KW homeostasis; cosmetic; pharmaceutival; biochip; ds.

XX

OS Homo sapiens.

XX

PN DE10260931-A1.

XX

PD 08-JUL-2004.

XX

PF 20-DEC-2002; 2002DE-01060931.

XX

PR 20-DEC-2002; 2002DE-01060931.

XX

PA (HENK ) HENKEL KGAA.

XX

PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;

PI Conradt M, Hofmann K;

XX

DR WPI; 2004-518857/50.

XX

PT In vitro identification of genes important for hair-bearing skin, useful

PT for assessing homeostasis and in screening for pharmaceutical or cosmetic

PT agents, based on differential expression analysis.

XX

PS Claim 5; SEQ ID NO 473; 250pp; German.

XX

CC This invention describes a novel in vitro method for identifying genes

CC that are significant for hair-bearing skin in humans. The method

CC comprises recovering, from hair-bearing skin, a first mixture of

CC genetically expressed (transcribed and optionally translated) factors

CC (i.e. proteins, mRNA or their fragments), recovering a second, similar

CC mixture from skin on which hair does not grow and subjecting both

CC mixtures to serial analysis of gene expression (SAGE) to identify those

CC genes for which expression is markedly different between the two types of

CC skin. The invention also describes in vitro methods for determining

CC homeostasis of human hair-bearing skin and for determining activity of

CC cosmetic and pharmaceutical agents for use against disorders or

CC disturbances of the homeostasis of human hair-bearing skin. A biochip and

CC a test kit comprising a solid support (flexible or rigid) with

CC immobilised probes are also described for determining homeostasis. The

CC hair-bearing skin is from the scalp and the other skin is from the face.

CC The method allows identification of as many as possible of the genes

CC important for hair-bearing skin, and therefore, of a very wide range of

```
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC human DNA Tag fragments used to identify genes associated with hair-
CC bearing skin.
XX
SQ Sequence 11 BP; 1 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match          44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGCGCTG 10
Db 10 GGGCGCGCTG 1

RESULT 100
ADQ36012
ID ADQ36012 standard; DNA; 11 BP.
XX
AC ADQ36012;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 829.
XX
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS Homo sapiens.
XX
PN DE10260931-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060931.
XX
PR 20-DEC-2002; 2002DE-01060931.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518857/50.
XX
PT In vitro identification of genes important for hair-bearing skin, useful
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 5; SEQ ID NO 829; 250pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for hair-bearing skin in humans. The method
CC comprises recovering, from hair-bearing skin, a first mixture of
CC genetically expressed (transcribed and optionally translated) factors
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC mixture from skin on which hair does not grow and subjecting both
CC mixtures to serial analysis of gene expression (SAGE) to identify those
CC genes for which expression is markedly different between the two types of
CC skin. The invention also describes in vitro methods for determining
CC homeostasis of human hair-bearing skin and for determining activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC a test kit comprising a solid support (flexible or rigid) with
CC immobilised probes are also described for determining homeostasis. The
CC hair-bearing skin is from the scalp and the other skin is from the face.
CC The method allows identification of as many as possible of the genes
CC important for hair-bearing skin, and therefore, of a very wide range of
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC human DNA Tag fragments used to identify genes associated with hair-
CC bearing skin.
XX
SQ Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match          44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Query Match          44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14
Db 2 GGGCTGTGGC 11

RESULT 101
ADQ35381
ID ADQ35381 standard; DNA; 11 BP.
XX
AC ADQ35381;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 198.
XX
KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX
OS Homo sapiens.
XX
PN DE10260931-A1.
XX
PD 08-JUL-2004.
XX
PF 20-DEC-2002; 2002DE-01060931.
XX
PR 20-DEC-2002; 2002DE-01060931.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;
XX
DR WPI; 2004-518857/50.
XX
PT In vitro identification of genes important for hair-bearing skin, useful
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
PS Claim 6; SEQ ID NO 198; 250pp; German.
XX
CC This invention describes a novel in vitro method for identifying genes
CC that are significant for hair-bearing skin in humans. The method
CC comprises recovering, from hair-bearing skin, a first mixture of
CC genetically expressed (transcribed and optionally translated) factors
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC mixture from skin on which hair does not grow and subjecting both
CC mixtures to serial analysis of gene expression (SAGE) to identify those
CC genes for which expression is markedly different between the two types of
CC skin. The invention also describes in vitro methods for determining
CC homeostasis of human hair-bearing skin and for determining activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC a test kit comprising a solid support (flexible or rigid) with
CC immobilised probes are also described for determining homeostasis. The
CC hair-bearing skin is from the scalp and the other skin is from the face.
CC The method allows identification of as many as possible of the genes
CC important for hair-bearing skin, and therefore, of a very wide range of
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC human DNA Tag fragments used to identify genes associated with hair-
CC bearing skin.
XX
SQ Sequence 11 BP; 3 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match          44.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 93;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 9 TGTGGCGAAG 18  
Db 1 TGTGGCAAAG 10

RESULT 102  
ADQ32141/c  
ID ADQ32141 standard; DNA; 11 BP.  
XX  
AC ADQ32141;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 231.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 9; SEQ ID NO 231; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14  
Db 11 GCGCAGTGGC 2

RESULT 103  
ADQ34986  
ID ADQ34986 standard; DNA; 11 BP.  
XX  
AC ADQ34986;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human facial skin-associated DNA fragment SEQ ID NO 3076.  
XX  
KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10260928-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 20-DEC-2002; 2002DE-01060928.  
XX  
PR 20-DEC-2002; 2002DE-01060928.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX  
DR WPI; 2004-518855/50.  
XX  
PT In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX  
PS Claim 4; SEQ ID NO 3076; 577pp; German.  
XX  
CC This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX  
SQ Sequence 11 BP; 0 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14  
Db 2 GCGCTGTGGC 11

RESULT 104  
ADQ35029  
ID ADQ35029 standard; DNA; 11 BP.

XX AC ADQ35029;  
XX DT 23-SEP-2004 (first entry)  
XX DE Human facial skin-associated DNA fragment SEQ ID NO 3119.  
XX KW facial skin; human; serial analysis of gene expression; SAGE;  
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX OS Homo sapiens.  
XX PN DE10260928-A1.  
XX PD 08-JUL-2004.  
XX PF 20-DEC-2002; 2002DE-01060928.  
XX PR 20-DEC-2002; 2002DE-01060928.  
XX PA (HENK ) HENKEL KGAA.  
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX WPI; 2004-518855/50.  
XX In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX Claim 4; SEQ ID NO 3119; 577pp; German.  
XX This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX SQ Sequence 11 BP; 0 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 CGCTGTGGCG 15  
Db 1 CGCTGTGGCG 10  
RESULT 105  
ADQ34095/c  
ID ADQ34095 standard; DNA; 11 BP.  
XX AC ADQ34095;  
XX DT 23-SEP-2004 (first entry)

XX DE Human facial skin-associated DNA fragment SEQ ID NO 2185.  
XX KW facial skin; human; serial analysis of gene expression; SAGE;  
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.  
XX OS Homo sapiens.  
XX PN DE10260928-A1.  
XX PD 08-JUL-2004.  
XX PF 20-DEC-2002; 2002DE-01060928.  
XX PR 20-DEC-2002; 2002DE-01060928.  
XX PA (HENK ) HENKEL KGAA.  
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;  
PI Conradt M, Hofmann K;  
XX WPI; 2004-518855/50.  
XX In vitro identification of genes important for facial skin, useful for  
PT assessing homeostasis and in screening for pharmaceutical or cosmetic  
PT agents, based on differential expression analysis.  
XX Claim 4; SEQ ID NO 2185; 577pp; German.  
XX This invention describes a novel in vitro method for identifying genes  
CC that are significant for facial skin in humans. The method comprises  
CC recovering, from facial skin, a first mixture of genetically expressed  
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or  
CC their fragments), recovering a second, similar mixture from some other  
CC human tissue, preferably skin from a protected area, especially from the  
CC breast and subjecting the mixtures to serial analysis of gene expression  
CC (SAGE) to identify those genes for which expression is markedly different  
CC between facial skin and the other tissue. The invention also describes an  
CC in vitro method for determining homeostasis of human facial skin; a test  
CC kit which comprises a solid support (flexible or rigid) on which are  
CC immobilised probes that bind specifically to the factors of interest and  
CC a biochip for determining homeostasis of human facial skin. The products  
CC of the invention are also used in a method which determines activity of  
CC cosmetic and pharmaceutical agents for use against disorders or  
CC disturbances of the homeostasis of human skin and a screening method for  
CC identifying cosmetic and pharmaceutical agents. The method allows  
CC identification of as many as possible of the genes important for facial  
CC skin and thus of a very wide range of potential therapeutic and cosmetic  
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to  
CC identify the facial skin-associated genes described in the invention.  
XX SQ Sequence 11 BP; 1 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 93;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
Db 11 GTGGCGAAGG 2  
RESULT 106  
AAV65451  
ID AAV65451 standard; DNA; 12 BP.  
XX AC AAV65451;  
XX DT 08-DEC-1998 (first entry)  
XX DE Primer pBS800-23E used in the course of the invention.  
XX KW Nucleic acid determination; hybridisation; probe; mismatch; SBH;



KW sequencing by hybridisation; PCR primer; ss.  
XX Synthetic.  
OS  
PN JP10243785-A.  
XX  
PD 14-SEP-1998.  
XX  
PF 03-MAR-1997; 97JP-00047821.  
XX  
PR 03-MAR-1997; 97JP-00047821.  
XX  
PA (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.  
XX  
DR WPI; 1998-549781/47.  
XX  
PT Determination of nucleic acid base sequence - is sensitive and rapid  
PT without mismatch in hybridisation as in sequencing by hybridisation  
PT method.  
XX  
PS Example; Page 9; 20pp; Japanese.  
XX  
CC Sequences shown in AAV65401 to AAV65580 represent PCR primers used in the  
CC course of the invention which provides a method for determining a single  
CC stranded nucleic acid base sequence. The method comprises separation of  
CC 4k oligonucleotide probe as a primer from all combinations of k base  
CC sequences and hybridising the probe and the nucleic acid to be tested.  
CC The probe is elongated to make a primer using the nucleic acid to be  
CC tested as a template and the elongated primer is determined. The base  
CC sequence of the nucleic acid is determined based on the elongated amount.  
CC The method allows sensitive and rapid determination of nucleic acid base  
CC sequence without mismatch in hybridisation as in sequencing by  
CC hybridisation (SBH) method  
XX  
SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAG 18  
Db 1 TGTGGCGCAG 10  
  
RESULT 107  
AAV65548  
ID AAV65548 standard; DNA; 12 BP.  
XX  
AC AAV65548;  
XX  
DT 08-DEC-1998 (first entry)  
XX  
DE Forward primer 18 used in the course of the invention.  
XX  
KW Nucleic acid determination; hybridisation; probe; mismatch; SBH;  
KW sequencing by hybridisation; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP10243785-A.  
XX  
PD 14-SEP-1998.  
XX  
PF 03-MAR-1997; 97JP-00047821.  
XX  
PR 03-MAR-1997; 97JP-00047821.  
XX  
PA (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.  
XX  
DR WPI; 1998-549781/47.  
XX  
PT Determination of nucleic acid base sequence - is sensitive and rapid

PT without mismatch in hybridisation as in sequencing by hybridisation  
PT method.  
XX  
PS Example; Page 12; 20pp; Japanese.  
XX  
CC Sequences shown in AAV65401 to AAV65580 represent PCR primers used in the  
CC course of the invention which provides a method for determining a single  
CC stranded nucleic acid base sequence. The method comprises separation of  
CC 4k oligonucleotide probe as a primer from all combinations of k base  
CC sequences and hybridising the probe and the nucleic acid to be tested.  
CC The probe is elongated to make a primer using the nucleic acid to be  
CC tested as a template and the elongated primer is determined. The base  
CC sequence of the nucleic acid is determined based on the elongated amount.  
CC The method allows sensitive and rapid determination of nucleic acid base  
CC sequence without mismatch in hybridisation as in sequencing by  
CC hybridisation (SBH) method  
XX  
SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCCGCGCTG 10  
Db 1 GGTCCGCGCTG 10  
  
RESULT 108  
AAV65547  
ID AAV65547 standard; DNA; 12 BP.  
XX  
AC AAV65547;  
XX  
DT 08-DEC-1998 (first entry)  
XX  
DE Forward primer 17 used in the course of the invention.  
XX  
KW Nucleic acid determination; hybridisation; probe; mismatch; SBH;  
KW sequencing by hybridisation; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN JP10243785-A.  
XX  
PD 14-SEP-1998.  
XX  
PF 03-MAR-1997; 97JP-00047821.  
XX  
PR 03-MAR-1997; 97JP-00047821.  
XX  
PA (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.  
XX  
DR WPI; 1998-549781/47.  
XX  
PT Determination of nucleic acid base sequence - is sensitive and rapid  
PT without mismatch in hybridisation as in sequencing by hybridisation  
PT method.  
XX  
PS Example; Page 12; 20pp; Japanese.  
XX  
CC Sequences shown in AAV65401 to AAV65580 represent PCR primers used in the  
CC course of the invention which provides a method for determining a single  
CC stranded nucleic acid base sequence. The method comprises separation of  
CC 4k oligonucleotide probe as a primer from all combinations of k base  
CC sequences and hybridising the probe and the nucleic acid to be tested.  
CC The probe is elongated to make a primer using the nucleic acid to be  
CC tested as a template and the elongated primer is determined. The base  
CC sequence of the nucleic acid is determined based on the elongated amount.  
CC The method allows sensitive and rapid determination of nucleic acid base  
CC sequence without mismatch in hybridisation as in sequencing by  
CC hybridisation (SBH) method  
XX



```
SQ      Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCGCGGCTG 10
        ||||| ||||
Db       2 GGTCGGGCTG 11

RESULT 109
AAV65546
ID      AAV65546 standard; DNA; 12 BP.
XX
AC      AAV65546;
XX
DT      08-DEC-1998 (first entry)
XX
DE      Forward primer 16 used in the course of the invention.
XX
KW      Nucleic acid determination; hybridisation; probe; mismatch; SBH;
KW      sequencing by hybridisation; PCR primer; ss.
XX
OS      Synthetic.
XX
PN      JPI0243785-A.
XX
PD      14-SEP-1998.
XX
PF      03-MAR-1997; 97JP-00047821.
XX
PR      03-MAR-1997; 97JP-00047821.
XX
PA      (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
XX
DR      WPI; 1998-549781/47.
XX
PT      Determination of nucleic acid base sequence - is sensitive and rapid
PT      without mismatch in hybridisation as in sequencing by hybridisation
PT      method.
XX
PS      Example; Page 12; 20pp; Japanese.
XX
CC      Sequences shown in AAV65401 to AAV65580 represent PCR primers used in the
CC      course of the invention which provides a method for determining a single
CC      stranded nucleic acid base sequence. The method comprises separation of
CC      4k oligonucleotide probe as a primer from all combinations of k base
CC      sequences and hybridising the probe and the nucleic acid to be tested.
CC      The probe is elongated to make a primer using the nucleic acid to be
CC      tested as a template and the elongated primer is determined. The base
CC      sequence of the nucleic acid is determined based on the elongated amount.
CC      The method allows sensitive and rapid determination of nucleic acid base
CC      sequence without mismatch in hybridisation as in sequencing by
CC      hybridisation (SBH) method
XX
SQ      Sequence 12 BP; 0 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCGCGGCTG 10
        ||||| ||||
Db       3 GGTCGGGCTG 12

RESULT 110
AAA74607
ID      AAA74607 standard; DNA; 12 BP.
XX
AC      AAA74607;
XX
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```
DT      15-SEP-2003 (revised)
DT      01-DEC-2000 (first entry)
XX
DE      HIV-specific reverse transcription primer LTR8RT.
XX
KW      Human immunodeficiency virus type 1; HIV-1; HIV-2; HIV detection;
KW      reverse transcription primer; ss.
XX
OS      Human immunodeficiency virus 1.
XX
PN      EP1026263-A2.
XX
PD      09-AUG-2000.
XX
PF      01-FEB-2000; 2000EP-00300792.
XX
PR      02-FEB-1999; 99US-0118417P.
XX
PA      (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI      Patterson DR, Puskas JA, Song K, Linnen JM;
XX
DR      WPI; 2000-516096/47.
XX
PT      Reverse transcribing human immunodeficiency virus RNA in clinical samples
PT      with novel HIV-specific oligonucleotide reverse transcription primers.
XX
PS      Claim 9; Page 12; 15pp; English.
XX
CC      The present sequence is a reverse transcription primer used in a method
CC      for the detection of human immunodeficiency virus (HIV) RNA in a
CC      biological sample. The HIV RNA is reverse transcribed to generate cDNA.
CC      This is then amplified by PCR and the PCR product is detected either by
CC      gel electrophoresis, followed by ethidium bromide staining, or using 5'-
CC      biotin-labelled primers during amplification. The use of HIV-specific
CC      reverse transcription primers provides a sensitive method for detecting
CC      HIV-1 and/or HIV-2 in plasma. This method can reduce the incidence of
CC      false negative results in screening of patients or blood supply for HIV.
CC      (Updated on 15-SEP-2003 to standardise OS field)
XX
SQ      Sequence 12 BP; 0 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGCG 15
        ||||| |||
Db       1 CCCTGTGGCG 10

RESULT 111
ABI23621
ID      ABI23621 standard; DNA; 12 BP.
XX
AC      ABI23621;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 323594 for detecting SNP TSC0031477.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
```

PR 07-APR-2000; 2000DE-01019173.  
XX (EPIG-) EPIGENOMICS AG.  
PA Olek A, Piepenbrock C, Berlin K;  
PI WPI; 2001-657177/75.  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX Claim 1; SEQ ID NO 323594; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAGG 19  
Db 1 GTGGCGAAGG 10  
  
RESULT 112  
ABI12916  
ID ABI12916 standard; DNA; 12 BP.  
XX  
AC ABI12916;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 312889 for detecting SNP TSC0025347.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 312889; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAGG 19  
Db 3 GTAGCGAAGG 12  
  
RESULT 113  
ABI06621/c  
ID ABI06621 standard; DNA; 12 BP.  
XX  
AC ABI06621;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 306594 for detecting SNP TSC0022080.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 306594; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
CC

```
XX
SQ      Sequence 12 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 0 Other;
      Query Match      44.2%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 85;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
      ||||| |||||
Db      10 GTGGAGAAGG 1

RESULT 114
ABI64116/C
ID      ABI64116 standard; DNA; 12 BP.
XX
AC      ABI64116;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 364089 for detecting SNP TSC0006574.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 364089; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
      Query Match      44.2%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 85;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
      ||||| |||||
Db      10 GTGGTGAAGG 1

RESULT 115
ABI64116/C
ID      ABI64116 standard; DNA; 12 BP.
XX
AC      ABI64116;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 364089 for detecting SNP TSC0006574.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 364089; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
      Query Match      44.2%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 85;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
      ||||| |||||
Db      10 GTGGTGAAGG 1

RESULT 116
ABI95969
ID      ABI95969 standard; DNA; 12 BP.
XX
AC      ABI95969;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 295962 for detecting SNP TSC0016826.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

```
ABH90350/c
ID      ABH90350 standard; DNA; 12 BP.
XX
AC      ABH90350;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 290343 for detecting SNP TSC0014318.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS      Homo sapiens.
XX
PN      WO200177384-A2.
XX
PD      18-OCT-2001.
XX
PF      06-APR-2001; 2001WO-IB000713.
XX
PR      07-APR-2000; 2000DE-01019173.
XX
PA      (EPIG-) EPIGENOMICS AG.
XX
PI      Olek A, Piepenbrock C, Berlin K;
XX      WPI; 2001-657177/75.
XX
PT      Set of oligonucleotides, useful for diagnosis and cell typing, is
PT      designed to detect single-nucleotide polymorphisms and cytosine
PT      methylation status.
XX
PS      Claim 1; SEQ ID NO 290343; 29pp + Sequence Listing; German.
XX
CC      This invention describes novel oligonucleotide primers or peptide nucleic
CC      acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC      and cytosine methylation status in chemically pretreated genomic DNA. The
CC      oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC      range of diseases including immune system, gastrointestinal, respiratory,
CC      central nervous system, cardiovascular and metabolic disorders. The
CC      oligomers are also used for detecting cell type differentiation. ABC00010
CC      -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC      represent the oligomers described in the invention. NOTE: The sequence
CC      data for this patent did not form part of the printed specification, but
CC      was obtained in electronic format from WIPO at
CC      ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
      Query Match      44.2%; Score 8.4; DB 1; Length 12;
      Best Local Similarity 90.0%; Pred. No. 85;
      Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TGTGGCGAAG 18
      ||||| |||||
Db      12 TGTGGCGAAG 3

RESULT 116
ABI95969
ID      ABI95969 standard; DNA; 12 BP.
XX
AC      ABI95969;
XX
DT      22-FEB-2002 (first entry)
XX
DE      Oligonucleotide primer SEQ ID NO 295962 for detecting SNP TSC0016826.
XX
KW      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW      peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW      central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
```

```
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 295962; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 44.2%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 85;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGTAGG 19
Db 1 GTGGCGTAGG 10

RESULT 117
ABH73785
ID ABH73785 standard; DNA; 12 BP.
XX
XX AC ABH73785;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 273770 for detecting SNP TSC0003303.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
```

```
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 273770; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 44.2%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 85;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 2 TGTGGTGAAG 11

RESULT 118
ABH90189
ID ABH90189 standard; DNA; 12 BP.
XX
XX AC ABH90189;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 290182 for detecting SNP TSC0014238.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB0000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 290182; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
```



CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 0 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCTGTGG 13  
| | | | |  
Db 2 CGCGCGGTGG 11

RESULT 119  
ABH72007  
ID ABH72007 standard; DNA; 12 BP.

XX  
AC ABH72007;

XX  
DT 22-FEB-2002 (first entry)

XX  
DE Oligonucleotide primer SEQ ID NO 271986 for detecting SNP TSC0002677.

XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX  
PD 18-OCT-2001.

XX  
PF 06-APR-2001; 2001WO-IB000713.

XX  
PR 07-APR-2000; 2000DE-01019173.

XX  
PA (EPIG-) EPIGENOMICS AG.

XX  
PI Olek A, Piepenbrock C, Berlin K;

XX  
DR WPI; 2001-657177/75.

XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX  
PS Claim 1; SEQ ID NO 271986; 29pp + Sequence Listing; German.

XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 12 BP; 3 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
| | | | |  
Db 2 GAGGCGAAGG 11

RESULT 120  
ABI25686  
ID ABI25686 standard; DNA; 12 BP.

XX  
AC ABI25686;

XX  
DT 22-FEB-2002 (first entry)

XX  
DE Oligonucleotide primer SEQ ID NO 325659 for detecting SNP TSC0032649.

XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX  
PD 18-OCT-2001.

XX  
PF 06-APR-2001; 2001WO-IB000713.

XX  
PR 07-APR-2000; 2000DE-01019173.

XX  
PA (EPIG-) EPIGENOMICS AG.

XX  
PI Olek A, Piepenbrock C, Berlin K;

XX  
DR WPI; 2001-657177/75.

XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

XX  
PS Claim 1; SEQ ID NO 325659; 29pp + Sequence Listing; German.

XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 12 BP; 1 A; 1 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
| | | | |  
Db 3 TGTGGCGAGG 12

RESULT 121  
ABI26828  
ID ABI26828 standard; DNA; 12 BP.

XX  
AC ABI26828;

XX



DT 22-FEB-2002 (first entry)  
XX Oligonucleotide primer SEQ ID NO 326801 for detecting SNP TSC0033283.  
DE  
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 326801; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
PS Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;  
XX  
CC  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAGG 19  
Db 1 GTGGGGAAGG 10  
  
RESULT 122  
ABH90031/c  
ID ABH90031 standard; DNA; 12 BP.  
XX  
AC ABH90031;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 290024 for detecting SNP TSC0014187.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB0000713.  
PF  
XX 07-APR-2000; 2000DE-01019173.  
PR  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
PI  
XX WPI; 2001-657177/75.  
DR  
XX  
XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 290024; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 4 A; 6 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAG 18  
Db 12 TGTGGCGAGG 3  
  
RESULT 123  
ABI29748/c  
ID ABI29748 standard; DNA; 12 BP.  
XX  
AC ABI29748;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 329721 for detecting SNP TSC0035109.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine

PT methylation status.  
XX Claim 1; SEQ ID NO 329721; 29pp + Sequence Listing; German.  
PS  
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
Db 11 TGTGGAGAAG 2  
||||| |||||

RESULT 124  
ABI12040  
ID ABI12040 standard; DNA; 12 BP.  
XX  
AC ABI12040;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 312013 for detecting SNP TSC0024800.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX  
PS Claim 1; SEQ ID NO 312013; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence

CC data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

CC  
XX  
SQ Sequence 12 BP; 1 A; 2 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGTG 12  
Db 3 TCGCGTTGTG 12  
||||| |||||

RESULT 125  
ABI17107  
ID ABI17107 standard; DNA; 12 BP.  
XX  
AC ABI17107;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 317080 for detecting SNP TSC0027806.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB0000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.  
XX  
PS Claim 1; SEQ ID NO 317080; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX  
SQ Sequence 12 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 0 Other;  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGA 16  
Db 3 GGTGTGGCGA 12  
||||| |||||

RESULT 126  
ABI50801  
ID ABI50801 standard; DNA; 12 BP.  
XX  
AC ABI50801;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 350774 for detecting SNP TSC0046869.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 350774; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 3 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 9 TGTGGCGAAG 18  
Db 2 TGTGGCGAAG 11  
RESULT 127  
ABH95967  
ID ABH95967 standard; DNA; 12 BP.  
XX  
AC ABH95967;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 295960 for detecting SNP TSC0016826.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 295960; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 1 A; 1 C; 6 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 10 GTGGCGAAGG 19  
Db 1 GTGGCGTAGG 10  
RESULT 128  
ABH90353/c  
ID ABH90353 standard; DNA; 12 BP.  
XX  
AC ABH90353;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE Oligonucleotide primer SEQ ID NO 290346 for detecting SNP TSC0014318.  
XX  
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
XX  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX

PA (EPIG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 290346; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAG 18  
Db ||||| |||||  
12 TGTGGGGAAG 3  
  
RESULT 129  
ADC33639/c  
ID ADC33639 standard; DNA; 12 BP.  
XX  
AC ADC33639;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE M. tuberculosis PCR primer #6.  
XX  
KW ss; PCR; primer; rifampin resistance; rpoB; tuberculosis.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN US2003104387-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 07-SEP-2001; 2001US-00949041.  
XX  
PR 07-SEP-2001; 2001US-00949041.  
XX  
PA (YANG/) YANG M.  
PA (WOOH/) WOO H S.  
XX  
PI Yang M, Woo HS;  
XX  
DR WPI; 2003-787043/74.  
XX  
PT Detecting tendency to rifampin resistance caused by mutation in RNA  
PT polymerase beta-subunit gene of Mycobacterium tuberculosis.  
XX  
PS Claim 50; SEQ ID NO 50; 27pp; English.  
XX  
CC The invention relates to a method of detecting a tendency to rifampin  
CC resistance caused by mutations in rpoB gene of Mycobacterium tuberculosis  
CC comprising extracting DNA from M. tuberculosis cells, amplifying rpoB

CC gene to produce fluorescently labelled product, contacting the labelled  
CC product with first and second array of oligonucleotide probes, detecting  
CC fluorescent hybridisation signal and correlating with tendency to  
CC rifampin resistance. The method is useful for detecting a tendency to  
CC rifampin resistance caused by mutations in a rpoB gene of M.  
CC tuberculosis. The method is easy to perform and is cost effective to be  
CC performed on a large-scale basis. The results produced is reliable and  
CC readily detectable. The method is easily adaptable to automation. The  
CC present sequence represents a M. tuberculosis PCR primer.  
XX  
SQ Sequence 12 BP; 1 A; 7 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGGC 14  
Db ||||| |||||  
11 GCGCTGGGGC 2  
  
RESULT 130  
ADZ45204/c  
ID ADZ45204 standard; DNA; 12 BP.  
XX  
AC ADZ45204;  
XX  
DT 14-JUL-2005 (first entry)  
XX  
DE Parallel stranded hairpin component oligonucleotide SEQ ID NO:28.  
XX  
KW aptamer; ss.  
XX  
OS Synthetic.  
XX  
PN US2005089893-A1.  
XX  
PD 28-APR-2005.  
XX  
PF 04-AUG-2004; 2004US-00912032.  
XX  
PR 06-AUG-2003; 2003US-0493092P.  
XX  
PA (LOPE/) LOPEZ M J.  
PA (MUNZ/) MUNZER M.  
PA (ERIT/) ERITJA R.  
XX  
PI Lopez MJ, Munzer M, Eritja R;  
XX  
DR WPI; 2005-314086/32.  
XX  
PT New nucleic acid ligand comprising a parallel-stranded hairpin, useful as  
PT aptamers, as artificial nucleic acid ligands and for detecting and  
PT eliminating molecules of interest.  
XX  
PS Disclosure; SEQ ID NO 28; 25pp; English.  
XX  
CC The invention relates to a nucleic acid ligand comprising a parallel-  
CC stranded hairpin. Also described: (1) a method for preparing a parallel-  
CC oligonucleotide duplex; and (2) a method for binding a target molecule.  
CC The parallel-stranded hairpin sequences or oligonucleotide triplexes are  
CC useful as aptamers. They are useful for detecting and eliminating  
CC molecules of interest. The ligand is useful as artificial nucleic acid  
CC ligand. The present sequence represents a parallel stranded hairpin  
CC component oligonucleotide from the present invention.  
XX  
SQ Sequence 12 BP; 0 A; 7 C; 1 G; 4 T; 0 U; 0 Other;  
  
Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 85;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAGG 19



Db | ||||| |  
12 GAGCGAAGG 3  
  
RESULT 131  
AAZ79106  
ID AAZ79106 standard; DNA; 10 BP.  
XX  
AC AAZ79106;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:1534.  
XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 109; 130pp; English.  
XX  
CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or

CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 TGGCGAAG 18  
Db 3 TGGCGAAG 10  
  
RESULT 132  
AAZ81742  
ID AAZ81742 standard; DNA; 10 BP.  
XX  
AC AAZ81742;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #976.  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
XX antimetastatic; vaccine; diagnosis; ss.  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX



PI Roberts BL, Shankara S;  
XX WPI; 2000-106079/09.  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX Claim 1; Page 84; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX immunotherapy  
SQ Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGGC 14  
|||  
Db 2 GCTGTGGC 9

RESULT 133  
AAZ85240  
ID AAZ85240 standard; DNA; 10 BP.

XX AAZ85240;

AC AAZ85240;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #4474.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;

KW non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.  
XX Roberts BL, Shankara S;  
XX WPI; 2000-106079/09.  
DR Isolated polynucleotides differentially expressed between metastatic and  
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
PT Claim 1; Page 179; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX immunotherapy  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15  
|||  
Db 2 CTGTGGCG 9

RESULT 134  
AAZ85260/C  
ID AAZ85260 standard; DNA; 10 BP.

XX AAZ85260;

AC AAZ85260;

DT 07-APR-2000 (first entry)

XX Metastatic breast tumour cell downregulated transcript tag #4494.

DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;

XX non-metastatic breast tumour tissue; gene therapy; anticancer;

KW antimetastatic; vaccine; diagnosis; ss.

XX Homo sapiens.

XX WO9965928-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

XX 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX

PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
DR Isolated polynucleotides differentially expressed between metastatic and  
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
PT  
XX  
PS Claim 1; Page 179; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGTG 12  
|||||||  
Db 8 GCGCTGTG 1

RESULT 135  
AAZ84921  
ID AAZ84921 standard; DNA; 10 BP.  
XX  
AC AAZ84921;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #4155.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX

OS Homo sapiens.  
XX  
XX WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
XX WPI; 2000-106079/09.  
DR  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
PT  
XX  
XX Claim 1; Page 169; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAAG 18  
|||||||  
Db 3 TGGCGAAG 10

RESULT 136  
AAZ84042  
ID AAZ84042 standard; DNA; 10 BP.  
XX  
AC AAZ84042;  
XX  
DT 07-APR-2000 (first entry)  
XX

DE Metastatic breast tumour cell downregulated transcript tag #3276.  
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX

OS Homo sapiens.  
XX  
XX WO9965928-A2.  
PN  
XX 23-DEC-1999.  
PD  
XX 18-JUN-1999; 99WO-US013647.  
PF  
XX 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-00900039P.  
PR 19-JUN-1998; 98US-00900040P.  
PR 19-JUN-1998; 98US-00900041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 146; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCGCGCTG 10  
Db 2 TCGCGCTG 9

RESULT 137  
AAZ79746  
ID AAZ79746 standard; DNA; 10 BP.  
XX  
AC AAZ79746;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human colon preferentially expressed gene SAGE tag, SEQ ID NO:37.  
XX  
KW SAGE tag; serial analysis of gene expression; diagnosis;  
KW differential gene expression; characterisation; targetted expression;  
KW tumour; cancer; immunotherapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9966303-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 17-JUN-1999; 99WO-US013820.  
XX

PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106132/09.  
XX  
PT New polynucleotide useful in cancer immunotherapy.  
XX  
PS Claim 1; Page 53; 97pp; English.  
XX  
CC Sequences AAZ79710-Z79916 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts which are  
CC differentially expressed in a variety of normal or malignant cell types.  
CC Some of the transcripts correspond to known genes or ESTs (expressed  
CC sequence tags) which were previously unknown to be preferentially or  
CC differentially expressed in that particular cell type, while other  
CC transcripts correspond to novel genes. The invention also provides a  
CC nucleotide comprising a promoter sequence derived from one of the  
CC differentially expressed genes, which may optionally be operably linked  
CC to a foreign nucleotide sequence, and gene delivery vehicles and host  
CC cells comprising the polynucleotides of the invention. A nucleotide  
CC comprising sequences AAZ79710-Z79916 may be used in diagnostic procedures  
CC to characterise a cell of a specific tissue type and to determine whether  
CC it is normal or malignant. They may be used to screen for agents that  
CC modulate expression of differentially expressed genes compound. The  
CC promoter/foreign gene construct of the invention may be used for  
CC targetted expression of the foreign gene in a particular cell type. For  
CC example, a promoter derived from a gene preferentially expressed in  
CC dendritic cells (antigen-presenting cells, or APCs), may be operably  
CC linked to a sequence encoding an immunostimulatory molecule and a  
CC sequence encoding an antigen. Such a construct could be transduced into  
CC APCs and would be useful for inducing an immune response by educating  
CC immune effector cells in vivo, or in cancer immunotherapy  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCGCGCTG 10

Db                   |                  |  
                    2 TCGCGCTG 9  
  
RESULT 138  
AAH63878  
ID   AAH63878 standard; cDNA; 10 BP.  
XX  
AC   AAH63878;  
XX  
DT   20-SEP-2001   (first entry)  
XX  
DE   Human ubiquitously expressed transcriptome sequence SEQ ID NO: 718.  
XX  
KW   Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW   cancer diagnosis; cell specific gene expression; ss.  
XX  
OS   Homo sapiens.  
XX  
PN   WO200138577-A2.  
XX  
PD   31-MAY-2001.  
XX  
PF   21-NOV-2000; 2000WO-US031922.  
XX  
PR   24-NOV-1999;   99US-00448480.  
XX  
PA   (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI   Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR   WPI; 2001-367706/38.  
XX  
PT   New isolated polynucleotides, useful for identifying specific cell type,  
PT   such as cancer cell, comprises transcriptomes expressed in particular  
PT   cell types.  
XX  
PS   Claim 13; Page 55; 94pp; English.  
XX  
CC   The present invention describes a method of identifying the type of cell  
CC   in a sample, involving determining which of the sequences AAH63161-  
CC   AAH64724 is expressed by the cell. The transcriptomes described in the  
CC   invention are cell-type specific, cancer specific or ubiquitously  
CC   expressed in humans. They can also be used to screen for drugs, reduce  
CC   cancer specific gene expression, standardise expression and restore the  
CC   function of a diseased cell or tissue. The present sequence is one of the  
CC   transcriptomes described in the exemplification of the invention  
XX  
SQ   Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match           42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;  
  
QY           5 GCGCTGTG 12  
             |             |  
Db           3 GCGCTGTG 10  
  
RESULT 139  
AAH32681  
ID   AAH32681 standard; cDNA; 10 BP.  
XX  
AC   AAH32681;  
XX  
DT   13-AUG-2001   (first entry)  
XX  
DE   LPS activated human monocyte expression gene cDNA tag SEQ:54.  
XX  
KW   Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
KW   expressed sequence tag; diagnosis; human disease; treatment; ss.  
XX  
OS   Homo sapiens.

XX                   |                  |  
PN                   JP2001069993-A.  
XX  
PD   21-MAR-2001.  
XX  
PF   28-APR-2000; 2000JP-00131079.  
XX  
PR   08-JUL-1999;   99JP-00195103.  
XX  
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR   WPI; 2001-304369/32.  
XX  
PT   LPS activated human monocyte expression gene group.  
XX  
PS   Claim 10; Page 18; 52pp; Japanese.  
XX  
CC   The present invention describes an lipopolysaccharide (LPS) activated  
CC   human monocyte expression gene group consisting of the high-ranking 50  
CC   genes of the highest expression among the genes expressed by human  
CC   monocyte stimulated by LPS in which the cDNA of each gene has the base  
CC   sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-  
CC   CATG-3' nearest to the polyA region. The gene group is useful for the  
CC   development of new means for the diagnosis and the treatment of various  
CC   human diseases in which human monocyte plays an important role. AAH32628  
CC   to AAH32943 represent specifically claimed LPS activated human monocyte  
CC   expression gene cDNA tags from the present invention. AAH32944 represents  
CC   an LPS activated human monocyte expression gene cDNA sequence encoding  
CC   AAB98009, which are given in the exemplification of the present invention  
XX  
SQ   Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match           42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches   8; Conservative   0; Mismatches   0; Indels   0; Gaps   0;  
  
QY           8 CTGTGGCG 15  
             |             |  
Db           2 CTGTGGCG 9  
  
RESULT 140  
ABA06193  
ID   ABA06193 standard; cDNA; 10 BP.  
XX  
AC   ABA06193;  
XX  
DT   10-JAN-2002   (first entry)  
XX  
DE   Human normal hepatocyte expression gene cDNA, SEQ ID NO: 170.  
XX  
KW   Human; hepatocyte; gene expression; hepatopathy; ss.  
XX  
OS   Homo sapiens.  
XX  
PN   JP2001211883-A.  
XX  
PD   07-AUG-2001.  
XX  
PF   31-JAN-2000; 2000JP-00023170.  
XX  
PR   31-JAN-2000; 2000JP-00023170.  
XX  
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR   WPI; 2001-629566/73.  
XX  
PT   Human normal hepatocyte expression gene group.  
XX  
PS   Claim 1; Page 9; 26pp; Japanese.  
XX  
CC   The invention relates to a human normal hepatocyte expression gene group  
CC   comprising 200 genes in the human normal hepatocyte. The cDNA of each



CC gene comprises one of 200 fully defined nucleotide sequences as given in  
CC the specification. The gene group and the cDNAs corresponding to each of  
CC the genes in the group are useful in the diagnosis and treatment of human  
CC hepatopathy. The present sequence is a cDNA corresponding to a gene  
CC expressed by normal human hepatocytes  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTG 12  
Db 3 GCGCTGTG 10  
|||||  
|  
RESULT 141  
ABA83148  
ID ABA83148 standard; cDNA; 10 BP.  
XX  
AC ABA83148;  
XX  
DT 08-FEB-2002. (first entry)  
XX  
DE Claudin 2 ovarian tumour marker gene SAGE tag, SEQ ID NO:108.  
XX  
KW Ovarian tumour marker gene; human; overexpression; upregulation;  
KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;  
KW identification; serous cystadenoma; borderline serous tumour;  
KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;  
KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;  
KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;  
KW adenofibroma; Brenner tumour; serial analysis of gene expression;  
KW immune response pathway; cell proliferation regulation; protein folding;  
KW membrane localised; secreted; therapeutic target; cytostatic;  
KW gene therapy; vaccine; SAGE tag; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200175177-A2.  
XX  
XX 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010947.  
XX  
PR 03-APR-2000; 2000US-0194336P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;  
PI  
XX WPI; 2001-626450/72.  
DR  
XX  
PT Detecting and identifying ovarian tumor, identifying increased risk for  
PT developing ovarian cancer, and determining effectiveness of ovarian  
PT cancer treatment, by measuring expression level of ovarian tumor marker  
PT gene.  
XX  
PS Claim 26; Page 41; 140pp; English.  
XX  
CC The invention relates to methods for diagnosing and prognosing ovarian  
CC tumours in an individual via the detection and measurement of the  
CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,  
CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,  
CC ABA83181 and ABA83183). The methods of the invention are useful for  
CC detecting an ovarian tumour in a patient, for identifying an individual  
CC at increased risk for developing ovarian cancer, in prognostic tests for  
CC assessing the relative severity of ovarian cancer, in tests for  
CC monitoring a patient in remission from ovarian cancer, and in tests for  
CC monitoring disease status in a patient being treated for ovarian cancer.  
CC The methods can additionally be used to identify a particular tumour as  
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from

CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,  
CC mucinous cystadenoma, borderline mucinous tumour, mucinous  
CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,  
CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner  
CC tumour. The ovarian tumour marker genes of the invention were identified  
CC using SAGE (serial analysis of gene expression) and were found to be  
CC overexpressed in a broad variety of ovarian epithelial tumour cells  
CC relative to normal ovarian epithelial cells. The marker genes are  
CC implicated in immune response pathways, in the regulation of cell  
CC proliferation and in protein folding, and many of these are membrane-  
CC localised or secreted. In addition to their use as diagnostic and  
CC prognostic markers, the ovarian tumour marker genes or their encoded  
CC proteins may be used as therapeutic targets for the treatment and  
CC prevention of ovarian cancer. Sequences ABA83123-ABA83169, ABA83179,  
CC ABA83181 and ABA83183 represent SAGE tags derived from the ovarian tumour  
CC marker genes of the invention  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 TCGCGCTG 10  
Db 2 TCGCGCTG 9  
|||||  
|  
RESULT 142  
AAF43250  
ID AAF43250 standard; DNA; 10 BP.  
XX  
AC AAF43250;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11389.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
XX Example; Page 356; 419pp; English.  
PS The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate



CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 TGGCGAAG 18  
Db 1 TGGCGAAG 8  
  
RESULT 143  
ABL42674  
ID ABL42674 standard; cDNA; 10 BP.  
XX  
AC ABL42674;  
XX  
DT 12-APR-2002 (first entry)  
XX  
DE Human maturation/activation dendritic cell expression gene tag #48.  
XX  
KW Human; maturation/activation dendritic cell expression gene; tag;  
KW maturation; activation; dendritic cell; ss.  
XX Homo sapiens.  
OS  
PN JP2001327293-A.  
XX  
PD 27-NOV-2001.  
XX  
PF 22-MAY-2000; 2000JP-00150562.  
XX  
PR 22-MAY-2000; 2000JP-00150562.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-127070/17.  
XX  
PT Human maturation/activation dendritic cell expression gene group.  
PS Claim 1; Page 9; 41pp; Japanese.  
XX  
CC The present invention describes a human maturation/activation dendritic  
CC cell (DC) expression gene group consisting of 100 genes which show the  
CC highest expression among the genes expressed in human maturation/  
CC activation DC. Also described are: (1) a protein expressed by the above  
CC human maturation/activation DC expression gene; (2) an antibody against  
CC the protein; and (3) an antagonist against the expression of each gene  
CC belonging to the above gene group. The gene group is useful for the  
CC treatment and the diagnosis of various human diseases related to human  
CC DC. ABL42627 to ABL42926 represent specifically claimed human  
CC maturation/activation DC expression gene tags from the present invention  
XX

SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 CTGTGGCG 15  
Db 2 CTGTGGCG 9  
  
RESULT 144  
ABL42776  
ID ABL42776 standard; cDNA; 10 BP.  
XX  
AC ABL42776;  
XX  
DT 12-APR-2002 (first entry)  
XX  
DE Human maturation/activation dendritic cell expression gene tag #150.  
XX  
KW Human; maturation/activation dendritic cell expression gene; tag;  
KW maturation; activation; dendritic cell; ss.  
XX Homo sapiens.  
OS  
PN JP2001327293-A.  
XX  
PD 27-NOV-2001.  
XX  
PF 22-MAY-2000; 2000JP-00150562.  
XX  
PR 22-MAY-2000; 2000JP-00150562.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-127070/17.  
XX  
PT Human maturation/activation dendritic cell expression gene group.  
PS Claim 10; Page 13; 41pp; Japanese.  
XX  
CC The present invention describes a human maturation/activation dendritic  
CC cell (DC) expression gene group consisting of 100 genes which show the  
CC highest expression among the genes expressed in human maturation/  
CC activation DC. Also described are: (1) a protein expressed by the above  
CC human maturation/activation DC expression gene; (2) an antibody against  
CC the protein; and (3) an antagonist against the expression of each gene  
CC belonging to the above gene group. The gene group is useful for the  
CC treatment and the diagnosis of various human diseases related to human  
CC DC. ABL42627 to ABL42926 represent specifically claimed human  
CC maturation/activation DC expression gene tags from the present invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 CTGTGGCG 15  
Db 2 CTGTGGCG 9  
  
RESULT 145  
ABK96054  
ID ABK96054 standard; DNA; 10 BP.  
XX  
AC ABK96054;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Human LIPE gene polymorphism detection oligonucleotide primer #29.

XX Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;  
KW polymorphism; primer; ss.  
XX Homo sapiens.  
OS  
XX WO200240502-A2.  
PN  
XX 23-MAY-2002.  
PD  
XX 16-NOV-2001; 2001WO-US043518.  
PF  
XX 16-NOV-2000; 2000US-0249302P.  
PR  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;  
PI WPI; 2002-519369/55.  
XX  
PT Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for  
PT improving efficiency and reliability in drug development for treating  
PT diseases associated with LIPE activity, e.g. obesity and male sterility.  
XX  
XX Claim 17; Page 16; 142pp; English.  
PS  
XX The present invention relates to a new polynucleotide comprising a  
CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)  
CC isogenes. The invention is useful in screening for drugs targeting LIPE  
CC isogenes that are useful for treating obesity and male sterility. The  
CC methods of the invention are useful for improving the efficiency and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with LIPE activity. The polynucleotide  
CC is useful in studying the expression and function of LIPE, and in  
CC expressing LIPE protein for use in screening for candidate drugs to treat  
CC diseases related to LIPE activity. It is also useful in studying the  
CC effect of the variation on the biological activity of LIPE as well as on  
CC the binding affinity of candidate drugs targeting LIPE for the treatment  
CC of obesity and male sterility. The invention is useful for studying the  
CC expression of LIPE isogenes in vivo, for in vivo screening and testing of  
CC drugs targeted against LIPE protein, and for testing the efficacy of  
CC therapeutic agents and compounds for treating obesity and male sterility  
CC in a biological system. The present nucleic acid sequence represents one  
CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were  
CC used in the invention to detect polymorphisms in the human LIPE gene  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGGC 14  
Db |||||||  
2 GCTGTGGC 9  
  
RESULT 146  
AAL48073  
ID AAL48073 standard; DNA; 10 BP.  
XX  
AC AAL48073;  
XX  
DT 27-SEP-2002 (first entry)  
XX  
DE Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 51.  
XX  
KW Human; colony stimulating factor 3 (granulocyte); CSF3; SNP; isogene;  
KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;  
KW neutropenia; promyelocytic leukaemia; haematological disorder;  
KW gene therapy; PCR; primer extension oligonucleotide; ss.  
XX  
OS Homo sapiens.

XX WO200194364-A2.  
PN  
XX 13-DEC-2001.  
PD  
XX 11-JUN-2001; 2001WO-US018913.  
PF  
XX 09-JUN-2000; 2000US-0210380P.  
PR  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Duda A, Kazemi A, Messer C, Sausker EA;  
PI WPI; 2002-566435/60.  
XX  
PT New variants of colony stimulating factor 3 (CSF3) isogenes, useful for  
PT improving efficiency and reliability in the development of drugs for  
PT treating diseases associated with CSF3 activity e.g. neutropenia.  
XX  
PS Claim 19; Page 13; 68pp; English.  
XX  
CC The present invention provides the protein, gene and cDNA sequences of  
CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are  
CC single nucleotide polymorphisms (SNPs) identified within these sequences.  
CC The sequences can be used in the treatment of neutropenia, promyelocytic  
CC leukaemia and haematological disorders. The present sequence is an allele  
CC specific primer extension oligonucleotide used to isolate the coding  
CC sequences of the invention  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 GGCGAAGG 19  
Db |||||||  
2 GGCGAAGG 9  
  
RESULT 147  
ABK23699  
ID ABK23699 standard; DNA; 10 BP.  
XX  
AC ABK23699;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Transcript tag DNA sequence #288 induced or suppressed by N-myc.  
XX  
KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;  
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;  
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200185941-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 11-MAY-2001; 2001WO-NL000361.  
XX  
PR 11-MAY-2000; 2000EP-00201698.  
PR 29-JUN-2000; 2000EP-00202284.  
XX  
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
XX  
PI Versteeg R, Caron HN;  
XX  
DR WPI; 2002-066603/09.  
XX  
PT A new nucleic acid library of myc-dependent downstream genes capable of  
PT supporting a neoplastic characteristic of cancer is useful to find new

PT therapies and diagnoses for cancer.  
XX  
PS Disclosure; Page 57; 69pp; English.  
XX  
CC The present invention relates to a nucleic acid library comprising myc-  
CC dependent downstream genes or their functional fragments essentially  
CC capable of supporting a neoplastic character of cancer such as growth,  
CC invasion or spread. These myc target or tag sequences are identified by  
CC SAGE (serial analysis of gene expression). The library is useful to find  
CC new diagnoses and treatments for cancer. The invention is also useful to  
CC enhance production of recombinant proteins in a production system with  
CC high expression of endogenous or transfected myc oncogenes. ABK23412-  
CC ABK23828 represent transcript tag DNA sequences that are activated or  
CC repressed by N-myc in human neuroblastoma  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTG 12  
Db 3 GCGCTGTG 10  
| | | | | | | |  
3 GCGCTGTG 10  
  
RESULT 148  
ACA94662  
ID ACA94662 standard; DNA; 10 BP.  
XX  
AC ACA94662;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DE DNA tag from human transcript repressed in adenomas/cancers #195.  
XX  
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;  
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;  
KW kidney proximal tubule.  
XX  
OS Homo sapiens.  
XX  
PN WO2003022863-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028518.  
XX  
PR 07-SEP-2001; 2001US-0317494P.  
PR 30-MAY-2002; 2002US-0383805P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Buckhaults P, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2003-313220/30.  
XX  
PT Detecting colorectal cancer in a subject, involves detecting macrophage  
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood  
PT of the subject.  
XX  
PS Disclosure; Page 32; 59pp; English.  
XX  
CC The invention relates to detecting CC (colorectal cancer e.g. colorectal  
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)  
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing  
CC amount of MIC or RDP detected to that in normal subjects, where an  
CC elevated amount of MIC or RDP in the subject is an indicator of CC in  
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting  
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP  
CC mRNA detected to that in normal subjects, where an elevated amount of MIC  
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)  
CC isolating epithelial cells from blood of a subject, isolating an mRNA

CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP  
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in  
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where  
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative  
CC of CC in the subject; (d) contacting blood or faeces of a subject, with  
CC an RDP substrate, detecting activity of RDP in the blood or faeces by  
CC detection of increased reaction product or decreased RDP substrate, and  
CC comparing the amount of activity of RDP in blood or faeces of the subject  
CC to that in normal subjects, where an elevated amount of activity of RDP  
CC in the blood or faeces of the subject is an indicator of CC in the  
CC subject; (e) administering to a subject an antibody which specifically  
CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is  
CC labeled with a moiety which is detectable from outside of the subject and  
CC detecting the moiety in the subject from outside of the subject, where an  
CC area of localisation of the moiety within the subject but outside the  
CC proximal tubules of the kidney identifies CC; or (f) administering to a  
CC subject a substrate for RDP, the substrate being labeled with a  
CC detectable moiety, isolating faeces or blood from the subject, and  
CC detecting in the faeces or blood RDP reaction product or RDP substrate  
CC with the detectable moiety, where increased product or decreased  
CC substrate in the faeces or blood indicates CC in the subject. The methods  
CC are useful for detecting colorectal cancer in a subject. The present  
CC sequence is a DNA tag derived from a human transcript whose expression is  
CC repressed in colorectal cancer or colorectal adenoma  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTG 12  
Db 3 GCGCTGTG 10  
| | | | | | | |  
3 GCGCTGTG 10  
  
RESULT 149  
ACA94515  
ID ACA94515 standard; DNA; 10 BP.  
XX  
AC ACA94515;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DE DNA tag from human transcript repressed in adenomas/cancers #48.  
XX  
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;  
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;  
KW kidney proximal tubule.  
XX  
OS Homo sapiens.  
XX  
PN WO2003022863-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028518.  
XX  
PR 07-SEP-2001; 2001US-0317494P.  
PR 30-MAY-2002; 2002US-0383805P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Buckhaults P, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2003-313220/30.  
XX  
PT Detecting colorectal cancer in a subject, involves detecting macrophage  
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood  
PT of the subject.  
XX  
PS Disclosure; Page 27; 59pp; English.  
XX

CC The invention relates to detecting CC (colorectal cancer e.g. colorectal  
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)  
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing  
CC amount of MIC or RDP detected to that in normal subjects, where an  
CC elevated amount of MIC or RDP in the subject is an indicator of CC in  
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting  
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP  
CC mRNA detected to that in normal subjects, where an elevated amount of MIC  
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)  
CC isolating epithelial cells from blood of a subject, isolating an mRNA  
CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP  
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in  
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where  
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative  
CC of CC in the subject; (d) contacting blood or faeces of a subject, with  
CC an RDP substrate, detecting activity of RDP in the blood or faeces by  
CC detection of increased reaction product or decreased RDP substrate, and  
CC comparing the amount of activity of RDP in blood or faeces of the subject  
CC to that in normal subjects, where an elevated amount of activity of RDP  
CC in the blood or faeces of the subject is an indicator of CC in the  
CC subject; (e) administering to a subject an antibody which specifically  
CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is  
CC labeled with a moiety which is detectable from outside of the subject and  
CC detecting the moiety in the subject from outside of the subject, where an  
CC area of localisation of the moiety within the subject but outside the  
CC proximal tubules of the kidney identifies CC; or (f) administering to a  
CC subject a substrate for RDP, the substrate being labeled with a  
CC detectable moiety, isolating faeces or blood from the subject, and  
CC detecting in the faeces or blood RDP reaction product or RDP substrate  
CC with the detectable moiety, where increased product or decreased  
CC substrate in the faeces or blood indicates CC in the subject. The methods  
CC are useful for detecting colorectal cancer in a subject. The present  
CC sequence is a DNA tag derived from a human transcript whose expression is  
CC repressed in colorectal cancer or colorectal adenoma  
XX

SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGCG 15  
|||  
Db 2 CTGTGGCG 9

RESULT 150  
ADS76513  
ID ADS76513 standard; DNA; 10 BP.

XX  
AC ADS76513;  
XX 30-DEC-2004 (first entry)  
XX Breast cancer detection oligonucleotide #295.  
DE  
XX ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.

OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX 07-OCT-2004.  
XX 22-MAR-2004; 2004WO-US008866.  
XX 20-MAR-2003; 2003US-0456735P.  
PR (DAND ) DANA FARBER CANCER INST INC.  
PA

XX Polyak K, Porter D, Allinen M;  
PI WPI; 2004-728732/71.  
XX Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX Example 2; SEQ ID NO 295; 149pp; English.  
PS The invention relates to a method of diagnosis (M1) comprising: (a)  
XX providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC diamutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.

SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCTG 10  
|||  
Db 2 TCGCGCTG 9

RESULT 151  
ADS78031  
ID ADS78031 standard; DNA; 10 BP.

XX  
AC ADS78031;  
XX 30-DEC-2004 (first entry)  
XX Breast cancer detection oligonucleotide #1813.  
DE  
XX ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.

OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX 07-OCT-2004.  
XX 22-MAR-2004; 2004WO-US008866.  
XX 20-MAR-2003; 2003US-0456735P.  
XX (DAND ) DANA FARBER CANCER INST INC.

PI Polyak K, Porter D, Allinen M;  
XX WPI; 2004-728732/71.  
XX Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX Example 6; SEQ ID NO 1813; 149pp; English.  
PS The invention relates to a method of diagnosis (M1) comprising: (a)  
CC



CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.

XX  
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCGCGCTG 10  
| | | | |  
Db 2 TCGCGCTG 9

RESULT 152  
AD576514  
ID ADS76514 standard; DNA; 10 BP.

XX  
AC ADS76514;

XX  
DT 30-DEC-2004 (first entry)

XX  
DE Breast cancer detection oligonucleotide #296.

XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.

XX Homo sapiens.

XX  
PN WO2004085621-A2.

XX  
PD 07-OCT-2004.

XX  
PF 22-MAR-2004; 2004WO-US008866.

XX  
PR 20-MAR-2003; 2003US-0456735P.

XX  
PA (DAND ) DANA FARBER CANCER INST INC.

XX  
PI Polyak K, Porter D, Allinen M;

XX  
DR WPI; 2004-728732/71.

XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.

XX  
PS Example 2; SEQ ID NO 296; 149pp; English.

XX The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.

XX  
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCGCGCTG 10  
| | | | |  
Db 2 TCGCGCTG 9

RESULT 153  
ADU19803  
ID ADU19803 standard; DNA; 10 BP.  
XX  
AC ADU19803;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Hypoxia-related tumorigenesis-related SAGE tag #1594.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.

XX  
PN WO2004092198-A2.

XX  
PD 28-OCT-2004.

XX  
PF 09-APR-2004; 2004WO-US011087.

XX  
PR 09-APR-2003; 2003US-0461712P.

XX  
PA (GENZ ) GENZYME CORP.

XX  
PI Nacht M;

XX  
DR WPI; 2004-758333/74.

XX  
PT Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.

XX  
PS Disclosure; Page 88; 100pp; English.

XX The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.

XX  
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 42.1%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCGCGCTG 10  
| | | | |  
Db 2 TCGCGCTG 9

RESULT 154  
ABV69823/c  
ID ABV69823 standard; cDNA; 11 BP.

XX  
AC ABV69823;

XX  
DT 21-OCT-2002 (first entry)



DE Human skin EST 7609.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 241; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGC 14  
Db 8 GCTGTGGC 1  
  
RESULT 155  
ABV62402/c  
ID ABV62402 standard; cDNA; 11 BP.  
XX  
AC ABV62402;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 188.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGC 14  
Db 8 GCTGTGGC 1  
  
RESULT 155  
ABV62402/c  
ID ABV62402 standard; cDNA; 11 BP.  
XX  
AC ABV62402;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 188.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.

XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 31; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGC 14  
Db 8 GCTGTGGC 1  
  
RESULT 156  
ABV67604/c  
ID ABV67604 standard; cDNA; 11 BP.  
XX  
AC ABV67604;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 5390.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX

PS Disclosure; Page 174; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 5 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 42.1%; Score 8; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGC 14  
Db 8 GCTGTGGC 1  
  
RESULT 157  
AAC85261  
ID AAC85261 standard; DNA; 11 BP.  
XX  
AC AAC85261;  
XX  
DT 22-MAR-2001 (first entry)  
XX  
DE mutD promoter sequence pOS102.  
XX  
KW E. coli; mutD; evolved microorganism; heterologous; mutator gene;  
KW mutation rate; DNA repair gene; proof reading; selective pressure; ss.  
XX  
OS Synthetic.  
XX  
PN WO200070037-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 15-MAY-2000; 2000WO-US013337.  
XX  
PR 19-MAY-1999; 99US-00314847.  
XX  
PA (GEMV ) GENENCOR INT INC.  
XX  
PI Schellenberger V, Liu AD, Selifonova OV;  
XX  
DR WPI; 2001-070775/08.  
XX  
PT Directing evolution of microorganisms to produce microorganisms able to  
PT grow under conditions suitable for production of useful products,  
PT comprises using mutator genes and extreme conditions.  
XX  
PS Disclosure; Page 12; 47pp; English.  
XX  
CC The sequences given in AAC85259-64 represent mutated promoter sequences  
CC which were used with the E. coli mutD coding sequence in the method of  
CC the invention to prepare an evolved microorganism. The method comprises  
CC culturing a microorganism having a heterologous mutator gene, for at  
CC least 20 doublings to select an evolved microorganism, where the gene  
CC generates a mutation rate of at least 5 - 100 000 fold relative to wild  
CC type. The evolved microorganism is then restored to a wild type mutation  
CC rate. A mutator gene is defined in the specification as being a DNA  
CC repair gene which comprises a mutation and which has impaired proof  
CC reading function. The method is useful for directing the evolution of a  
CC microorganism, i.e., directing desired genetic change in microorganisms  
CC in response to selective pressure. Microorganisms are produced that are

CC capable of producing, e.g., enzymes, growth factors, hormones, vitamins,  
CC amino acids, dyes or other chemicals. The method can be used to produce  
CC microorganisms which can grow under extreme conditions, e.g., high  
CC temperature, pH extremes, high salt concentrations or the presence of  
CC solvent  
XX  
SQ Sequence 11 BP; 0 A; 3 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 GTCGCGCTGTG 12  
Db 1 GTCGCGCTGTG 11  
  
RESULT 158  
ABQ87267  
ID ABQ87267 standard; cDNA; 11 BP.  
XX  
AC ABQ87267;  
XX  
DT 10-SEP-2002 (first entry)  
XX  
DE Human skin stress/ageing related EST SEQ ID NO 1022.  
XX  
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253773-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015178.  
XX  
PR 03-JAN-2001; 2001DE-01000121.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-528865/56.  
XX  
PT Identifying genes involved in skin stress and aging, useful e.g. in  
PT screening for cosmetic or therapeutic agents, based on differential gene  
PT expression.  
XX  
PS Claim 8; Page 79; 325pp; German.  
XX  
CC The invention relates to identifying (M1) genes in vitro that, in humans  
CC or animals, are important for skin ageing and/or skin stress by serial  
CC analysis of gene expression between mixtures of transcribed and  
CC optionally translated, genetically encoded factors (A) obtained from  
CC young and aged skin, to identify that genes that show strong differential  
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is  
CC useful for: identifying markers of skin ageing and/or stress; determining  
CC skin ageing and/or stress; and identifying or determining the effects of  
CC pharmaceutical or cosmetic agents for control of skin ageing. The present  
CC sequence is one of a group of human skin ageing/stress related expressed  
CC sequence tags (ABQ86246-ABQ87680) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 8 CTGTGGCGAAG 18  
Db 1 CTGGGGGGAAG 11

```
RESULT 159
ABQ87096/c
ID  ABQ87096 standard; cDNA; 11 BP.
XX
AC  ABQ87096;
XX
DT  10-SEP-2002 (first entry)
XX
DE  Human skin stress/ageing related EST SEQ ID NO 851.
XX
KW  Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS  Homo sapiens.
XX
PN  WO200253773-A2.
XX
PD  11-JUL-2002.
XX
PF  20-DEC-2001; 2001WO-EP015178.
XX
PR  03-JAN-2001; 2001DE-01000121.
XX
PA  (HENK ) HENKEL KGAA.
XX
PI  Petersohn D, Conradt M, Hofmann K;
XX
DR  WPI; 2002-528865/56.
XX
PT  Identifying genes involved in skin stress and aging, useful e.g. in
PT  screening for cosmetic or therapeutic agents, based on differential gene
PT  expression.
XX
PS  Claim 8; Page 72; 325pp; German.
XX
CC  The invention relates to identifying (M1) genes in vitro that, in humans
CC  or animals, are important for skin ageing and/or skin stress by serial
CC  analysis of gene expression between mixtures of transcribed and
CC  optionally translated, genetically encoded factors (A) obtained from
CC  young and aged skin, to identify that genes that show strong differential
CC  expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC  useful for: identifying markers of skin ageing and/or stress; determining
CC  skin ageing and/or stress; and identifying or determining the effects of
CC  pharmaceutical or cosmetic agents for control of skin ageing. The present
CC  sequence is one of a group of human skin ageing/stress related expressed
CC  sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ  Sequence 11 BP; 2 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
Db 11 CTCGCTGGGCG 1

RESULT 160
ABQ87230/c
ID  ABQ87230 standard; cDNA; 11 BP.
XX
AC  ABQ87230;
XX
DT  10-SEP-2002 (first entry)
XX
DE  Human skin stress/ageing related EST SEQ ID NO 985.
XX
KW  Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
OS  Homo sapiens.
XX
PN  WO200253773-A2.
PT  In vitro identification of skin-expressed genes, useful for determining
```

```
XX
PD  11-JUL-2002.
XX
PF  20-DEC-2001; 2001WO-EP015178.
XX
PR  03-JAN-2001; 2001DE-01000121.
XX
PA  (HENK ) HENKEL KGAA.
XX
PI  Petersohn D, Conradt M, Hofmann K;
XX
DR  WPI; 2002-528865/56.
XX
PT  Identifying genes involved in skin stress and aging, useful e.g. in
PT  screening for cosmetic or therapeutic agents, based on differential gene
PT  expression.
XX
PS  Claim 8; Page 78; 325pp; German.
XX
CC  The invention relates to identifying (M1) genes in vitro that, in humans
CC  or animals, are important for skin ageing and/or skin stress by serial
CC  analysis of gene expression between mixtures of transcribed and
CC  optionally translated, genetically encoded factors (A) obtained from
CC  young and aged skin, to identify that genes that show strong differential
CC  expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC  useful for: identifying markers of skin ageing and/or stress; determining
CC  skin ageing and/or stress; and identifying or determining the effects of
CC  pharmaceutical or cosmetic agents for control of skin ageing. The present
CC  sequence is one of a group of human skin ageing/stress related expressed
CC  sequence tags (ABQ86246-ABQ87680) of the invention
XX
SQ  Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGGAAG 18
Db 11 CTGGGGGCTAAG 1

RESULT 161
ABV68460/c
ID  ABV68460 standard; cDNA; 11 BP.
XX
AC  ABV68460;
XX
DT  21-OCT-2002 (first entry)
XX
DE  Human skin EST 6246.
XX
KW  Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW  immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW  psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS  Homo sapiens.
XX
PN  WO200253774-A2.
XX
PD  11-JUL-2002.
XX
PF  20-DEC-2001; 2001WO-EP015179.
XX
PR  03-JAN-2001; 2001DE-01000127.
XX
PA  (HENK ) HENKEL KGAA.
XX
PI  Petersohn D, Conradt M, Hofmann K;
XX
DR  WPI; 2002-590638/63.
XX
PT  In vitro identification of skin-expressed genes, useful for determining
```

PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 198; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GGTCGGCGCTGT 11  
Db 11 GGTCACCCCTGT 1  
  
RESULT 162  
ABV69665  
ID ABV69665 standard; cDNA; 11 BP.  
XX  
AC ABV69665;  
XX  
XX 21-OCT-2002 (first entry)  
DT Human skin EST 7451.  
DE  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
XX  
DT 21-OCT-2002 (first entry)  
XX Human skin EST 7451.  
DE  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 234; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 CGCGCTGTGGC 14  
Db 1 CACGCAGTGGC 11  
  
RESULT 163  
ABV65281  
ID ABV65281 standard; cDNA; 11 BP.  
XX  
AC ABV65281;  
XX  
XX 21-OCT-2002 (first entry)  
DT Human skin EST 3067.  
DE  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
DR WPI; 2002-590638/63.  
XX  
XX In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 110; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGAAG 18  
||| ||| |||







XX (HENK ) HENKEL KGAA.  
PA  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 59; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGGAAG 18  
Db 11 CTGGGGCTAAG 1  
  
RESULT 167  
ABV72108/c  
ID ABV72108 standard; cDNA; 11 BP.  
XX  
AC ABV72108;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 9894.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 9894.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Claim 24; Page 323; 1345pp; German.  
XX

CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX  
SQ Sequence 11 BP; 2 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAAGG 19  
Db 11 TGTGCCCAAGG 1  
  
RESULT 168  
ABV66734  
ID ABV66734 standard; cDNA; 11 BP.  
XX  
AC ABV66734;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Human skin EST 4520.  
XX  
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;  
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;  
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200253774-A2.  
XX  
PD 11-JUL-2002.  
XX  
PF 20-DEC-2001; 2001WO-EP015179.  
XX  
PR 03-JAN-2001; 2001DE-01000127.  
XX  
PA (HENK ) HENKEL KGAA.  
XX  
PI Petersohn D, Conradt M, Hofmann K;  
XX  
XX WPI; 2002-590638/63.  
XX  
PT In vitro identification of skin-expressed genes, useful for determining  
PT homeostasis and identifying cosmetic or pharmaceutical agents against  
PT e.g. skin cancer.  
XX  
PS Disclosure; Page 149; 1345pp; German.  
XX  
CC The invention relates to in vitro identification (M1) of genes expressed  
CC in the skin of humans or animals by subjecting a mixture of genetically  
CC encoded factors from skin, to serial analysis of gene expression (SAGE)  
CC so as to identify skin-expressed genes and quantify their expression.  
CC (M1) is useful for identifying genes involved in skin homeostasis; to  
CC determine skin homeostasis and to test agent (A) that maintains or  
CC promotes skin homeostasis or that can be used for treating skin  
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;  
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;  
CC rosacea; melanoma; basal cell carcinoma; and carcinoma of the  
CC skin. The present sequence is that of a human expressed sequence tag  
CC (EST) of the invention  
XX

SQ	Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;	
	Query Match 41.1%; Score 7.8; DB 1; Length 11;	
	Best Local Similarity 81.8%; Pred. No. 1.3e+02;	
	Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	8 CTGTGGCGAAG 18	
Db	1 CTGTGTCCAAG 11	
RESULT 169		
ABV62244		
ID	ABV62244 standard; cDNA; 11 BP.	
XX		
AC	ABV62244;	
XX		
DT	21-OCT-2002 (first entry)	
XX		
DE	Human skin EST 30.	
XX		
KW	Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;	
KW	immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;	
KW	psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200253774-A2.	
XX		
PD	11-JUL-2002.	
XX		
PF	20-DEC-2001; 2001WO-EP015179.	
XX		
PR	03-JAN-2001; 2001DE-01000127.	
XX		
PA	(HENK ) HENKEL KGAA.	
XX		
PI	Petersohn D, Conradt M, Hofmann K;	
XX		
DR	WPI; 2002-590638/63.	
XX		
PT	In vitro identification of skin-expressed genes, useful for determining	
PT	homeostasis and identifying cosmetic or pharmaceutical agents against	
PT	e.g. skin cancer.	
XX		
PS	Disclosure; Page 26; 1345pp; German.	
XX		
CC	The invention relates to in vitro identification (M1) of genes expressed	
CC	in the skin of humans or animals by subjecting a mixture of genetically	
CC	encoded factors from skin, to serial analysis of gene expression (SAGE)	
CC	so as to identify skin-expressed genes and quantify their expression.	
CC	(M1) is useful for identifying genes involved in skin homeostasis; to	
CC	determine skin homeostasis and to test agent (A) that maintains or	
CC	promotes skin homeostasis or that can be used for treating skin	
CC	disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;	
CC	ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;	
CC	rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the	
CC	skin. The present sequence is that of a human expressed sequence tag	
CC	(EST) of the invention	
XX		
SQ	Sequence 11 BP; 2 A; 4 C; 4 G; 1 T; 0 U; 0 Other;	
	Query Match 41.1%; Score 7.8; DB 1; Length 11;	
	Best Local Similarity 81.8%; Pred. No. 1.3e+02;	
	Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	4 CGCGCTGTGGC 14	
Db	1 CACGCAGTGGC 11	
RESULT 170		
ADQ36355		

SQ	Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;	
	Query Match 41.1%; Score 7.8; DB 1; Length 11;	
	Best Local Similarity 81.8%; Pred. No. 1.3e+02;	
	Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	5 GCGCTGTGGCG 15	
Db	1 GCGCTGTGGAG 11	
RESULT 171		
ADQ35677		
ID	ADQ35677 standard; DNA; 11 BP.	
XX		
AC	ADQ35677;	
XX		
DT	23-SEP-2004 (first entry)	

ID	ADQ36355 standard; DNA; 11 BP.	
XX		
AC	ADQ36355;	
XX		
DT	23-SEP-2004 (first entry)	
XX		
DE	Human hair-bearing skin-associated DNA fragment SEQ ID NO 1172.	
XX		
KW	hair-bearing skin; human; serial analysis of gene expression; SAGE;	
KW	homeostasis; cosmetic; pharmaceutical; biochip; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	DE10260931-A1.	
XX		
PD	08-JUL-2004.	
XX		
PF	20-DEC-2002; 2002DE-01060931.	
XX		
PR	20-DEC-2002; 2002DE-01060931.	
XX		
PA	(HENK ) HENKEL KGAA.	
XX		
PI	Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;	
PI	Conradt M, Hofmann K;	
XX		
DR	WPI; 2004-518857/50.	
XX		
PT	In vitro identification of genes important for hair-bearing skin, useful	
PT	for assessing homeostasis and in screening for pharmaceutical or cosmetic	
PT	agents, based on differential expression analysis.	
XX		
PS	Claim 4; SEQ ID NO 1172; 250pp; German.	
XX		
CC	This invention describes a novel in vitro method for identifying genes	
CC	that are significant for hair-bearing skin in humans. The method	
CC	comprises recovering, from hair-bearing skin, a first mixture of	
CC	genetically expressed (transcribed and optionally translated) factors	
CC	(i.e. proteins, mRNA or their fragments), recovering a second, similar	
CC	mixture from skin on which hair does not grow and subjecting both	
CC	mixtures to serial analysis of gene expression (SAGE) to identify those	
CC	genes for which expression is markedly different between the two types of	
CC	skin. The invention also describes in vitro methods for determining	
CC	homeostasis of human hair-bearing skin and for determining activity of	
CC	cosmetic and pharmaceutical agents for use against disorders or	
CC	disturbances of the homeostasis of human hair-bearing skin. A biochip and	
CC	a test kit comprising a solid support (flexible or rigid) with	
CC	immobilised probes are also described for determining homeostasis. The	
CC	hair-bearing skin is from the scalp and the other skin is from the face.	
CC	The method allows identification of as many as possible of the genes	
CC	important for hair-bearing skin, and therefore, of a very wide range of	
CC	potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent	
CC	human DNA tag fragments used to identify genes associated with hair-	
CC	bearing skin.	
XX		
SQ	Sequence 11 BP; 1 A; 1 C; 7 G; 2 T; 0 U; 0 Other;	
	Query Match 41.1%; Score 7.8; DB 1; Length 11;	
	Best Local Similarity 81.8%; Pred. No. 1.3e+02;	
	Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	5 GCGCTGTGGCG 15	
Db	1 GCGCTGTGGAG 11	
RESULT 171		
ADQ35677		
ID	ADQ35677 standard; DNA; 11 BP.	
XX		
AC	ADQ35677;	
XX		
DT	23-SEP-2004 (first entry)	

```
XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 494.
XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX OS Homo sapiens.
XX XX DE10260931-A1.
XX PN 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060931.
XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518857/50.
XX PS Claim 5; SEQ ID NO 494; 250pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
CC that are significant for hair-bearing skin in humans. The method
CC comprises recovering, from hair-bearing skin, a first mixture of
CC genetically expressed (transcribed and optionally translated) factors
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC mixture from skin on which hair does not grow and subjecting both
CC mixtures to serial analysis of gene expression (SAGE) to identify those
CC genes for which expression is markedly different between the two types of
CC skin. The invention also describes in vitro methods for determining
CC homeostasis of human hair-bearing skin and for determining activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC a test kit comprising a solid support (flexible or rigid) with
CC immobilised probes are also described for determining homeostasis. The
CC hair-bearing skin is from the scalp and the other skin is from the face.
CC The method allows identification of as many as possible of the genes
CC important for hair-bearing skin, and therefore, of a very wide range of
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC human DNA Tag fragments used to identify genes associated with hair-
CC bearing skin.
XX SQ Sequence 11 BP; 3 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 1 TGTGGGGAAG 11

RESULT 172
ADQ34103/c
ID ADQ34103 standard; DNA; 11 BP.
XX AC ADQ34103;
XX XX 23-SEP-2004 (first entry)
DT Human facial skin-associated DNA fragment SEQ ID NO 2193.
DE facial skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
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```
XX OS Homo sapiens.
XX XX DE10260928-A1.
XX PN 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060928.
XX PR 20-DEC-2002; 2002DE-01060928.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PI Conradt M, Hofmann K;
XX DR WPI; 2004-518855/50.
XX PS Claim 4; SEQ ID NO 2193; 577pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.
XX SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGT 11
Db 11 GGTCACCCCTGT 1

RESULT 173
ADT79188
ID ADT79188 standard; DNA; 11 BP.
XX AC ADT79188;
XX XX 30-DEC-2004 (first entry)
DT Oligonucleotide #1 used in detection of Cx26 35deltaG mutation.
DE Connexin 26; Cx26; non-syndromic hearing impairment; NSH1;
XX KW gap-junction beta 2; GJB2; ss.
XX OS Unidentified.
XX PN US2004203035-A1.
```

XX PD 14-OCT-2004.  
XX PF 09-JAN-2004; 2004US-00754408.  
XX PR 09-JAN-2003; 2003US-0438963P.  
XX PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
XX PI Mast AL, Dorn E, Kwiatkowski RJ, Accola M, Wigdal SS;  
XX DR WPI; 2004-746972/73.  
XX  
PT New kit comprises non-amplified oligonucleotide detection assay  
PT configured for detecting at least one Connexin 26 allele, useful for  
PT screening nucleic acid samples for the presence of mutations in the  
PT connexin 26 or gap-junction beta 2 gene.  
XX  
PS Disclosure; SEQ ID NO 8; 25pp; English.  
XX  
CC The present invention relates to a method which comprises of a non-  
CC amplified oligonucleotide detection assay configured for detecting at  
CC least one Connexin 26 (Cx26) allele. The method of the invention is  
CC useful for the detection and characterisation of mutations associated  
CC with non-syndromic hearing impairment (NSHI). The invention is also  
CC useful for using invasive cleavage structure assays to screen nucleic  
CC acid samples for the presence of mutations in the connexin 26 or gap-  
CC junction beta 2 gene (GJB2) associated with non-syndromic hearing loss.  
CC The present sequence is an oligonucleotide used in the detection of Cx26  
CC 35deltaG mutation.  
XX  
SQ Sequence 11 BP; 1 A; 5 C; 5 G; 0 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 CGCGCTGTGGC 14  
Db | || || | || ||  
1 CGCGCCGAGGC 11  
  
RESULT 174  
ADZ24827/C  
ID ADZ24827 standard; DNA; 11 BP.  
XX  
AC ADZ24827;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human SNP detection related oligonucleotide #1794.  
XX  
KW ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasia;  
KW immune disorder; cardiovascular disease; metabolic disorder;  
KW respiratory disease; musculoskeletal disease; renal disease;  
KW nephrotropic; endocrine disease; genitourinary disease.  
XX  
OS Homo sapiens.  
XX  
PN WO2005030952-A1.  
XX  
PD 07-APR-2005.  
XX  
PF 30-SEP-2004; 2004WO-JP014784.  
XX  
PR 30-SEP-2003; 2003JP-00342519.  
PR 28-MAY-2004; 2004JP-00158717.  
XX  
PA (RIKE ) RIKEN KK.  
PA (STAG-) STAGEN CO LTD.  
PA (SEKI/) SEKINE A.  
PA (IIDA/) IIDA A.  
PA (SAIT/) SAITO S.

XX PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;  
XX DR WPI; 2005-305936/31.  
XX  
PT Analyzing haplotype, by detecting polymorphism in drug-related genes,  
PT electing common polymorphism (CP), building haplotype block using CP,  
PT specifying CP within block, specifying tag polymorphism from CP within  
PT block.  
XX  
PS Disclosure; SEQ ID NO 1794; 1290pp; Japanese.  
XX  
CC The invention relates to a method of analyzing haplotype, by detecting  
CC gene polymorphism in drug-related genes such as aryl acetylamine  
CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,  
CC sub-family A (ABC1), member 1. The method is useful for analyzing  
CC haplotype. The method is useful for estimating the sensitivity or disease  
CC of a medicine or a foreign material, for selecting appropriate dosage for  
CC preventing or treating diseases, for determining appropriate dosage of  
CC medicine for preventing or treating a disease, for analyzing a drug  
CC interaction, and for determining the related polymorphism relative to the  
CC sensitivity of the medicine, foreign material or disease. The diseases  
CC include malignant tumor, immune disorder circulatory disease, metabolic  
CC disease, kidney disease, respiratory disease and muscle associated  
CC disease. The method enables analysis of the individual differences  
CC related to the sensitivity of a medicine, using a haplotype, without  
CC using each single nucleotide polymorphism. The present sequence  
CC represents a human SNP detection related oligonucleotide.  
XX  
SQ Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 41.1%; Score 7.8; DB 1; Length 11;  
Best Local Similarity 81.8%; Pred. No. 1.3e+02;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCTGT 11  
Db | || || | || ||  
11 GCTCGCACTGT 1  
  
RESULT 175  
AAQ71089/C  
ID AAQ71089 standard; cDNA; 10 BP.  
XX  
AC AAQ71089;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1995 (first entry)  
XX  
DE Merlin exon 7 splice acceptor site.  
XX  
KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D2S28;  
KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
KW merlin-associated tumour; D2S1; posterior capsular lens opacity;  
KW deafness; balance disorder; paralysis; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP613945-A2.  
XX  
PD 07-SEP-1994.  
XX  
PF 25-FEB-1994; 94EP-00301367.  
XX  
PR 25-FEB-1993; 93US-00022034.  
PR 04-MAR-1993; 93US-00026063.  
PR 19-AUG-1993; 93US-00108808.  
PR 22-DEC-1993; 93US-00171718.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX



PI Trofatter JA, Maccollin MM, Gusella JF;  
XX  
DR WPI; 1994-272992/34.  
XX  
PT The tumour suppressor gene merlin - for treatment and diagnosis of  
XX tumours and neurofibromatosis (NF2).  
PT  
XX  
PS Example 6; Page 26; 86pp; English.  
XX  
CC The sequences given in AAQ71078-109 represent the splice donor and  
CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-  
CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
CC The missing or mutated gene in NF2 patients has been shown to be the  
CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-  
CC like protein), which possesses tumour suppressor activity, and whose  
CC tumour suppressor activity is mediated by inter- actions with the  
CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
CC is either lost or mutated. A mutant merlin protein may be encoded by a  
CC gene in which a mutation of A to T at the first position of the codon  
CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
CC merlin gene may be used in gene therapy for the treatment of a merlin-  
CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
CC posterior capsular lens opacities, deafness or hearing loss, balance  
CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGA 16  
Db ||||| |  
10 CTGTGGGGA 2  
  
RESULT 176  
AAQ71095/c  
ID AAQ71095 standard; cDNA; 10 BP.  
XX  
AC AAQ71095;  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1995 (first entry)  
XX  
DE Merlin exon 10 splice acceptor site.  
XX  
KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;  
KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
KW deafness; balance disorder; paralysis; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP613945-A2.  
XX  
PD 07-SEP-1994.  
XX  
PF 25-FEB-1994; 94EP-00301367.  
XX  
PR 25-FEB-1993; 93US-00022034.  
PR 04-MAR-1993; 93US-00026063.  
PR 19-AUG-1993; 93US-00108808.  
PR 22-DEC-1993; 93US-00171718.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI Trofatter JA, Maccollin MM, Gusella JF;  
XX

DR WPI; 1994-272992/34.  
XX  
PT The tumour suppressor gene merlin - for treatment and diagnosis of  
PT tumours and neurofibromatosis (NF2).  
XX  
PS Example 6; Page 26; 86pp; English.  
XX  
CC The sequences given in AAQ71078-109 represent the splice donor and  
CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-  
CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
CC The missing or mutated gene in NF2 patients has been shown to be the  
CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-  
CC like protein), which possesses tumour suppressor activity, and whose  
CC tumour suppressor activity is mediated by inter- actions with the  
CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
CC is either lost or mutated. A mutant merlin protein may be encoded by a  
CC gene in which a mutation of A to T at the first position of the codon  
CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
CC merlin gene may be used in gene therapy for the treatment of a merlin-  
CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
CC posterior capsular lens opacities, deafness or hearing loss, balance  
CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGA 16  
Db ||||| |  
10 CTGTGGCCA 2  
  
RESULT 177  
AAQ96664/c  
ID AAQ96664 standard; DNA; 10 BP.  
XX  
AC AAQ96664;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)  
XX  
DE HIV-1 NL4-3 nef gene nucleotide deletion 259.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.  
XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.  
XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX  
DR WPI; 1995-293115/38.  
XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.  
XX  
PS Claim 13; Page 191; 301pp; English.



XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
Db 9 GTGGCTAAG 1

RESULT 178  
AAQ96663/c  
ID AAQ96663 standard; DNA; 10 BP.  
XX  
AC AAQ96663;  
XX  
DT 16-OCT-2003 (revised)  
DT 22-MAR-1996 (first entry)

DE HIV-1 NL4-3 nef gene nucleotide deletion 258.  
XX  
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
OS Human immunodeficiency virus 1.  
XX  
PN WO9521912-A1.

XX  
PD 17-AUG-1995.  
XX  
PF 14-FEB-1995; 95WO-AU0000063.  
XX  
PR 14-FEB-1994; 94AU-00003864.  
PR 21-FEB-1994; 94AU-00004002.  
PR 23-DEC-1994; 94AU-00000284.

XX  
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
PA (AURE-) AUSTRALIAN RED CROSS SOC.  
XX  
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
XX WPI; 1995-293115/38.

XX  
PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
PT LTR region - can be used in a vaccine to inhibit/reduce productive  
PT infection in an individual by a pathogenic strain.

PS Claim 13; Page 191; 301pp; English.  
XX  
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
CC resulting avirulent HIV strains are still capable of inducing an immune  
CC response in humans, and enable the generation of therapeutic, diagnostic  
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
CC standardise OS field)

XX  
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
Db 10 GTGGCTAAG 2  
  
RESULT 179  
AAX18633  
ID AAX18633 standard; DNA; 10 BP.  
XX  
AC AAX18633;

XX  
DT 06-MAY-1999 (first entry)  
XX  
DE p53 serial analysis of gene expression tag #31.  
XX

KW p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic;  
KW rat embryo fibroblast; REF; tumour suppressor; cell cycle control;  
KW tumorigenesis; diagnosis; ss.

XX Synthetic.  
OS Rattus sp.  
XX  
PN WO9901581-A1.  
XX  
PD 14-JAN-1999.  
XX  
PF 02-JUL-1998; 98WO-US013903.  
XX  
PR 02-JUL-1997; 97US-0051573P.

XX (GENZ ) GENZYME CORP.  
XX  
PI Madden SL, Galella EA, Bertelsen AH, Beaudry GA;  
XX WPI; 1999-106079/09.

XX  
PT Diagnosis of cancer in potentially neoplastic samples - by comparing the  
PT level of transcription between RNA transcripts in two tissue samples,  
PT useful for providing an extensive profile of gene expression in rat  
PT embryo fibroblast (REF) cells.

XX  
PS Example 2; Page 15; 32pp; English.  
XX  
CC A method has been developed for the diagnosis of cancer in potentially  
CC neoplastic samples. The method comprises comparing the level of  
CC transcription between RNA transcripts in two tissue samples (which are of  
CC the same type), where the first sample is potentially neoplastic, and the  
CC second sample is normal human tissue. The first sample is categorized as  
CC neoplastic if its level of transcription is lower than that of the second  
CC sample. The transcript is selected from Alu, RAS, U6 snRNA, 16S RNA, EGR-  
CC 1, ribosomal protein S27, ETS-1, 28S RNA, CGR11, and LIMK-2, and it is  
CC identified by a tag selected from ribosomal protein L13a, alpha-tubulin  
CC (T1) and (T2), thymosin beta-4, and gamma- actin. The present sequence  
CC represents a serial analysis of gene expression (SAGE) tag from the  
CC present invention. The use of SAGE tags provides an extensive profile of  
CC gene expression in rat embryo fibroblast (REF) cells containing the (non)  
CC -functional p53 tumour suppression gene. The discovery of new SAGE tags,  
CC which are regulated by p53, enables the diagnosis of genes that are  
CC related to cell cycle control and tumorigenesis

SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGCGCAAGG 19  
Db 2 TGCTGAAGG 10

RESULT 180

AAZ79074/c  
ID AAZ79074 standard; DNA; 10 BP.  
XX  
AC AAZ79074;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:1502.  
XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 108; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell

CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGCG 15  
| | | | | | | |  
Db 10 GCTGTGGGG 2  
  
RESULT 181  
AAZ79675  
ID AAZ79675 standard; DNA; 10 BP.  
XX  
AC AAZ79675;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:2103.  
XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 108; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell

PR 19-JUN-1998; 98US-00900040P.  
PR 19-JUN-1998; 98US-00900041P.  
PR 19-JUN-1998; 98US-00900042P.  
PR 19-JUN-1998; 98US-00900043P.  
PR 19-JUN-1998; 98US-00900044P.  
PR 19-JUN-1998; 98US-00900045P.  
PR 19-JUN-1998; 98US-00900047P.  
PR 19-JUN-1998; 98US-00900048P.  
PR 19-JUN-1998; 98US-00900072P.  
PR 19-JUN-1998; 98US-00900076P.  
PR 19-JUN-1998; 98US-00900077P.  
PR 19-JUN-1998; 98US-00900078P.  
PR 19-JUN-1998; 98US-00900079P.  
PR 19-JUN-1998; 98US-00900080P.  
PR 08-DEC-1998; 98US-01111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 124; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
expression) tags used to identify mRNA transcripts encoding  
immunostimulatory cofactor proteins which are preferentially or  
differentially expressed in monocyte-derived dendritic cells compared  
with monocytes. Some of the transcripts correspond to known genes or ESTs  
(expressed sequence tags) which were previously unknown to be  
preferentially or differentially expressed in dendritic cells, while  
other transcripts correspond to novel genes. Antigen-presenting cell  
(APC)-associated costimulatory factors play an important role in the  
activation of the cytotoxic immune response, particularly against tumour  
cells. Tumour antigen presentation via the MHC (major histocompatibility  
complex) and subsequent recognition by T-cell receptors is alone  
insufficient to activate a robust cytotoxic immune response that can lyse  
the tumour cells, immunostimulatory cofactors also being required for  
efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
sequences identified using the SAGE tags have several potential uses.  
They may be used in vaccines to induce an immune response, particularly  
against a tumour antigen; to modulate the genotype of an APC; to screen  
for agents that modulate expression of differentially expressed genes in  
an APC; and as hybridisation probes/amplification primers for the  
diagnosis, prognosis and monitoring of diseases related to abnormal  
expression of these genes. Detection of the dendritic cell differentially  
expressed genes, or of their encoded proteins, can be used to identify  
cells as belonging to the monocyte lineage. Cells containing these genes  
can be used in active immunotherapy (or to stimulate production of a  
population of antigen-specific effector cells) and vectors containing  
them are used in gene therapy. Co-administration of tumour antigens and  
APC-associated costimulatory factors ensures adequate antigen  
presentation to endogenous APCs and upregulates the APCs for the  
presentation of co-stimulatory signals, migration to T cell-rich sites,  
secretion of T cell growth factors and secretion of chemokines for  
recruitment of immune effector cells

SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 GCGCTGTGG 13  
| | | | |  
Db 2 GGGCTGTGG 10

RESULT 182  
AAZ79480  
ID AAZ79480 standard; DNA; 10 BP.  
XX  
AC AAZ79480;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:1908.  
XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
APC; monocyte-derived dendritic cell; differential gene expression;  
immunostimulatory cofactor; costimulatory factor; CTL;  
cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-01111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 119; 130pp; English.  
XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
expression) tags used to identify mRNA transcripts encoding  
immunostimulatory cofactor proteins which are preferentially or  
differentially expressed in monocyte-derived dendritic cells compared  
with monocytes. Some of the transcripts correspond to known genes or ESTs  
(expressed sequence tags) which were previously unknown to be  
preferentially or differentially expressed in dendritic cells, while

CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 0 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15  
|||||||  
Db 2 GCTGTGGGG 10

RESULT 183

AAZ78781/c  
ID AAZ78781 standard; DNA; 10 BP.

XX AAZ78781;

DT 10-APR-2000 (first entry)

DE Human dendritic cell SAGE tag, SEQ ID NO:1209.

XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

PF 18-JUN-1999; 99WO-US013800.

XX 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-0089991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106077/09.

XX

PT Isolated polynucleotides differentially expressed in antigen-presenting

XX cells, useful in gene vaccines against cancer.

PS Claim 1; Page 99; 130pp; English.

XX  
CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.

CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells

XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 38.9%; Score 7.4; DB 1; Length 10;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

|||||

Db 10 TGGAGAAGG 2



RESULT 184  
AAZ82348/C  
ID AAZ82348 standard; DNA; 10 BP.  
XX  
AC AAZ82348;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1582.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 100; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
| | | | | | | |

Db 10 CTCTGTGGC 2  
RESULT 185  
AAZ81963/C  
ID AAZ81963 standard; DNA; 10 BP.  
XX  
AC AAZ81963;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1197.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 90; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY	6	CGCTGTGGC 14	
Db	9	CTCTGTGGC 1	
RESULT 186			
AAZ85441/c			
ID	AAZ85441 standard; DNA; 10 BP.		
XX			
AC	AAZ85441;		
XX			
DT	07-APR-2000 (first entry)		
XX			
DE	Metastatic breast tumour cell downregulated transcript tag #4675.		
XX			
KW	Human; metastatic breast tumour tissue; breast cancer; tag; primer;		
KW	non-metastatic breast tumour tissue; gene therapy; anticancer;		
KW	antimetastatic; vaccine; diagnosis; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO9965928-A2.		
XX			
PD	23-DEC-1999.		
XX			
PF	18-JUN-1999; 99WO-US013647.		
XX			
PR	19-JUN-1998; 98US-0089853P.		
PR	19-JUN-1998; 98US-0089997P.		
PR	19-JUN-1998; 98US-0090039P.		
PR	19-JUN-1998; 98US-0090040P.		
PR	19-JUN-1998; 98US-0090041P.		
XX			
PA	(GENZ ) GENZYME CORP.		
PA	(ROBE/) ROBERTS B L.		
PA	(SHAN/) SHANKARA S.		
XX			
PI	Roberts BL, Shankara S;		
XX			
DR	WPI; 2000-106079/09.		
XX			
PPT	Isolated polynucleotides differentially expressed between metastatic and		
PPT	non-metastatic breast cancer cells, useful for diagnosis, prevention and		
PPT	treatment of cancer.		
XX			
PS	Claim 1; Page 184; 219pp; English.		
XX			
CCC	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts		
CCC	that are preferentially transcribed in the metastatic breast tumour		
CCC	tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942		
CCC	to AAZ86677 represent tags corresponding to distinct transcripts that are		
CCC	preferentially transcribed in the primary or non-metastatic breast tumour		
CCC	tissue (i.e. are downregulated in metastatic breast tumour cells). These		
CCC	transcripts can be used for diagnosis, prognosis, monitoring and		
CCC	treatment of breast cancer, particularly where metastatic. Diagnosis is		
CCC	by standard immunoassays or hybridisation/amplification reactions.		
CCC	Compounds that modulate expression of the transcripts are potentially		
CCC	useful for treatment of (metastatic) breast cancer, while promoters from		
CCC	the transcripts are used to direct expression, in selected cell types, of		
CCC	e.g. therapeutic genes (also ribozymes or antisense sequences),		
CCC	particularly an antigen-encoding sequence for use in gene or cell-based		
CCC	vaccines. Polypeptides encoded by the transcripts are also useful in		
CCC	vaccines; for diagnosing breast cancer and for raising specific		
CCC	antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic		
CCC	agents. Host cells that produce the polypeptides can be used to expand		
CCC	and isolate populations of educated, antigen-specific immune effector		
CCC	cells, e.g. cytotoxic T lymphocytes, and these used for adoptive		
CCC	immunotherapy		
XX			
SQ	Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;		
Query Match 38.9%; Score 7.4; DB 1; Length 10;			
Best Local Similarity 88.9%; Pred.No. 1.7e+02;			

Matches	8;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	2	GTGCGGCTG	10						
Db	10	GCGCGGCTG	2						
RESULT 187									
AAZ83525									
ID	AAZ83525 standard; DNA; 10 BP.								
XX									
AC	AAZ83525;								
XX									
DT	07-APR-2000 (first entry)								
XX									
DE	Metastatic breast tumour cell upregulated transcript tag #2759.								
XX									
KW	Human; metastatic breast tumour tissue; breast cancer; tag; primer;								
KW	non-metastatic breast tumour tissue; gene therapy; anticancer;								
KW	antimetastatic; vaccine; diagnosis; ss.								
XX									
OS	Homo sapiens.								
XX									
PN	WO9965928-A2.								
XX									
PD	23-DEC-1999.								
XX									
PF	18-JUN-1999; 99WO-US013647.								
XX									
PR	19-JUN-1998; 98US-0089853P.								
PR	19-JUN-1998; 98US-0089997P.								
PR	19-JUN-1998; 98US-0090039P.								
PR	19-JUN-1998; 98US-0090040P.								
PR	19-JUN-1998; 98US-0090041P.								
XX									
PA	(GENZ ) GENZYME CORP.								
PA	(ROBE/) ROBERTS B L.								
PA	(SHAN/) SHANKARA S.								
XX									
PI	Roberts BL, Shankara S;								
XX									
DR	WPI; 2000-106079/09.								
XX									
PT	Isolated polynucleotides differentially expressed between metastatic and								
PT	non-metastatic breast cancer cells, useful for diagnosis, prevention and								
PT	treatment of cancer.								
XX									
PS	Claim 1; Page 133; 219pp; English.								
XX									
CC	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts								
CC	that are preferentially transcribed in the metastatic breast tumour								
CC	tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942								
CC	to AAZ86677 represent tags corresponding to distinct transcripts that are								
CC	preferentially transcribed in the primary or non-metastatic breast tumour								
CC	tissue (i.e. are downregulated in metastatic breast tumour cells). These								
CC	transcripts can be used for diagnosis, prognosis, monitoring and								
CC	treatment of breast cancer, particularly where metastatic. Diagnosis is								
CC	by standard immunoassays or hybridisation/amplification reactions.								
CC	Compounds that modulate expression of the transcripts are potentially								
CC	useful for treatment of (metastatic) breast cancer, while promoters from								
CC	the transcripts are used to direct expression, in selected cell types, of								
CC	e.g. therapeutic genes (also ribozymes or antisense sequences),								
CC	particularly an antigen-encoding sequence for use in gene or cell-based								
CC	vaccines. Polypeptides encoded by the transcripts are also useful in								
CC	vaccines; for diagnosing breast cancer and for raising specific								
CC	antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic								
CC	agents. Host cells that produce the polypeptides can be used to expand								
CC	and isolate populations of educated, antigen-specific immune effector								
CC	cells, e.g. cytotoxic T lymphocytes, and these used for adoptive								
CC	immunotherapy								
XX									
SQ	Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;								

Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
||| |||||  
Db 2 CGCGGTGGC 10

RESULT 188  
AAZ82033  
ID AAZ82033 standard; DNA; 10 BP.  
XX  
AC AAZ82033;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1267.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
PI WPI; 2000-106079/09.  
DR  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 92; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
XX immunotherapy

SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18  
||| |||||  
Db 1 GTGGCAAAG 9

RESULT 189  
AAZ84603  
ID AAZ84603 standard; DNA; 10 BP.  
XX  
AC AAZ84603;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #3837.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
PI WPI; 2000-106079/09.  
DR  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 161; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
XX immunotherapy

CC immunotherapy  
XX  
SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 5 GCGCTGTGG 13  
} |||||  
Db 2 GGGCTGTGG 10  
  
RESULT 190  
AAZ81044/c  
ID AAZ81044 standard; DNA; 10 BP.  
XX  
AC AAZ81044;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #278.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 65; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand

CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGGCG 15  
} |||||  
Db 10 GCTGTGGGG 2  
  
RESULT 191  
AAZ81349  
ID AAZ81349 standard; DNA; 10 BP.  
XX  
AC AAZ81349;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #583.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 74; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 GCTGTGGCG 15  
||| |||||  
Db 1 GCGGTGGCG 9  
  
RESULT 192  
AAZ82759/C  
ID AAZ82759 standard; DNA; 10 BP.  
XX  
AC AAZ82759;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1993.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 113; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CGCTGTGGC 14  
||| |||||  
Db 9 CGCTGGGGC 1  
  
RESULT 193  
AAZ81572/C  
ID AAZ81572 standard; DNA; 10 BP.  
XX  
AC AAZ81572;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #806.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 79; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of



CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 11 TGGCGAAGG 19  
Db 10 TGGAGAAGG 2  
||| |||||  
  
RESULT 194  
AAZ81415/C  
ID AAZ81415 standard; DNA; 10 BP.  
XX  
AC AAZ81415;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #649.  
XX  
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 75; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 10 GTGGCGAAG 18  
Db 10 GTGGCGAAG 2  
||||| |||||  
  
RESULT 195  
AAZ82829/C  
ID AAZ82829 standard; DNA; 10 BP.  
XX  
AC AAZ82829;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #2063.  
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 115; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is



CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
||| ||||  
Db 10 GGTCCCGCT 2

RESULT 196  
AAZ84942/c  
ID AAZ84942 standard; DNA; 10 BP.

XX AAZ84942;

AC AAZ84942;

XX 07-APR-2000 (first entry)

DE Metastatic breast tumour cell downregulated transcript tag #4176.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

XX WO9965928-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

PF 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX Claim 1; Page 170; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX

SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
||| |||||  
Db 10 CGCAGTGGC 2

RESULT 197  
AAZ80867/c  
ID AAZ80867 standard; DNA; 10 BP.

XX AAZ80867;

AC AAZ80867;

XX 07-APR-2000 (first entry)

DE Metastatic breast tumour cell upregulated transcript tag #101.

XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.

OS Homo sapiens.

XX WO9965928-A2.

PN 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013647.

PF 19-JUN-1998; 98US-0089853P.

XX 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090041P.

XX (GENZ ) GENZYME CORP.

PA (ROBE/) ROBERTS B L.

PA (SHAN/) SHANKARA S.

XX Roberts BL, Shankara S;

PI WPI; 2000-106079/09.

XX Isolated polynucleotides differentially expressed between metastatic and

PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX Claim 1; Page 61; 219pp; English.  
PS  
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy

XX  
SQ Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
||| |||||  
Db 10 TGGTGAAGG 2

RESULT 198

AAC74122  
ID AAC74122 standard; cDNA; 10 BP.

XX  
AC AAC74122;

XX  
DT 02-FEB-2001 (first entry)

XX  
DE Human monocyte and dendritic cell expressed gene oligonucleotide #209.

XX  
KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;  
KW autoimmune disease; tumour; ss.

OS Homo sapiens.

XX  
PN WO200060074-A1.

XX  
PD 12-OCT-2000.

XX  
PF 30-MAR-2000; 2000WO-JP002019.

XX  
PR 01-APR-1999; 99JP-00095481.

XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX  
PI Hashimoto S, Matsushima K, Suzuki T;

XX  
DR WPI; 2000-619172/59.

XX  
PT Groups of genes expressed in human dendritic cells at a greater or lesser  
PT extent than in monocytes for investigation and diagnosis of autoimmune  
PT disease and tumors.

XX  
PS Claim 19; Page 15; 95pp; Japanese.

XX  
CC The present invention describes a group of genes consisting of 100 genes  
CC which are highly expressed in human dendritic cells; a group of genes  
CC which are expressed at a higher frequency in human dendritic cells than  
CC in human monocytes; and a group of genes which are expressed at lower  
CC frequency in human dendritic cells than in human monocytes. Each group of  
CC genes are characterised in that cDNAs of these genes respectively have  
CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID  
CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114  
CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'

CC located most closely to the poly-A region. The sequences can be used for  
CC the investigation of the role and mechanism of the involvement of  
CC dendritic cells in the immune system and for the study and diagnosis of  
CC diseases in which dendritic cells play a significant role, e.g. cancers  
CC and autoimmune diseases

XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15  
||||| |||  
Db 1 GCTGTGGCG 9

RESULT 199

AAC73917

ID AAC73917 standard; cDNA; 10 BP.

XX  
AC AAC73917;

XX  
DT 02-FEB-2001 (first entry)

XX  
DE Human dendritic cell cDNA base sequence oligonucleotide #4.

XX  
KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;  
KW autoimmune disease; tumour; ss.

XX  
OS Homo sapiens.

XX  
PN WO200060074-A1.

XX  
PD 12-OCT-2000.

XX  
PF 30-MAR-2000; 2000WO-JP002019.

XX  
PR 01-APR-1999; 99JP-00095481.

XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX  
PI Hashimoto S, Matsushima K, Suzuki T;

XX  
DR WPI; 2000-619172/59.

XX  
PT Groups of genes expressed in human dendritic cells at a greater or lesser  
PT extent than in monocytes for investigation and diagnosis of autoimmune  
PT disease and tumors.

XX  
PS Claim 1; Page 9; 95pp; Japanese.

XX  
CC The present invention describes a group of genes consisting of 100 genes  
CC which are highly expressed in human dendritic cells; a group of genes  
CC which are expressed at a higher frequency in human dendritic cells than  
CC in human monocytes; and a group of genes which are expressed at lower  
CC frequency in human dendritic cells than in human monocytes. Each group of  
CC genes are characterised in that cDNAs of these genes respectively have  
CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID  
CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114  
CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'  
CC located most closely to the poly-A region. The sequences can be used for  
CC the investigation of the role and mechanism of the involvement of  
CC dendritic cells in the immune system and for the study and diagnosis of  
CC diseases in which dendritic cells play a significant role, e.g. cancers  
CC and autoimmune diseases

XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10

RESULT 200  
AAC74079/c  
ID AAC74079 standard; cDNA; 10 BP.  
XX  
AC AAC74079;  
XX  
DT 02-FEB-2001 (first entry)  
XX  
DE Human dendritic cell and monocyte expressed gene oligonucleotide #166.  
XX  
KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;  
KW autoimmune disease; tumour; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200060074-A1.  
XX  
PD 12-OCT-2000.  
XX  
PF 30-MAR-2000; 2000WO-JP002019.  
XX  
PR 01-APR-1999; 99JP-00095481.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Hashimoto S, Matsushima K, Suzuki T;  
XX WPI; 2000-619172/59.  
DR  
XX  
PT Groups of genes expressed in human dendritic cells at a greater or lesser  
PT extent than in monocytes for investigation and diagnosis of autoimmune  
PT disease and tumors.  
XX  
PS Claim 10; Page 13; 95pp; Japanese.  
XX  
CC The present invention describes a group of genes consisting of 100 genes  
CC which are highly expressed in human dendritic cells; a group of genes  
CC which are expressed at a higher frequency in human dendritic cells than  
CC in human monocytes; and a group of genes which are expressed at lower  
CC frequency in human dendritic cells than in human monocytes. Each group of  
CC genes are characterised in that cDNAs of these genes respectively have  
CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID  
CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114  
CC to AAC74213), each is continuous with the base sequence 5'-CATG-3'  
CC located most closely to the poly-A region. The sequences can be used for  
CC the investigation of the role and mechanism of the involvement of  
CC dendritic cells in the immune system and for the study and diagnosis of  
CC diseases in which dendritic cells play a significant role, e.g. cancers  
CC and autoimmune diseases  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
Db 10 TGGAGAAGG 2

RESULT 201  
AAA56244  
ID AAA56244 standard; DNA; 10 BP.  
XX  
AC AAA56244;  
XX  
XX 07-SEP-2000 (first entry)  
DT

XX Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:138.  
DE  
XX  
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;  
KW granulocyte-macrophage colony-stimulating factor; characterisation;  
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;  
KW disease onset mechanism; genetic disease; drug development; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200024892-A1.  
XX  
PD 04-MAY-2000.  
XX  
PF 28-OCT-1999; 99WO-JP005982.  
XX  
PR 28-OCT-1998; 98JP-00307532.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX  
PI Hashimoto S, Matsushima K, Suzuki T;  
XX WPI; 2000-350734/30.  
DR  
XX  
PT Genes most frequently expressed in human monocytes and GM-macrophages and  
PT M-macrophages studied and with cDNAs characterized, for study of gene  
PT specificity, disease onset mechanism, drug development and diagnosis.  
XX  
PS Claim 7; Page 66; 138pp; Japanese.  
XX  
CC The present invention describes 100 human genes, which are expressed most  
CC frequently in human monocytes. The cDNA of each gene has a sequence fully  
CC defined in the specification, and lacking the CATG sequence located  
CC adjacent to polyA region. Also described are: (1) an antibody  
CC specifically for the protein encoded by any of the genes; (2)  
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes  
CC which are expressed most frequently in human macrophages, differentiated  
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,  
CC the cDNA of each gene has a fully defined sequence, given in the  
CC specification, lacking the base sequence CATG located most closely to the  
CC poly A region; (4) an antibody specifically for the protein encoded by  
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA  
CC sequences of (3). The genes and cDNAs, are used for the study of gene  
CC specificity and disease onset mechanism e.g. oncogenesis, genetic  
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent  
CC specifically claimed oligonucleotide tag sequences for human genes  
CC expressed in monocytes and macrophages  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10

RESULT 202  
AAA56333  
ID AAA56333 standard; DNA; 10 BP.  
XX  
AC AAA56333;  
XX  
DT 07-SEP-2000 (first entry)  
XX  
DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:227.  
XX  
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;  
KW granulocyte-macrophage colony-stimulating factor; characterisation;  
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;  
KW disease onset mechanism; genetic disease; drug development; ss.

XX Homo sapiens.  
OS  
XX  
XX WO200024892-A1.  
PN  
XX  
XX 04-MAY-2000.  
PD  
XX  
XX 28-OCT-1999; 99WO-JP005982.  
PF  
XX  
XX 28-OCT-1998; 98JP-00307532.  
PR  
XX  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
PA  
XX  
XX Hashimoto S, Matsushima K, Suzuki T;  
PI  
XX  
XX WPI; 2000-350734/30.  
DR  
XX  
XX Genes most frequently expressed in human monocytes and GM-macrophages and  
PT M-macrophages studied and with cDNAs characterized, for study of gene  
PT specificity, disease onset mechanism, drug development and diagnosis.  
XX  
XX Claim 13; Page 84; 138pp; Japanese.  
PS  
XX The present invention describes 100 human genes, which are expressed most  
CC frequently in human monocytes. The cDNA of each gene has a sequence fully  
CC defined in the specification, and lacking the CATG sequence located  
CC adjacent to polyA region. Also described are: (1) an antibody  
CC specifically for the protein encoded by any of the genes; (2)  
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes  
CC which are expressed most frequently in human macrophages, differentiated  
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,  
CC the cDNA of each gene has a fully defined sequence, given in the  
CC specification, lacking the base sequence CATG located most closely to the  
CC poly A region; (4) an antibody specifically for the protein encoded by  
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA  
CC sequences of (3). The genes and cDNAs, are used for the study of gene  
CC specificity and disease onset mechanism e.g. oncogenesis, genetic  
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent  
CC specifically claimed oligonucleotide tag sequences for human genes  
CC expressed in monocytes and macrophages  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10  
  
RESULT 203  
AAA56136  
ID AAA56136 standard; DNA; 10 BP.  
XX  
AC AAA56136;  
XX  
DT 07-SEP-2000 (first entry)  
XX  
DE Human monocyte gene Tag oligonucleotide sequence SEQ ID NO:30.  
XX  
KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;  
KW granulocyte-macrophage colony-stimulating factor; characterisation;  
KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;  
KW disease onset mechanism; genetic disease; drug development; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200024892-A1.  
PN  
XX  
XX 04-MAY-2000.  
PD  
XX

PF 28-OCT-1999; 99WO-JP005982.  
XX  
PR 28-OCT-1998; 98JP-00307532.  
XX  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
PA  
XX  
XX Hashimoto S, Matsushima K, Suzuki T;  
PI  
XX  
XX WPI; 2000-350734/30.  
DR  
XX  
XX Genes most frequently expressed in human monocytes and GM-macrophages and  
PT M-macrophages studied and with cDNAs characterized, for study of gene  
PT specificity, disease onset mechanism, drug development and diagnosis.  
XX  
XX Claim 1; Page 45; 138pp; Japanese.  
PS  
XX The present invention describes 100 human genes, which are expressed most  
CC frequently in human monocytes. The cDNA of each gene has a sequence fully  
CC defined in the specification, and lacking the CATG sequence located  
CC adjacent to polyA region. Also described are: (1) an antibody  
CC specifically for the protein encoded by any of the genes; (2)  
CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes  
CC which are expressed most frequently in human macrophages, differentiated  
CC from human monocytes by granulocyte-macrophage colony-stimulating factor,  
CC the cDNA of each gene has a fully defined sequence, given in the  
CC specification, lacking the base sequence CATG located most closely to the  
CC poly A region; (4) an antibody specifically for the protein encoded by  
CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA  
CC sequences of (3). The genes and cDNAs, are used for the study of gene  
CC specificity and disease onset mechanism e.g. oncogenesis, genetic  
CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent  
CC specifically claimed oligonucleotide tag sequences for human genes  
CC expressed in monocytes and macrophages  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10  
  
RESULT 204  
AAA14154  
ID AAA14154 standard; DNA; 10 BP.  
XX  
AC AAA14154;  
XX  
DT 15-SEP-2003 (revised)  
DT 21-JUL-2000 (first entry)  
XX  
DE E. coli K-12 leading strand PCR primer, SEQ ID NO:52.  
XX  
KW Polymorphism detection; over-represented sequence; strand bias;  
KW organism identification; genomic mapping; octamer; leading strand;  
KW Escherichia coli 0157:H7; PCR primer; ss.  
XX  
OS Escherichia coli K12.  
XX  
XX WO200017399-A2.  
PN  
XX  
XX 30-MAR-2000.  
PD  
XX  
XX 17-SEP-1999; 99WO-US021379.  
PF  
XX  
XX 18-SEP-1998; 98US-0101011P.  
PR  
XX  
XX (UYNE-) UNIV NEBRASKA-LINCOLN.  
PA  
XX  
PI Benson AK;



XX WPI; 2000-283618/24.

XX Detecting DNA polymorphisms, useful e.g. for identifying organisms by

PT species, strain or serotype, comprises amplification with primers based

PT on over-represented oligonucleotide sequences.

XX Example; Page 28; 49pp; English.

XX The invention relates to a novel method for the detection of

CC polymorphisms in a DNA sequence. Test DNA and a second DNA are amplified

CC with at least one pair of primers, and the sequence differences between

CC the amplicons are compared. The primers are based on oligonucleotide

CC sequences that are over-represented in the genome of the relevant

CC organism, and which are biased to one strand. The method can be used to

CC identify an organism by species, serotype or strain, in which case

CC amplicons are analysed for products, common to all members of the

CC species, and those specific for strain or serotype, and the results

CC compared with an existing database. The method can also be used to

CC identify an individual, by comparison of results for a test DNA with an

CC existing database. When applied to differential display analysis, pattern

CC differences in the amplicons are determined, particularly by a

CC quantitative method such as densitometry, fluorimetry or radiometry. The

CC method of the invention is used to identify individuals, to classify

CC organisms by species, strain or serotype, and to identify genes based on

CC differential display. The method can also be used for genomic mapping,

CC detecting changes in expression patterns, genetic linkage studies,

CC medical diagnosis, epidemiology, forensics, and agriculture. The method

CC uses over-represented sequences to prime amplification. These sequences

CC are distributed over the entire genome, so analysis is not restricted to

CC particular regions, and a single primer pair can amplify up to 5% of the

CC complete Escherichia coli genome. The primers are rationally designed, so

CC non-specific amplification is limited and the method does not require

CC restriction enzymes or adapters. Sequences AAA14149-A14154 represent PCR

CC primers based on over-represented octamer sequences biased to the leading

CC strand of the E. coli K-12 genome and are fluorescently labelled at the

CC 5' end. These primers, and lagging strand primers AAA14155- AAA14160 were

CC used in the exemplifications of the invention to differentiate and

CC further characterise two strains of E. coli 0157:H7 (strains FR1K 1641

CC and FR1K 533) and two strains from the ECOR collection (ECOR 20 and ECOR

CC 50). (Updated on 15-SEP-2003 to standardise OS field)

XX

SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17

Db 2 TCTGGCGAA 10

RESULT 205

AAA73645/c

ID AAA73645 standard; DNA; 10 BP.

XX AAA73645;

XX 30-JAN-2001 (first entry)

DE Probe #14 for sequencing by hybridisation.

XX Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.

OS Synthetic.

XX WO200040758-A2.

XX 13-JUL-2000.

XX 06-JAN-2000; 2000WO-US000458.

XX

PR

XX 06-JAN-1999; 99US-0115284P.

PA (HYSE-) HYSEQ INC.

PI Drmanac R, Drmanac S, Kita D, Cooke C, Xu C;

XX WPI; 2000-475839/41.

XX Identifying one or more sequences of a target nucleic acid (NA), useful

PT for parallel analyses, comprises contacting the NA with a set of pools of

PT probes comprising mixture of probes with different information regions.

PS Disclosure; Page 53; 196pp; English.

XX The present sequence is a probe used to demonstrate the method of the

CC invention, which is concerned with the use of pools of probes to enable

CC sequencing by hybridisation, a process known as SBH. Overlapping probes

CC are used which allows the identification of sequences longer than the

CC probe length, and either the target nucleic acid or the probe is

CC labelled. The method of the invention is useful for assembling sequences

CC and in parallel analyses

SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16

Db 10 CTGTGGCAA 2

RESULT 206

AAA73646/c

ID AAA73646 standard; DNA; 10 BP.

XX AAA73646;

XX 30-JAN-2001 (first entry)

DE Probe #15 for sequencing by hybridisation.

XX Nucleic acid sequencing; sequencing by hybridisation; SBH; probe; ss.

OS Synthetic.

XX WO200040758-A2.

XX 13-JUL-2000.

XX 06-JAN-2000; 2000WO-US000458.

XX 06-JAN-1999; 99US-0115284P.

XX (HYSE-) HYSEQ INC.

PI Drmanac R, Drmanac S, Kita D, Cooke C, Xu C;

XX WPI; 2000-475839/41.

XX Identifying one or more sequences of a target nucleic acid (NA), useful

PT for parallel analyses, comprises contacting the NA with a set of pools of

PT probes comprising mixture of probes with different information regions.

PS Disclosure; Page 53; 196pp; English.

XX The present sequence is a probe used to demonstrate the method of the

CC invention, which is concerned with the use of pools of probes to enable

CC sequencing by hybridisation, a process known as SBH. Overlapping probes

CC are used which allows the identification of sequences longer than the

CC probe length, and either the target nucleic acid or the probe is

CC labelled. The method of the invention is useful for assembling sequences



CC and in parallel analyses  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGA 16  
Db ||||| |  
9 CTGTGGCAA 1  
  
RESULT 207  
AAI70450  
ID AAI70450 standard; DNA; 10 BP.  
XX  
AC AAI70450;  
XX  
DT 21-JAN-2002 (first entry)  
XX  
DE Oligonucleotide used in mismatch discrimination.  
XX  
KW Probe; hybridisation; array; microarray; mismatch; detection; ss.  
XX  
OS Synthetic.  
XX  
PN WO200164958-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 01-MAR-2001; 2001WO-US006900.  
XX  
PR 01-MAR-2000; 2000US-0186046P.  
PR 28-NOV-2000; 2000US-00724959.  
XX  
PA (EPOC-) EPOCH BIOSCIENCE INC.  
XX  
PI Dempcy RO, Gall AA, Lohkov SG, Afonina IA, Singer MJ;  
PI Kutyaivin IV, Vermeulen NMJ;  
XX  
DR WPI; 2001-648247/74.  
XX  
PT New modified oligonucleotides containing pyrazolo-pyrimidine and/or 5-  
PT substituted pyrimidine bases, useful as probes or primers in assays,  
PT especially for mismatch discrimination.  
XX  
PS Example 9; Page 84; 116pp; English.  
XX  
CC The present sequence is that of one of a set of oligonucleotides (see  
CC AAI70448-64) used in a mismatch discrimination experiment. The experiment  
CC compared the thermodynamic discrimination of mismatched base pairs formed  
CC by modified oligonucleotides containing 4-amino-3-(3-hydroxyprop-1-  
CC ynyl)pyrazolo(3,4-d)pyrimidine (HOPPPA) or 5-(3-hydroxyprop-1-yl)-1,3-  
CC dihydropyrimidine-2,4-dione (HOPU) versus those containing 4-amino-3-  
CC (prop-1-yny)pyrazolo(3,4-d)pyrimidine (pppa) and 5-prop-1-yny-1,3-  
CC dihydropyrimidine-2,4-dione (PU) at 37 degree C. Oligonucleotides  
CC containing the modified bases and also including a 3' minor groove binder  
CC (MGB), were hybridised to their complements, such as the present  
CC sequence. HOPPPA and HOPU substitution generally increased mismatch  
CC discrimination compared to PPPA and PU. The invention provides modified  
CC oligonucleotides for mismatch discrimination. Also provides are methods  
CC for distinguishing related polynucleotides, detecting target sequences,  
CC sequencing, primer extension, for examining gene expression, and for  
CC identifying a mutation or polymorphism  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGA 16

Db | ||||| |  
2 CAGTGGCGA 10  
  
RESULT 208  
AAH19999  
ID AAH19999 standard; DNA; 10 BP.  
XX  
AC AAH19999;  
XX  
DT 07-AUG-2001 (first entry)  
XX  
DE Mouse Treg immunoregulatory network related tag #70.  
XX  
KW Mouse; EST; expressed sequence tag; contig; immunoregulation;  
KW immunosuppression; Treg immunoregulatory network; inflammatory;  
KW immune disorder; T regulatory lymphocyte; T helper cell; dermatological;  
KW antiinflammatory; immunosuppressive; antiarteriosclerotic; antiallergic;  
KW antidiabetic; neuroprotective; osteopathic; antiarthritic; anti-ulcer;  
KW rheumatoid arthritis; osteoarthritis; glomerular nephritis; diabetes;  
KW inflammatory bowel disease; vascular disease; atherosclerosis; psoriasis;  
KW vasculitis; skin disease; dermatitis; Crohn's disease; lung disease;  
KW ulcerative colitis; lupus erythematosus; autoimmune disorder; emphysema;  
KW hypersensitivity; multiple sclerosis; chronic bronchitis; asthma;  
KW idiopathic pulmonary fibrosis; primer; probe; tag; ss.  
XX  
OS Mus musculus.  
OS Synthetic.  
XX  
PN WO200127267-A2.  
XX  
PD 19-APR-2001.  
XX  
PF 06-OCT-2000; 2000WO-GB003821.  
XX  
PR 08-OCT-1999; 99GB-00023790.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX  
PI Adams E, Waldmann H, Cobbold S, Zelenika D;  
PI WPI; 2001-300216/31.  
DR  
XX  
PT Isolated genes differentially expressed in T helper 1 (Th1) and 2 (Th2)  
PT and T regulatory (Treg) lymphocytes useful in prophylaxis, diagnosis and  
PT therapy of inflammatory and immune diseases.  
XX  
PS Example 4; Page 5; 29pp; English.  
XX  
CC The present invention describes an isolated gene (I) obtainable by: (a)  
CC comparing the expression of one or more genes in populations of T helper  
CC 1 lymphocytes (Th1)-, Th2- and T regulatory cells (Treg)-enriched cell  
CC populations to identify a gene which is differentially expressed in the  
CC populations; and (b) isolating the gene. (I) can have dermatological,  
CC antiinflammatory, immunosuppressive, antiarteriosclerotic, antiallergic,  
CC antidiabetic, neuroprotective, osteopathic, antiarthritic and anti-ulcer  
CC activities. (I) can be used in anti-inflammatory and immunoregulatory  
CC compositions for use in therapy, prophylaxis, or diagnosis and/or in a  
CC pharmaceutical excipient, a unit dosage form or in a form suitable for  
CC local or systemic administration. Methods from the present invention can  
CC be used for detecting Th1 and/or Th2 and/or Treg cells in a biological  
CC sample, for cell typing or for determining the number of Th1 and/or Th2  
CC and/or Treg cells in a biological sample. Diseases which may be treated  
CC by compositions of the invention include rheumatoid and osteoarthritis,  
CC glomerular nephritis, diabetes, inflammatory bowel disease, vascular  
CC diseases e.g. atherosclerosis and vasculitis, skin diseases such as  
CC psoriasis and dermatitis, Crohn's disease, ulcerative colitis, lupus  
CC erythematosus, autoimmune disorders, hypersensitivity, multiple  
CC sclerosis, and lung diseases e.g. chronic bronchitis, emphysema,  
CC idiopathic pulmonary fibrosis and asthma. (I) can also be used as markers  
CC for analysis of serum, urine and biopsy, particularly during and after  
CC therapy for multiple sclerosis. AAH19930 to AAH20034 and AAB75133  
CC represent sequence used in the exemplification of the present invention

```
XX
SQ      Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

      Query Match      38.9%; Score 7.4; DB 1; Length 10;
      Best Local Similarity 88.9%; Pred. No. 1.7e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 TGGCGAAGG 19
      ||| |||||
Db      2 TGGTGAAGG 10

RESULT 209
AAI67372
ID      AAI67372 standard; DNA; 10 BP.
XX
AC      AAI67372;
XX
DT      11-FEB-2002 (first entry)
XX
DE      Human FKBP8 gene polymorphism detecting primer.
XX
KW      FK506-binding protein 8; FKBP8; haplotyping; polymorphism; cancer;
KW      immunosuppression; human; primer; ss.
XX
OS      Homo sapiens.
XX
PN      WO200172965-A2.
XX
PD      04-OCT-2001.
XX
PF      26-MAR-2001; 2001WO-US009718.
XX
PR      24-MAR-2000; 2000US-0192125P.
XX
PA      (GENA-) GENAISSANCE PHARM INC.
XX
PI      Anastasio AE, Bentivegna SC, Choi JY, Kliem SE, Koshy B;
PI      Stephens JC;
XX
WPI; 2001-626261/72.
XX
New haplotypes of the FK506-binding protein 8 gene, useful for genotyping
PT      that gene in individual and to design new therapy for associated disease
PT      such as immunosuppression and cancer.
XX
PS      Claim 16; Page 14; 98pp; English.
XX
The invention relates to haplotyping the FK506-binding protein 8 (38kD)
CC      (FKBP8) gene in an individual. The method involves determining the
CC      identity of the nucleotide pair at one or more polymorphic sites selected
CC      from P1 to P26 (described in the specification). The invention is useful
CC      to improve the efficiency and reliability of several steps in the
CC      discovery and development of drugs for treating diseases associated with
CC      FKBP8 activity, for example immunosuppression and cancer. Sequences
CC      AAI67352-403 represent oligonucleotide primers for detecting FKBP8 gene
CC      polymorphisms by primer extension techniques
XX
SQ      Sequence 10 BP; 0 A; 2 C; 7 G; 1 T; 0 U; 0 Other;

      Query Match      38.9%; Score 7.4; DB 1; Length 10;
      Best Local Similarity 88.9%; Pred. No. 1.7e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCG 15
      ||| |||||
Db      1 GCTGGGGCG 9

RESULT 210
AAS09210/c
ID      AAS09210 standard; DNA; 10 BP.
XX
```

```
AC      AAS09210;
XX
DT      07-NOV-2001 (first entry)
XX
DE      Oligonucleotide ON 10 relating to VEGF receptor-1 peptide ligand #1.
XX
KW      Vascular endothelial growth factor receptor-1; VEGF; psoriasis;
KW      angiogenesis mediated disease; birth control; neovascularisation;
KW      inflammatory disorder; neoplastic disorder; anti tumour; anti rheumatic;
KW      anti arthritic; anti psoriatic; anti diabetic; anti atherosclerotic;
KW      anti ulcer; osteopathic; cytostatic; anti inflammatory; ophthalmological;
KW      dermatological; ON 10; ss.
XX
OS      Synthetic.
XX
PN      WO200157067-A1.
XX
PD      09-AUG-2001.
XX
PF      02-FEB-2001; 2001WO-IB0000135.
XX
PR      04-FEB-2000; 2000US-0180568P.
XX
PA      (SUPR-) SUPRATEK PHARMA INC.
XX
PI      Tchistiakova L, Li S, Pietrzynski G, Alakhov V;
XX
WPI; 2001-529780/58.
XX
Composition for treating angiogenesis mediated diseases such as tumor and
PT      psoriasis, comprises a peptide or its derivative capable of specific
PT      binding with high affinity vascular endothelial growth factor receptor-1.
XX
PS      Example 16; Page 71; 86pp; English.
XX
The present invention relates to a pharmaceutical composition comprising
CC      of a peptide ligand, or its derivative, which is capable of specific
CC      binding with high affinity to vascular endothelial growth factor (VEGF)
CC      receptor-1 or its derivative and structurally similar receptors. The
CC      invention also provides peptide ligands that are capable of inhibiting
CC      angiogenesis induced by VEGF. The peptide ligands of the invention are
CC      useful for treating a disease associated with angiogenesis in a patient.
CC      They are also useful for treating angiogenesis mediated diseases e.g.
CC      solid tumours, rheumatoid arthritis and psoriasis, for treating diseases
CC      of excessive or abnormal stimulation of endothelial cells e.g. Crohn's
CC      disease, atherosclerosis and scleroderma, for treating diseases that have
CC      angiogenesis as a pathological consequence e.g. cat scratch disease and
CC      ulcers, as a birth control agent, and for treating diseases associated
CC      with neovascularisation of the eye e.g. atopic keratitis and Paget's
CC      disease, inflammatory disorders e.g. ulcerative colitis and inflammatory
CC      bowel disease, and neoplastic and non-neoplastic diseases and disorders.
CC      The peptide ligands are also useful as a targeting group to improve the
CC      delivery of a biological agent used for therapeutic or diagnostic
CC      purpose. The present sequence for oligonucleotide ON 10 is used to
CC      construct phage expressing VEGF receptor-1 peptide ligand #1 (AAU07801)
XX
SQ      Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

      Query Match      38.9%; Score 7.4; DB 1; Length 10;
      Best Local Similarity 88.9%; Pred. No. 1.7e+02;
      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCGCGCT 9
      ||| |||||
Db      10 GGTCGCGCT 2

RESULT 211
AAH63607/c
ID      AAH63607 standard; cDNA; 10 BP.
XX
AC      AAH63607;
XX
```

DT 20-SEP-2001 (first entry)  
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 447.  
DE  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 2001-367706/38.  
XX  
PT New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
cell types.  
XX  
PS Claim 13; Page 49; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 6 CGCTGTGGC 14  
Db 9 CGCTGGGC 1  
  
RESULT 212  
AAH63746/c  
ID AAH63746 standard; cDNA; 10 BP.  
XX  
AC AAH63746;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 586.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;  
PI WPI; 2001-367706/38.  
XX  
DR New isolated polynucleotides, useful for identifying specific cell type,  
XX such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
PT  
XX  
PS Claim 11; Page 52; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Oy 6 CGCTGTGGC 14  
Db 10 CGCAGTGGC 2  
  
RESULT 213  
AAH64224  
ID AAH64224 standard; cDNA; 10 BP.  
XX  
AC AAH64224;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1064.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 2001-367706/38.  
XX  
PT New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 13; Page 63; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention

```
CC transcripts described in the exemplification of the invention
XX
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
Db 2 TGGTGAAGG 10

RESULT 214
AAH63440
ID AAH63440 standard; cDNA; 10 BP.
XX
AC AAH63440;
XX
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 280.
DE
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
OS
XX WO200138577-A2.
Db 2 TGGTGAAGG 10

RESULT 215
AAH63439
ID AAH63439 standard; cDNA; 10 BP.
XX
AC AAH63439;
```

```
XX 20-SEP-2001 (first entry)
DT Human ubiquitously expressed transcriptome sequence SEQ ID NO: 279.
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
DE cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
OS
XX WO200138577-A2.
PN 31-MAY-2001.
XX
PD 21-NOV-2000; 2000WO-US031922.
XX
PF 24-NOV-1999; 99US-00448480.
XX
PR (UYJO ) UNIV JOHNS HOPKINS.
XX Velculescu VE, Vogelstein B, Kinzler KW;
PI WPI; 2001-367706/38.
XX New isolated polynucleotides, useful for identifying specific cell type,
PT such as cancer cell, comprises transcriptomes expressed in particular
PT cell types.
XX Claim 13; Page 45; 94pp; English.
PS The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
CC AAH64724 is expressed by the cell. The transcriptomes described in the
CC invention are cell-type specific, cancer specific or ubiquitously
CC expressed in humans. They can also be used to screen for drugs, reduce
CC cancer specific gene expression, standardise expression and restore the
CC function of a diseased cell or tissue. The present sequence is one of the
CC transcriptomes described in the exemplification of the invention
XX
SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
Db 2 GGGCTGTGG 10

RESULT 216
AAH64185
ID AAH64185 standard; cDNA; 10 BP.
XX
AC AAH64185;
XX
DT 20-SEP-2001 (first entry)
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1025.
DE Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX Homo sapiens.
OS
XX WO200138577-A2.
PN 31-MAY-2001.
XX
PF 21-NOV-2000; 2000WO-US031922.
XX
PR 24-NOV-1999; 99US-00448480.
XX
```



PA (UYJO ) UNIV JOHNS HOPKINS.  
XX Velculescu VE, Vogelstein B, Kinzler KW;  
PI  
XX WPI; 2001-367706/38.  
DR  
XX New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
PT  
XX  
PS Claim 13; Page 62; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 GCTGTGGCG 15  
| | | | |  
Db 1 GCTGTTGCG 9  
  
RESULT 217  
AAH63894/c  
ID AAH63894 standard; cDNA; 10 BP.  
XX  
AC AAH63894;  
XX  
DT 20-SEP-2001 (first entry)  
XX  
DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 734.  
XX  
KW Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 2001-367706/38.  
XX  
XX New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 13; Page 56; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the

CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 0 G; 4 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAGG 19  
| | | | |  
Db 10 TGGAGAAGG 2  
  
RESULT 218  
AAD20721/c  
ID AAD20721 standard; DNA; 10 BP.  
XX  
AC AAD20721;  
XX  
DT 03-JAN-2002 (first entry)  
XX  
DE Primer #13 used to detect human GPIBA gene polymorphism.  
XX  
KW Human; haplotyping; glycoprotein Ib (platelet) alpha protein; GPIBA;  
KW Bernard-Soulier syndrome; platelet-type von Willebrand disease; HIV;  
KW Alzheimer's disease; polymorphism; human immunodeficiency virus; primer;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175065-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010671.  
XX  
PR 03-APR-2000; 2000US-0194341P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Choi JY, Klien SE, Koshy B, Parks KE;  
XX  
XX WPI; 2001-626427/72.  
DR  
XX  
PT New haplotypes of the glycoprotein Ib platelet alpha polypeptide gene are  
PT useful for diagnosis and drug discovery for treating Bernard Soulier  
PT syndrome, platelet-type von Willebrand disease, HIV and Alzheimer's  
PT disease.  
XX  
PS Claim 18; Page 14; 66pp; English.  
XX  
CC The invention relates to methods for haplotyping glycoprotein Ib  
CC (platelet) alpha polypeptide (GPIBA) gene of an individual. The method  
CC involves determining if the individual has one of the GPIBA haplotypes or  
CC haplotype pairs. The methods of the invention are useful for disease  
CC diagnosis and in the discovery and development of drugs for treating  
CC diseases associated with GPIBA activity e.g. Bernard-Soulier syndrome,  
CC platelet-type von Willebrand disease, HIV and Alzheimer's disease. The  
CC present sequence is a primer used for detecting human GPIBA gene  
CC polymorphisms  
XX  
SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GTCGGGCTG 10  
| | | | |  
Db 10 GTCGGGCTG 2



RESULT 219  
AAH32655  
ID AAH32655 standard; cDNA; 10 BP.  
XX  
AC AAH32655;  
XX  
DT 13-AUG-2001 (first entry)  
XX  
DE LPS activated human monocyte expression gene cDNA tag SEQ:28.  
XX  
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
XX expressed sequence tag; diagnosis; human disease; treatment; ss.  
OS Homo sapiens.  
XX  
PN JP2001069993-A.  
XX  
PD 21-MAR-2001.  
XX  
PF 28-APR-2000; 2000JP-00131079.  
XX  
PR 08-JUL-1999; 99JP-00195103.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2001-304369/32.  
XX  
PT LPS activated human monocyte expression gene group.  
XX  
PS Claim 1; Page 15; 52pp; Japanese.  
CC The present invention describes an lipopolysaccharide (LPS) activated  
CC human monocyte expression gene group consisting of the high-ranking 50  
CC genes of the highest expression among the genes expressed by human  
CC monocyte stimulated by LPS in which the cDNA of each gene has the base  
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-  
CC CATG-3' nearest to the polyA region. The gene group is useful for the  
CC development of new means for the diagnosis and the treatment of various  
CC human diseases in which human monocyte plays an important role. AAH32628  
CC to AAH32943 represent specifically claimed LPS activated human monocyte  
CC expression gene cDNA tags from the present invention. AAH32944 represents  
CC an LPS activated human monocyte expression gene cDNA sequence encoding  
CC AAB98009, which are given in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
PT LPS activated human monocyte expression gene group.  
XX  
PS Claim 1; Page 15; 52pp; Japanese.  
CC The present invention describes an lipopolysaccharide (LPS) activated  
CC human monocyte expression gene group consisting of the high-ranking 50  
CC genes of the highest expression among the genes expressed by human  
CC monocyte stimulated by LPS in which the cDNA of each gene has the base  
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-  
CC CATG-3' nearest to the polyA region. The gene group is useful for the  
CC development of new means for the diagnosis and the treatment of various  
CC human diseases in which human monocyte plays an important role. AAH32628  
CC to AAH32943 represent specifically claimed LPS activated human monocyte  
CC expression gene cDNA tags from the present invention. AAH32944 represents  
CC an LPS activated human monocyte expression gene cDNA sequence encoding  
CC AAB98009, which are given in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10  
RESULT 220  
AAH32828  
ID AAH32828 standard; cDNA; 10 BP.  
XX  
AC AAH32828;  
XX  
DT 13-AUG-2001 (first entry)  
XX  
DE LPS activated human monocyte expression gene cDNA tag SEQ:201.  
XX  
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
XX expressed sequence tag; diagnosis; human disease; treatment; ss.  
OS Homo sapiens.  
XX  
PN JP2001069993-A.  
XX  
PD 21-MAR-2001.  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10

XX  
PF 28-APR-2000; 2000JP-00131079.  
XX  
PR 08-JUL-1999; 99JP-00195103.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2001-304369/32.  
XX  
PT LPS activated human monocyte expression gene group.  
XX  
PS Claim 19; Page 36; 52pp; Japanese.  
XX  
CC The present invention describes an lipopolysaccharide (LPS) activated  
CC human monocyte expression gene group consisting of the high-ranking 50  
CC genes of the highest expression among the genes expressed by human  
CC monocyte stimulated by LPS in which the cDNA of each gene has the base  
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-  
CC CATG-3' nearest to the polyA region. The gene group is useful for the  
CC development of new means for the diagnosis and the treatment of various  
CC human diseases in which human monocyte plays an important role. AAH32628  
CC to AAH32943 represent specifically claimed LPS activated human monocyte  
CC expression gene cDNA tags from the present invention. AAH32944 represents  
CC an LPS activated human monocyte expression gene cDNA sequence encoding  
CC AAB98009, which are given in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 7 GCTGTGGCG 15  
Db 1 GCTGTTGCG 9  
RESULT 221  
AAH32746/c  
ID AAH32746 standard; cDNA; 10 BP.  
XX  
AC AAH32746;  
XX  
DT 13-AUG-2001 (first entry)  
XX  
DE LPS activated human monocyte expression gene cDNA tag SEQ:119.  
XX  
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;  
XX expressed sequence tag; diagnosis; human disease; treatment; ss.  
OS Homo sapiens.  
XX  
PN JP2001069993-A.  
XX  
PD 21-MAR-2001.  
XX  
PF 28-APR-2000; 2000JP-00131079.  
XX  
PR 08-JUL-1999; 99JP-00195103.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2001-304369/32.  
XX  
PT LPS activated human monocyte expression gene group.  
XX  
PS Claim 10; Page 26; 52pp; Japanese.  
XX  
CC The present invention describes an lipopolysaccharide (LPS) activated  
CC human monocyte expression gene group consisting of the high-ranking 50  
CC genes of the highest expression among the genes expressed by human  
CC monocyte stimulated by LPS in which the cDNA of each gene has the base  
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-

CC CATG-3' nearest to the polyA region. The gene group is useful for the  
CC development of new means for the diagnosis and the treatment of various  
CC human diseases in which human monocyte plays an important role. AAH32628  
CC to AAH32943 represent specifically claimed LPS activated human monocyte  
CC expression gene cDNA tags from the present invention. AAH32944 represents  
CC an LPS activated human monocyte expression gene cDNA sequence encoding  
CC AAB98009, which are given in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGGCG 15  
||| |||||  
Db 10 GCTTTGGCG 2

RESULT 222  
ABA81653/C  
ID ABA81653 standard; DNA; 10 BP.

XX ABA81653;

DT 24-JAN-2002 (first entry)

XX Human phospholipid transfer protein gene PCR primer SEQ ID NO: 102.

XX Human; phospholipid transfer protein; PLTP; SNP; atherosclerosis;  
KW single nucleotide polymorphism; high-density lipoprotein metabolism;  
KW PCR primer; ss.

XX Homo sapiens.

XX WO200172761-A2.

PD 04-OCT-2001.

XX 15-MAR-2001; 2001WO-US008283.

XX 24-MAR-2000; 2000US-0192127P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Chew A, Choi JY, Koshy B;

DR WPI; 2001-662922/76.

XX Genotyping phospholipid transfer protein gene of individual for  
PT haplotyping individual's gene, comprises determining identity of  
PT nucleotide pair at polymorphic sites for two copies of PLTP gene present  
PT in the individual.

XX Claim 17; Page 14; 98pp; English.

XX The present invention relates to a method for haplotyping the human  
CC phospholipid transfer protein (PLTP) gene, involving determining the  
CC identity of the nucleotide present at one or more of the 25 polymorphic  
CC sites within the gene. This can be used to aid drug development for the  
CC treatment of diseases associated with different haplotypes of the PLTP  
CC gene, possibly including atherosclerosis. The present sequence is a PCR  
CC primer used for detecting polymorphisms in the PLTP gene

XX Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTGGCGAAG 18  
||||| |||||  
Db 10 GTGGCCAAG 2

RESULT 223  
ABA06025  
ID ABA06025 standard; cDNA; 10 BP.

XX ABA06025;

DT 10-JAN-2002 (first entry)

XX Human normal hepatocyte expression gene cDNA, SEQ ID NO: 2.

XX Human; hepatocyte; gene expression; hepatopathy; ss.

XX Homo sapiens.

PN JP2001211883-A.

PD 07-AUG-2001.

XX 31-JAN-2000; 2000JP-00023170.

PR 31-JAN-2000; 2000JP-00023170.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2001-629566/73.

XX Human normal hepatocyte expression gene group.

PS Claim 1; Page 6; 26pp; Japanese.

XX The invention relates to a human normal hepatocyte expression gene group  
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each in  
CC gene comprises one of 200 fully defined nucleotide sequences as given in  
CC the specification. The gene group and the cDNAs corresponding to each of  
CC the genes in the group are useful in the diagnosis and treatment of human  
CC hepatopathy. The present sequence is a cDNA corresponding to a gene  
CC expressed by normal human hepatocytes

XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGCGCT 9  
||| |||||  
Db 2 GGACGCGCT 10

RESULT 224  
ABA06218  
ID ABA06218 standard; cDNA; 10 BP.

XX ABA06218;

DT 10-JAN-2002 (first entry)

XX Human normal hepatocyte expression gene cDNA, SEQ ID NO: 195.

XX Human; hepatocyte; gene expression; hepatopathy; ss.

XX Homo sapiens.

PN JP2001211883-A.

PD 07-AUG-2001.

XX 31-JAN-2000; 2000JP-00023170.

XX 31-JAN-2000; 2000JP-00023170.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX WPI; 2001-629566/73.  
XX Human normal hepatocyte expression gene group.  
PT Claim 1; Page 9; 26pp; Japanese.  
XX The invention relates to a human normal hepatocyte expression gene group  
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each  
CC gene comprises one of 200 fully defined nucleotide sequences as given in  
CC the specification. The gene group and the cDNAs corresponding to each of  
CC the genes in the group are useful in the diagnosis and treatment of human  
CC hepatopathy. The present sequence is a cDNA corresponding to a gene  
CC expressed by normal human hepatocytes  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10  
||| |||||  
  
RESULT 225  
AAA91471  
ID AAA91471 standard; DNA; 10 BP.  
XX  
AC AAA91471;  
XX 12-JUL-2001 (first entry)  
DT  
DE Human CHRM5 gene, allele specific oligonucleotide #39.  
XX  
KW CHRM5; human; cholinergic receptor muscarinic 5; polymorphic variant;  
KW genotyping; haplotype; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200128995-A2.  
XX  
PD 26-APR-2001.  
XX  
PF 19-OCT-2000; 2000WO-US029071.  
XX  
PR 21-OCT-1999; 99US-0160647P.  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Chew A, Choi JY, Nandabalan K, Stephens JC;  
PI WPI; 2001-300313/31.  
XX  
DR Isolated polynucleotide encoding the cholinergic receptor, muscarinic 5  
XX (CHRM5), used to genotype/haplotype the CHRM5 gene, and to identify an  
PT association between a trait and a polymorphism, comprises novel  
PT polymorphisms.  
XX  
PS Claim 15; Page 49; 53pp; English.  
XX  
CC This sequence is a the human cholinergic receptor, muscarinic 5 (CHRM5)  
CC gene, allele specific oligonucleotide. The invention relates to a  
CC polymorphic variant of the CHRM5 gene sequence. The polymorphic sequence  
CC is useful to genotype or haplotype the CHRM5 gene, to predict a haplotype  
CC pair for the CHRM5 gene, and for identifying an association between a  
CC trait (such as a clinical response to a drug targeting CHRM5). It is also  
CC useful in gene therapy in patients who lack the CHRM5 isogene or have  
CC only one copy of it, and in assays to measure the binding affinities of  
CC one or more candidate drugs targeting CHRM5. The DNA sequence is used in  
CC the treatment of disorders affected by expression or function of a novel

CC CHRM5 isogene of the invention. The protein encoded by the CHRM5 variant  
CC is useful to identify drugs which target the CHRM5 polymorphic variant  
CC protein. Antibodies against the protein can be used to neutralise the  
CC CHRM5 isoform activity expressed in an individual, and is useful in  
CC detection of CHRM5 in immunocytochemical, immunohistochemical and  
CC immunofluorescence. A composition containing a genotyping oligonucleotide  
CC for detecting a polymorphism in the CHRM5 gene is used to detect novel  
CC CHRM5 polymorphisms of the invention  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAG 18  
Db 2 GTGGCCAAG 10  
||||| |||  
  
RESULT 226  
AAF36041/C  
ID AAF36041 standard; DNA; 10 BP.  
XX  
AC AAF36041;  
XX 23-MAR-2001 (first entry)  
DT  
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2780.  
DE  
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA  
XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
DR  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 99; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the classes of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTGCGGCT 9  
||| |||||  
Db 10 GGTGCGCT 2  
  
RESULT 227  
AAF43354  
ID AAF43354 standard; DNA; 10 BP.  
XX  
AC AAF43354;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11493.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 360; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the classes of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 GTCGCGCTG 10  
|||| |||||  
Db 2 GTCGTCGCTG 10  
  
RESULT 228  
AAF39191/c  
ID AAF39191 standard; DNA; 10 BP.  
XX  
AC AAF39191;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5930.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 211; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression



CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 3 TCGGCTGT 11  
Db 9 TCGCACTGT 1  
  
RESULT 229  
AAF34571  
ID AAF34571 standard; DNA; 10 BP.  
XX  
AC AAF34571;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1310.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 46; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGG 13  
Db 2 GCTCTGTGG 10  
  
RESULT 230  
AAF35628  
ID AAF35628 standard; DNA; 10 BP.  
XX  
AC AAF35628;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2367.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 84; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log



CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAG 18  
Db 2 GTGGCGAGG 10  
  
RESULT 231  
AAF37416  
ID AAF37416 standard; DNA; 10 BP.  
XX AAF37416;  
AC  
XX 23-MAR-2001 (first entry)  
DT  
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4155.  
DE  
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX WO200077214-A2.  
PN  
XX 21-DEC-2000.  
PD  
XX 14-JUN-2000; 2000WO-US016223.  
PF  
XX 16-JUN-1999; 99US-00335032.  
PR  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA  
XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
XX Example; Page 148; 419pp; English.  
PS  
XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 CGCGCTGTG 12  
Db 2 CGCGCTGCG 10  
  
RESULT 232  
AAF36771/c  
ID AAF36771 standard; DNA; 10 BP.  
XX AAF36771;  
AC  
XX 23-MAR-2001 (first entry)  
DT  
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3510.  
DE  
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX WO200077214-A2.  
PN  
XX 21-DEC-2000.  
PD  
XX 14-JUN-2000; 2000WO-US016223.  
PF  
XX 16-JUN-1999; 99US-00335032.  
PR  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA  
XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX

PS Example; Page 125; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16

Db |||||

9 CTGAGGCGA 1

RESULT 233

AAF37531

ID AAF37531 standard; DNA; 10 BP.

XX

AC AAF37531;

XX

DT 23-MAR-2001 (first entry)

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4270.

XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

PD 21-DEC-2000.

XX

PF 14-JUN-2000; 2000WO-US016223.

XX

PR 16-JUN-1999; 99US-00335032.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Velculescu V, Vogelstein B, Kinzler K;

XX

DR WPI; 2001-061874/07.

XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX

PS Example; Page 152; 419pp; English.

XX

CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

Db |||||

2 TGGCGAAGC 10

RESULT 234

AAF43175/c

ID AAF43175 standard; DNA; 10 BP.

XX

AC AAF43175;

XX

DT 23-MAR-2001 (first entry)

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11314.

XX

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

PD 21-DEC-2000.

XX

PF 14-JUN-2000; 2000WO-US016223.

XX

PR 16-JUN-1999; 99US-00335032.

XX

PA (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Velculescu V, Vogelstein B, Kinzler K;

XX

DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 354; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
||||| |||  
Db 10 CGCTGAGGC 2

RESULT 235  
AAF43253  
ID AAF43253 standard; DNA; 10 BP.

XX AAF43253;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11392.

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PA (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
XX  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 356; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
||||| |||  
Db 1 TGGCGATGG 9

RESULT 236  
AAF43167  
ID AAF43167 standard; DNA; 10 BP.

XX AAF43167;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11306.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
DE nor previously assigned open reading frame; nonannotated ORF; SAGE;  
DE serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
KW Saccharomyces cerevisiae.

XX WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
PA Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR Yeast gene coding sequences comprising NORF genes with serial analysis of  
XX gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
PT Example; Page 353; 419pp; English.  
PS The present invention describes an isolated DNA molecule comprising a  
XX coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 GCGCTGTGG 13  
Db 2 GCCCTGTGG 10  
RESULT 237  
AAS19671  
ID AAS19671 standard; DNA; 10 BP.  
XX AAS19671;  
AC AAS19671;  
XX 26-MAR-2002 (first entry)  
DT Primer-extension oligonucleotide #24 to detect human GHRHR polymorphisms.  
XX Human; single nucleotide polymorphism; SNP; GHRHR; chromosome 7p14;  
KW growth hormone releasing hormone receptor; haplotyping; genotyping;  
KW isolated growth hormone deficiency; IGHD; pituitary adenoma; primer; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO200179239-A2.  
PN 25-OCT-2001.  
XX Novel polymorphic variants of aldo-keto reductase family 1, member b1  
PT gene useful in studying expression and function of the protein, useful  
PT for screening drugs to treat diseases e.g. diabetes.

PF 17-APR-2001; 2001WO-US012453.  
XX PR 17-APR-2000; 2000US-0197978P.  
XX (GENA-) GENAISSANCE PHARM INC.  
PA Chew A, Choi JY, Denton RR, Nandabalan K, Sausker EA;  
XX WPI; 2002-066342/09.  
PI Genotyping human Growth hormone releasing hormone receptor gene of  
XX individual for determining haplotype of individual by determining  
PT identity of nucleotide pair at specific polymorphic sites for two copies  
PT of gene.  
XX Claim 18; Page 15; 90pp; English.  
PS The present invention relates to novel single nucleotide polymorphisms  
XX (SNPs) in the human growth hormone releasing hormone receptor (GHRHR)  
CC gene located on chromosome 7p14, and methods for haplotyping and/or  
CC genotyping the GHRHR gene. The methods of the invention make use of  
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or  
CC primer-extension oligonucleotides for detecting the GHRHR gene  
CC polymorphisms. The polymorphisms and screened compounds are useful for  
CC the treatment of diseases associated with GHRHR activity, such as  
CC isolated growth hormone deficiency (IGHD) and pituitary adenomas.  
CC AAS19648-AAS19673 represent primer-extension oligonucleotides for  
CC detecting human GHRHR gene polymorphisms  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 8 CTGTGGCGA 16  
Db 1 CTGTGGTGA 9  
RESULT 238  
ABL01179/c  
ID ABL01179 standard; DNA; 10 BP.  
XX ABL01179;  
AC ABL01179;  
XX 12-MAR-2002 (first entry)  
DT Human AKR1B1 gene polymorphism detection primer SEQ ID NO:76.  
XX Human; aldo-keto reductase family 1 member B1; aldose reductase; ss;  
KW AKR1B1; chromosome 7q35; detection; polymorphism; ASO; probe; primer;  
KW allele-specific oligonucleotide; antidiabetic; gene therapy; diabetes.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO200179223-A2.  
PN 25-OCT-2001.  
XX 12-APR-2001; 2001WO-US011944.  
PF 12-APR-2000; 2000US-0196315P.  
XX (GENA-) GENAISSANCE PHARM INC.  
PA Choi JY, Nandabalan K, Rounds E, Sanchis A;  
XX WPI; 2002-075056/10.  
DR Novel polymorphic variants of aldo-keto reductase family 1, member b1  
XX gene useful in studying expression and function of the protein, useful  
PT for screening drugs to treat diseases e.g. diabetes.  
PT



XX Claim 18; Page 15; 103pp; English.

PS The present invention describes an isolated polynucleotide (I) comprising

XX a sequence which is a polymorphic variant (PV) of a reference sequence

CC for aldo-keto reductase family 1, member B1 (AKR1B1) gene or its

CC fragment, having the 22214 base pair sequence given in ABL01105. AKR1B1

CC has antidiabetic activity and can be used in gene therapy. AKR1B1 can be

CC used in the treatment of diabetes. The human AKR1B1 gene is located on

CC chromosome 7q35. ABL01107 to ABL01129 represent allele-specific

CC oligonucleotide (ASO) probes used in the detection of polymorphisms in

CC the human AKR1B1 gene; ABL01130 to ABL01175 represent ASO primers used in

CC the detection of polymorphisms in the human AKR1B1 gene; and ABL01176 to

CC ABL01221 represent preferred primers used in the detection of

CC polymorphisms in the human AKR1B1 gene

XX

SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

Db 9 TGGCGAGGG 1

RESULT 239

AAS98835/c

ID AAS98835 standard; DNA; 10 BP.

XX

AC AAS98835;

XX

DT 26-MAR-2002 (first entry)

XX

DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #201.

XX

KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;

KW cytostatic; gene therapy; malignant histiocytosis; isogene;

KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;

KW genotype; human; allele specific oligonucleotide; ASO; primer;

KW primer extension; ss.

XX

OS Homo sapiens.

XX

PN WO200179225-A2.

XX

PD 25-OCT-2001.

XX

PF 12-APR-2001; 2001WO-US012044.

XX

PR 12-APR-2000; 2000US-0196411P.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Chew A, Choi JY, Koshy B;

XX

DR WPI; 2002-075058/10.

XX

PT Novel polymorphic variants of colony stimulating factor 1 receptor useful

PT in studying expression and function of the protein, useful for screening

PT candidate drugs to treat diseases e.g. inflammatory disorders.

XX

PS Claim 17; Page 17; 164pp; English.

XX

CC The invention describes a novel isolated polynucleotide (I) comprising a

CC sequence which is a polymorphic variant (PV) of a reference sequence for

CC colony stimulating factor 1 receptor (CSF1R) gene, found on The

CC polypeptide are useful for improving the discovery and development of

CC drugs for treating diseases associated with CSF1R activity, e.g.,

CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders

CC and the haplotypes can be used to validate CSF1R as a candidate target

CC for treating a specific condition or disease predicted to be associated

CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also

CC be used in developing diagnostic tests and therapeutic treatments. (I) is

CC useful in studying the expression and function of CSF1R, and in

CC expressing CSF1R protein for use in screening for candidate drugs to

CC treat diseases related to CSF1R activity and in studying the effect of

CC the variation on the biological activity of CSF1R as well as on the

CC binding affinity of candidate drugs targeting CSF1R. Antibodies are

CC useful in a variety of diagnostic and prognostic formats and therapeutic

CC methods. A transgenic animal is useful in studying expression of the

CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs

CC targeted against CSF1R protein, and for testing the efficacy of

CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)

CC are useful as probes and primers, and for assaying a polymorphism in the

CC target region. Without requiring any a priori knowledge of the phenotypic

CC effect of any particular CSF1R or haplotype the invention provides a

CC method for identifying lead compounds that are more likely to show

CC efficacy in clinical trials. This sequence is a primer used to detect

CC CSF1R gene polymorphisms by primer extension, described in the method of

CC the invention

XX

SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15

Db 10 GGTGTGGCG 2

RESULT 240

ABL42636

ID ABL42636 standard; cDNA; 10 BP.

XX

AC ABL42636;

XX

DT 12-APR-2002 (first entry)

XX

DE Human maturation/activation dendritic cell expression gene tag #10.

XX

KW Human; maturation/activation dendritic cell expression gene; tag;

KW maturation; activation; dendritic cell; ss.

XX

OS Homo sapiens.

XX

PN JP2001327293-A.

XX

PD 27-NOV-2001.

XX

PF 22-MAY-2000; 2000JP-00150562.

XX

PR 22-MAY-2000; 2000JP-00150562.

XX

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX

DR WPI; 2002-127070/17.

XX

PT Human maturation/activation dendritic cell expression gene group.

XX

PS Claim 1; Page 9; 41pp; Japanese.

XX

CC The present invention describes a human maturation/activation dendritic

CC cell (DC) expression gene group consisting of 100 genes which show the

CC highest expression among the genes expressed in human maturation/

CC activation DC. Also described are: (1) a protein expressed by the above

CC human maturation/activation DC expression gene; (2) an antibody against

CC the protein; and (3) an antagonist against the expression of each gene

CC belonging to the above gene group. The gene group is useful for the

CC treatment and the diagnosis of various human diseases related to human

CC DC. ABL42627 to ABL42926 represent specifically claimed human

CC maturation/activation DC expression gene tags from the present invention

XX



SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
||| |||||  
Db 2 TGGTGAAGG 10

RESULT 241  
AAD25385/c  
ID AAD25385 standard; DNA; 10 BP.  
XX  
AC AAD25385;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human primer #2 to detect ADORA2A gene polymorphisms.  
XX  
KW Human; adenosine A2a receptor; ADORA2A; polymorphic site; PS; haplotype;  
KW drug screening; cellular stress; hypertension; antisense gene therapy;  
KW hypotensive; tranquilliser; chromosome 22q11.23; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200187905-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 16-MAY-2001; 2001WO-US015789.  
XX  
PR 18-MAY-2000; 2000US-0205120P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Duda AE, Kliem SE, Koshy B, Lee HH, Sanchis A;  
XX WPI; 2002-055678/07.  
XX  
PT Genetic variants of human adenosine A2a receptors, ADORA2A gene useful  
PT for studying expression, function of the gene and expressing ADORA2A  
PT proteins for use in screening for drugs to treat hypertension and  
PT cellular stress.  
XX  
PS Claim 18; Page 13; 58pp; English.  
XX  
CC The present invention relates to a polynucleotide comprising a sequence  
CC which comprises adenosine A2a receptor (ADORA2A) isogene chosen from  
CC isogenes 1-2 and 4 having polymorphisms at polymorphic sites (PS)  
CC corresponding to nucleotide position 531 (PS1) of a sequence of 997 bp,  
CC 1345 (PS2), 1794 (PS3) and 1833 (PS4) of a sequence of 1906 bp, or which  
CC is a polymorphic variant of a coding sequence for ADORA2A isogene.  
CC ADORA2A gene is located on chromosome 22q11.23. ADORA2A is useful for  
CC screening for drugs targeting the polypeptide, by contacting the ADORA2A  
CC polymorphic variant with a candidate agent and assaying for binding  
CC activity. The polymorphism and haplotype data are useful for validating  
CC whether ADORA2A is a suitable target for drugs to treat cellular stress  
CC and hypertension, screening for such drugs and reducing bias in clinical  
CC trials of such drugs. A polymorphic variant of ADORA2A is useful in  
CC studying the effect of the variation on the biological activity of  
CC ADORA2A, on the binding affinity of candidate drugs targeting ADORA2A  
CC for the treatment of cellular stress and hypertension and in assays to  
CC measure the binding affinities of one or more candidate drugs targeting  
CC the ADORA2A protein. The present sequence is human primer used for  
CC detecting ADORA2A gene polymorphisms  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGA 16  
||| |||||  
Db 9 CTGTGGCCA 1

RESULT 242  
ABN81464  
ID ABN81464 standard; DNA; 10 BP.  
XX  
AC ABN81464;  
XX  
DT 16-AUG-2002 (first entry)  
XX  
DE Human HTATIP PCR primer SEQ ID NO 65.  
XX  
KW Human; HIV-1 Tat interactive protein; HTATIP; haplotyping; genotyping;  
KW transgenic; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200229089-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 05-OCT-2001; 2001WO-US031593.  
XX  
PR 06-OCT-2000; 2000US-0238655P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Armstrong B, Bentivegna SC, Choi JY, Gilson CR, Parks KE;  
PI Sausker EA;  
XX  
DR WPI; 2002-330173/36.  
XX  
PT New HIV-1 tat interactive protein, 60 kDa (HTATIP) gene polymorphic  
PT variants, for studying the expression and function of HTATIP and  
PT screening candidate drugs for treating familial glucocorticoid deficiency  
PT and cancer.  
XX  
PS Claim 16; Page 14; 89pp; English.  
XX  
CC The invention relates to novel genetic variants of the HIV-1 Tat  
CC interactive protein, 60 kDa (HTATIP) gene. The polymorphic variants are  
CC useful in studying the expression and function of HTATIP, in expressing  
CC HTATIP protein for use in screening for candidate drugs to treat diseases  
CC related to HTATIP activity, in studying the effect of the variation on  
CC the biological activity of HTATIP and the binding affinity of candidate  
CC drugs targeting HTATIP for the treatment of disorders. Haplotyping  
CC methods are useful in validating HTATIP as a candidate target for  
CC treating a specific condition or disease predicted to be associated with  
CC HTATIP activity or in the design of clinical trials of candidate drugs  
CC for treating a specific condition or disease associated with HTATIP  
CC activity. Transgenic animals are useful for studying expression of the  
CC HTATIP isogenes in vivo, for in vivo screening and testing of drugs  
CC targeted against HTATIP protein and for testing the efficacy of  
CC therapeutic agents and compounds for disorders. The present sequence is  
CC that of a HTATIP allele specific PCR primer of the invention  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGT 11  
||| |||||  
Db 1 TCGCGGTGT 9

RESULT 243  
ABK96027

ID ABK96027 standard; DNA; 10 BP.  
XX  
AC ABK96027;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Human LIPE gene polymorphism detection oligonucleotide primer #2.  
XX  
KW Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;  
KW polymorphism; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200240502-A2.  
XX  
PD 23-MAY-2002.  
XX  
PF 16-NOV-2001; 2001WO-US043518.  
XX  
PR 16-NOV-2000; 2000US-0249302P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
PI Anastasio AE, Bentivegna SC, Chew A, Koshy B, Rounds E;  
XX  
DR WPI; 2002-519369/55.  
XX  
PT Novel genetic variants of Lipase, Hormone-Sensitive isogenes, useful for  
PT improving efficiency and reliability in drug development for treating  
PT diseases associated with LIPE activity, e.g. obesity and male sterility.  
XX  
PS Claim 17; Page 15; 142pp; English.  
XX  
CC The present invention relates to a new polynucleotide comprising a  
CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)  
CC isogenes. The invention is useful in screening for drugs targeting LIPE  
CC isogenes that are useful for treating obesity and male sterility. The  
CC methods of the invention are useful for improving the efficiency and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with LIPE activity. The polynucleotide  
CC is useful in studying the expression and function of LIPE, and in  
CC expressing LIPE protein for use in screening for candidate drugs to treat  
CC diseases related to LIPE activity. It is also useful in studying the  
CC effect of the variation on the biological activity of LIPE as well as on  
CC the binding affinity of candidate drugs targeting LIPE for the treatment  
CC of obesity and male sterility. The invention is useful for studying the  
CC expression of LIPE isogenes in vivo, for in vivo screening and testing of  
CC drugs targeted against LIPE protein, and for testing the efficacy of  
CC therapeutic agents and compounds for treating obesity and male sterility  
CC in a biological system. The present nucleic acid sequence represents one  
CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were  
CC used in the invention to detect polymorphisms in the human LIPE gene  
XX  
SQ Sequence 10 BP; 0 A; 1 C; 5 G; 4 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 GCTGTGGCG 15  
Db 2 GCTGTGGTG 10  
  
RESULT 244  
AAL48067  
ID AAL48067 standard; DNA; 10 BP.  
XX  
AC AAL48067;  
XX  
DT 27-SEP-2002 (first entry)  
XX  
DE Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 45.

XX Human; colony stimulating factor 3(granulocyte); CSF3; SNP; isogene;  
KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;  
KW neutropenia; promyelocytic leukaemia; haematological disorder;  
KW gene therapy; PCR; primer extension oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200194364-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 11-JUN-2001; 2001WO-US018813.  
XX  
PR 09-JUN-2000; 2000US-0210380P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
PI Duda A, Kazemi A, Messer C, Sausker EA;  
XX  
DR WPI; 2002-566435/60.  
XX  
PT New variants of colony stimulating factor 3 (CSF3) isogenes, useful for  
PT improving efficiency and reliability in the development of drugs for  
PT treating diseases associated with CSF3 activity e.g. neutropenia.  
XX  
PS Claim 19; Page 13; 68pp; English.  
XX  
CC The present invention provides the protein, gene and cDNA sequences of  
CC human colony stimulating factor 3(granulocyte) CSF3. Also described are  
CC single nucleotide polymorphisms (SNPs) identified within these sequences.  
CC The sequences can be used in the treatment of neutropenia, promyelocytic  
CC leukaemia and haematological disorders. The present sequence is an allele  
CC specific primer extension oligonucleotide used to isolate the coding  
CC sequences of the invention  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CGCTGTGGC 14  
Db 2 CGCGGTGGC 10  
  
RESULT 245  
AAL48068/c  
ID AAL48068 standard; DNA; 10 BP.  
XX  
AC AAL48068;  
XX  
DT 27-SEP-2002 (first entry)  
XX  
DE Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 46.  
XX  
KW Human; colony stimulating factor 3(granulocyte); CSF3; SNP; isogene;  
KW chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;  
KW neutropenia; promyelocytic leukaemia; haematological disorder;  
KW gene therapy; PCR; primer extension oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200194364-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 11-JUN-2001; 2001WO-US018813.  
XX  
PR 09-JUN-2000; 2000US-0210380P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Kazemi A, Messer C, Sausker EA;  
XX WPI; 2002-566435/60.  
XX  
XX New variants of colony stimulating factor 3 (CSF3) isogenes, useful for  
PT improving efficiency and reliability in the development of drugs for  
PT treating diseases associated with CSF3 activity e.g. neutropenia.  
XX  
XX Claim 19; Page 13; 68pp; English.  
PS  
XX The present invention provides the protein, gene and cDNA sequences of  
CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are  
CC single nucleotide polymorphisms (SNPs) identified within these sequences.  
CC The sequences can be used in the treatment of neutropenia, promyelocytic  
CC leukaemia and haematological disorders. The present sequence is an allele  
CC specific primer extension oligonucleotide used to isolate the coding  
CC sequences of the invention  
XX  
SQ Sequence 10 BP; 3 A; 6 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 GCTGTGGCG 15  
Db 9 GCTGTGGTG 1  
  
RESULT 246  
AAD27409/c  
ID AAD27409 standard; DNA; 10 BP.  
XX  
AC AAD27409;  
XX  
DT 18-APR-2002 (first entry)  
XX  
DE Oligo #2, to construct a phage that express ligand #4 of the invention.  
XX  
KW Small intestine; blood brain barrier; central nervous system; CNS;  
KW circulatory system; gastrointestinal tract; pharmaceutical; ligand; ss.  
XX  
OS Synthetic.  
XX  
PN WO200190139-A2.  
XX  
PD 29-NOV-2001.  
XX  
PF 07-MAY-2001; 2001WO-IB0000926.  
XX  
PR 07-MAY-2001; 2001WO-IB0000926.  
XX  
PA (SUPR-) SUPRATEK PHARMA INC.  
XX  
PI Tchistiakova L, Li S, Pietrzynski G, Alakhov V;  
XX  
DR WPI; 2002-130449/17.  
XX  
XX New polypeptide capable of crossing the blood brain or intestine barrier  
PT for increasing the absorption of an orally administered therapeutic from  
PT the gastrointestinal tract into the circulatory system.  
XX  
PS Example 3; Page 45; 60pp; English.  
XX  
XX The present invention relates to novel ligands comprising a peptide  
CC capable of crossing the small intestine and blood brain barrier. The  
CC ligand is capable of enhancing oral and central nervous system (CNS)  
CC bioavailability of biological agents or formulations. The invention also  
CC relates to pharmaceutical compositions in which the ligand is used as  
CC targeting moiety to improve the delivery of a biological agent used for  
CC diagnostic or therapeutic purpose. The polypeptide is used to increase  
CC absorption of an orally delivered therapeutic agent into the circulatory

CC system from the gastrointestinal tract. The present DNA sequence is an  
CC oligonucleotide which is used for constructing a phage that express  
CC ligand #4 used in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCT 9  
Db 10 GGTCGCGCT 2  
  
RESULT 247  
ABL39499  
ID ABL39499 standard; DNA; 10 BP.  
XX  
AC ABL39499;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human ETVF primer-extension oligonucleotide 5.  
XX  
KW Human; electron-transfer flavoprotein beta polypeptide; ETVF;  
KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;  
KW novel polymorphic site; novel polymorphism; ETVF genotype; ss; GAI1;  
KW ETVF haplotype; transgenic animal; primer; probe; chromosome 19q13;  
KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.  
XX  
OS Homo sapiens.  
XX  
PN WO200202580-A2.  
XX  
PD 10-JAN-2002.  
XX  
PF 05-JUL-2001; 2001WO-US021306.  
XX  
PR 05-JUL-2000; 2000US-0215984P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;  
XX  
DR WPI; 2002-154722/20.  
XX  
XX Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,  
PT useful for therapeutic purposes, for studying the expression and function  
PT of the polynucleotide, and for expressing the flavoprotein.  
XX  
PS Claim 19; Page 15; 143pp; English.  
XX  
XX The invention comprises DNA, cDNA and protein sequences of the human  
CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on  
CC chromosome 19q13.3-13.4). The invention specifically relates to the  
CC identification of 27 novel polymorphic sites within the ETVF gene.  
CC Electron-transfer flavoprotein (ETF) is an obligatory electron acceptor  
CC for nine primary flavoprotein dehydrogenases and is located in the  
CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta  
CC (ETFB) subunit. Electrons accepted by ETF are transferred to the  
CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).  
CC Deficiency of ETF or ETFDH leads to glutaric acidemia type II (GAI1).  
CC Therefore ETVF is a pharmaceutically-important gene in the treatment of  
CC GAI1. The novel ETVF polymorphisms identified in the invention are useful  
CC for genotyping and haplotyping the ETVF gene of an individual. The ETVF  
CC protein and nucleic acids of the invention are useful for studying the  
CC expression and function of ETVF in vivo. The ETVF protein and nucleic  
CC acids are also useful for testing the efficacy of therapeutic agents and  
CC compounds for glutaric acidemia type II. The nucleic acids of the  
CC invention are useful in the production of a transgenic animal expressing  
CC the ETVF gene. Nucleic acids ABL39414-ABL39440 represent claimed ETVF  
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed

```
CC  ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC  represent claimed ETFB primer-extension oligonucleotides
XX
SQ  Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

    Query Match      38.9%; Score 7.4; DB 1; Length 10;
    Best Local Similarity 88.9%; Pred. No. 1.7e+02;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CTGTGGCGA 16
Db      1 CTGTGGGGA 9

RESULT 248
ABT05346
ID  ABT05346 standard; DNA; 10 BP.
XX
AC  ABT05346;
XX
DT  24-OCT-2002 (first entry)
XX
DE  Human NAGA-alpha gene primer extension oligonucleotide 6.
XX
KW  Human; PCR; primer; ss; gene therapy; N-acetylgalactosaminidase alpha;
KW  chromosome 22q13.2-q13.31; lysosomal glycohydrolase; screening; SNP;
KW  NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
KW  genotyping.
XX
OS  Homo sapiens.
XX
PN  WO200194637-A1.
XX
DT  24-OCT-2002 (first entry)
XX
DE  Human NAGA-alpha gene primer extension oligonucleotide 6.
XX
KW  Human; PCR; primer; ss; gene therapy; N-acetylgalactosaminidase alpha;
KW  chromosome 22q13.2-q13.31; lysosomal glycohydrolase; screening; SNP;
KW  NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
KW  genotyping.
XX
OS  Homo sapiens.
XX
PN  WO200194637-A1.
XX
DT  13-DEC-2001.
XX
PT  New genetic variants of isolated N-acetylgalactosaminidase (NAGA), Alpha
PT  gene, useful for therapeutic purposes, for studying the expression and
PT  function of the polynucleotide, and for expressing NAGA protein.
XX
PF  07-JUN-2001; 2001WO-US018456.
XX
PR  07-JUN-2000; 2000US-0210110P.
XX
PA  (GENA-) GENAISSANCE PHARM INC.
XX
PI  Duda A, Kazemi A, Koshy B, Parks KE;
XX
WPI; 2002-566449/60.
XX
PT  New genetic variants of isolated N-acetylgalactosaminidase (NAGA), Alpha
PT  gene, useful for therapeutic purposes, for studying the expression and
PT  function of the polynucleotide, and for expressing NAGA protein.
XX
PS  Claim 18; Page 14; 91pp; English.
XX
CC  The invention comprises the amino acid and coding sequence of the human N
CC  -acetylgalactosaminidase (NAGA) alpha protein. The invention specifically
CC  comprises novel polymorphic sites identified within the NAGA gene. The
CC  NAGA gene is located on chromosome 22q13.2-q13.31, and encodes a
CC  lysosomal glycohydrolase that cleaves alpha-N-acetylgalactosaminy
CC  moieties in glycoconjugates. The NAGA DNA and protein sequences of the
CC  invention are useful for studying the expression and function of NAGA and
CC  for screening candidate drugs to treat diseases related to NAGA activity.
CC  The NAGA gene polymorphisms identified in the present invention are
CC  useful for haplotyping and genotyping the NAGA gene of an individual. The
CC  present DNA sequence represents an N-acetylgalactosaminidase gene primer
CC  extension oligonucleotide
XX
SQ  Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

    Query Match      38.9%; Score 7.4; DB 1; Length 10;
    Best Local Similarity 88.9%; Pred. No. 1.7e+02;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGC 14
Db      1 CGCTGTGCC 9
```

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RESULT 249
ABT05344/C
ID  ABT05344 standard; DNA; 10 BP.
XX
AC  ABT05344;
XX
DT  24-OCT-2002 (first entry)
XX
DE  Human NAGA-alpha gene primer extension oligonucleotide 4.
XX
KW  Human; PCR; primer; ss; gene therapy; N-acetylgalactosaminidase alpha;
KW  chromosome 22q13.2-q13.31; lysosomal glycohydrolase; screening; SNP;
KW  NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
KW  genotyping.
XX
OS  Homo sapiens.
XX
PN  WO200194637-A1.
XX
DT  13-DEC-2001.
XX
PF  07-JUN-2001; 2001WO-US018456.
XX
PR  07-JUN-2000; 2000US-0210110P.
XX
PA  (GENA-) GENAISSANCE PHARM INC.
XX
PI  Duda A, Kazemi A, Koshy B, Parks KE;
XX
WPI; 2002-566449/60.
XX
PT  New genetic variants of isolated N-acetylgalactosaminidase (NAGA), Alpha
PT  gene, useful for therapeutic purposes, for studying the expression and
PT  function of the polynucleotide, and for expressing NAGA protein.
XX
PS  Claim 18; Page 13; 91pp; English.
XX
CC  The invention comprises the amino acid and coding sequence of the human N
CC  -acetylgalactosaminidase (NAGA) alpha protein. The invention specifically
CC  comprises novel polymorphic sites identified within the NAGA gene. The
CC  NAGA gene is located on chromosome 22q13.2-q13.31, and encodes a
CC  lysosomal glycohydrolase that cleaves alpha-N-acetylgalactosaminy
CC  moieties in glycoconjugates. The NAGA DNA and protein sequences of the
CC  invention are useful for studying the expression and function of NAGA and
CC  for screening candidate drugs to treat diseases related to NAGA activity.
CC  The NAGA gene polymorphisms identified in the present invention are
CC  useful for haplotyping and genotyping the NAGA gene of an individual. The
CC  present DNA sequence represents an N-acetylgalactosaminidase gene primer
CC  extension oligonucleotide
XX
SQ  Sequence 10 BP; 1 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

    Query Match      38.9%; Score 7.4; DB 1; Length 10;
    Best Local Similarity 88.9%; Pred. No. 1.7e+02;
    Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 TGGCGAAGG 19
Db      10 TGGGGAAGG 2

RESULT 250
AAS99201/C
ID  AAS99201 standard; DNA; 10 BP.
XX
AC  AAS99201;
XX
DT  12-MAR-2002 (first entry)
XX
DE  UDP glycosyltransferase 1 (UGT1A1) allele-specific oligonucleotide #68.
XX
```



KW UDP glycosyltransferase 1; UGT1A1; human; haplotyping; ss;  
KW drug discovery; Gilbert's syndrome; Crigler-Najjar syndrome;  
XX allele-specific oligonucleotide.  
OS Homo sapiens.  
XX WO200179230-A2.  
XX  
PD 25-OCT-2001.  
XX  
XX 13-APR-2001; 2001WO-US012273.  
PF  
XX 18-APR-2000; 2000US-0197514P.  
PR  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
PI Chew A, Choi JY, Koshy B, Rounds E;  
XX WPI; 2002-075063/10.  
DR  
XX  
PT Genotyping a human UDP glycosyltransferase 1 gene of an individual for  
PT determining the haplotype of an individual, involves determining the  
PT identity of a nucleotide pair at specific polymorphic sites for two  
PT copies of the gene.  
XX  
PS Claim 18; Page 14; 81pp; English.  
XX  
CC The invention relates to genotyping a human UDP glycosyltransferase  
CC (UGT1A1) gene of an individual, involving determining for the two copies  
CC of the UGT1A1 gene present in the individual, the identity of the  
CC nucleotide pair at one or more polymorphic sites. The new method is  
CC useful for determining whether an individual has a haplotype or haplotype  
CC pairs, given in the specification. It is useful for improving the  
CC efficacy and reliability of several steps in the discovery and  
CC development of drugs for treating diseases associated with UGT1A1  
CC activity, e.g., Gilbert's syndrome and Crigler-Najjar syndrome, to  
CC validate UGT1A1 as a candidate agent for treating a specific condition or  
CC disease predicted to be associated with UGT1A1 activity, and in the  
CC design of clinical trials of candidate drugs for treating a specific  
CC condition or disease predicted to be associated with UGT1A1 activity. The  
CC method is useful to screen for compounds targeting UGT1A1 to treat a  
CC specific condition or disease associated with UGT1A1 activity. A nucleic  
CC acid (I) comprising a polymorphic variant of a reference sequence for the  
CC UGT1A1 gene or cDNA (II) or its fragment is useful in studying the  
CC expression and function of UGT1A1, and in expressing UGT1A1 protein for  
CC use in screening for candidate drugs to treat diseases related to UGT1A1  
CC activity. (I) or (II) is useful for therapeutic purposes. (II) or a  
CC recombinant organism comprising (II) is useful for studying expression of  
CC the UGT1A1 isogenes in vivo, for in vivo screening and testing of drugs  
CC targeted against UGT1A1 protein, and for testing the efficacy of  
CC therapeutic agents and compounds for Gilbert's syndrome and Crigler-  
CC Najjar syndrome, in a biological system. AAS99134-AAS99203 represent UDP  
CC glycosyltransferase 1 gene allele-specific oligonucleotides used in the  
CC method of the invention  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTG 10  
||| ||||  
Db 10 GTCGTGCTG 2

RESULT 251  
ABV84886  
ID ABV84886 standard; cDNA; 10 BP.  
XX  
AC ABV84886;  
XX  
DT 12-DEC-2002 (first entry)

XX Human thymosin beta-4 SAGE tag #696.  
DE  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 55; Page 29; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly  
CC expressed in chronic hepatitis C liver tissue  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
||| ||||  
Db 2 TGGTGAAGG 10

RESULT 252  
ABV84695  
ID ABV84695 standard; cDNA; 10 BP.  
XX  
AC ABV84695;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Chronic hepatitis C/HCC differentially expressed gene SAGE tag #505.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; differential expression; ss.  
XX  
OS Homo sapiens.  
XX



PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 46; Page 25; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly  
CC expressed genes out of those genes which are underexpressed in  
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCT 9  
Db ||| |||||  
2 GGACGCGCT 10  
  
RESULT 253  
ABV84505  
ID ABV84505 standard; cDNA; 10 BP.  
XX  
AC ABV84505;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human apolipoprotein A-I SAGE tag #315.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; differential expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 28; Page 19; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84491-ABV84590 are SAGE tags representing the 100 least highly  
CC expressed genes out of those genes which are underexpressed in  
CC hepatocellular carcinoma compared with normal liver tissue  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCT 9  
Db ||| |||||  
2 GGACGCGCT 10  
  
RESULT 254  
ABV84523  
ID ABV84523 standard; cDNA; 10 BP.  
XX  
AC ABV84523;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human HCC underexpressed gene SAGE tag #333.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; differential expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 28; Page 19; 139pp; Japanese.

XX The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84491-ABV84590 are SAGE tags representing the 100 least highly  
CC expressed genes out of those genes which are underexpressed in  
CC hepatocellular carcinoma compared with normal liver tissue  
XX

SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
|| |||||  
Db 2 GGACGCGCT 10

RESULT 255  
ABV84710

ID ABV84710 standard; cDNA; 10 BP.  
XX  
AC ABV84710;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human apolipoprotein A-I SAGE tag #520.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; differential expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 46; Page 25; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve

CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly  
CC expressed genes out of those genes which are underexpressed in  
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue  
XX

SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
|| |||||  
Db 2 GGACGCGCT 10

RESULT 256  
ABV84764

ID ABV84764 standard; cDNA; 10 BP.  
XX  
AC ABV84764;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Chronic hepatitis C/HCC differentially expressed gene SAGE tag #574.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; differential expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 46; Page 26; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression

CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly  
CC expressed genes out of those genes which are underexpressed in  
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCGCGCTG 10  
| |||||  
Db 2 GACGCGCTG 10

RESULT 257  
ABV84791  
ID ABV84791 standard; cDNA; 10 BP.  
XX  
AC ABV84791;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human apolipoprotein A-I SAGE tag #601.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 55; Page 28; 139pp; Japanese.

CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly  
CC expressed in chronic hepatitis C liver tissue  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GGTGCGGCT 9  
|| |||||  
Db 2 GGACGGGCT 10

RESULT 258  
ABV84741  
ID ABV84741 standard; cDNA; 10 BP.  
XX  
AC ABV84741;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Chronic hepatitis C/HCC differentially expressed gene SAGE tag #551.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; differential expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.

XX Human chronic hepatitis C tissue expression exasperating gene group  
XX comprises 100 high-ranking genes.  
XX  
PS Claim 46; Page 26; 139pp; Japanese.  
CC  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84691-ABV84790 are SAGE tags representing the 100 least highly  
CC expressed genes out of those genes which are underexpressed in  
CC hepatocellular carcinoma compared with chronic hepatitis C liver tissue  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GGTGCGGCT 9  
|| |||||  
Db 2 GGACGGGCT 10

RESULT 259  
ABV84919  
ID ABV84919 standard; cDNA; 10 BP.  
XX  
AC ABV84919;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human apolipoprotein A-I SAGE tag #729.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 64; Page 30; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly  
CC expressed in hepatocellular carcinoma  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCT 9  
Db || |||||  
2 GGACGCGCT 10  
  
RESULT 260  
ABV84967  
ID ABV84967 standard; cDNA; 10 BP.  
XX  
AC ABV84967;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human thymosin beta-4 SAGE tag #777.

XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 64; Page 31; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84891-ABV84990 are SAGE tags representing 100 genes which are highly  
CC expressed in hepatocellular carcinoma  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAGG 19  
Db ||| |||||  
2 TGGTGAAGG 10  
  
RESULT 261  
ABK23578/c  
ID ABK23578 standard; DNA; 10 BP.  
XX  
AC ABK23578;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Transcript tag DNA sequence #167 induced or suppressed by N-myc.  
XX  
KW Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;  
KW spread; myc target; myc tag; SAGE; serial analysis of gene expression;  
KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200185941-A2.  
XX



PD 15-NOV-2001.  
XX  
PF 11-MAY-2001; 2001WO-NL000361.  
XX  
PR 11-MAY-2000; 2000EP-00201698.  
PR 29-JUN-2000; 2000EP-00202284.  
XX  
PA (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN.  
XX  
PI Versteeg R, Caron HN;  
XX  
DR WPI; 2002-066603/09.  
XX  
PT A new nucleic acid library of myc-dependent downstream genes capable of  
PT supporting a neoplastic characteristic of cancer is useful to find new  
PT therapies and diagnoses for cancer.  
XX  
PS Disclosure; Page 53; 69pp; English.  
XX  
CC The present invention relates to a nucleic acid library comprising myc-  
CC dependent downstream genes or their functional fragments essentially  
CC capable of supporting a neoplastic character of cancer such as growth,  
CC invasion or spread. These myc target or tag sequences are identified by  
CC SAGE (serial analysis of gene expression). The library is useful to find  
CC new diagnoses and treatments for cancer. The invention is also useful to  
CC enhance production of recombinant proteins in a production system with  
CC high expression of endogenous or transfected myc oncogenes. ABK23412-  
CC ABK23828 represent transcript tag DNA sequences that are activated or  
CC repressed by N-myc in human neuroblastoma  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCT 9  
Db ||||| |||||  
10 GGTCCCGCT 2  
  
RESULT 262  
ABA96213/c  
ID ABA96213 standard; DNA; 10 BP.  
XX  
AC ABA96213;  
XX  
DT 13-MAR-2002 (first entry)  
XX  
DE Half-site oligonucleotide ON-10.  
XX  
KW Multidimensional library; MDL; industrial; pharmaceutical; biomedicine;  
KW bioregulation; multidimensional peptide; MDP; vaccine; ss.  
XX  
OS Synthetic.  
XX  
PN WO200186293-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 11-MAY-2001; 2001WO-IB0000810.  
XX  
PR 12-MAY-2000; 2000US-00570477.  
XX  
PA (SUPR-) SUPRATEK PHARMA INC.  
PA (BIOP-) BIOPHAGE INC.  
XX  
PI Popkov M, Mandeville R, Romar O, Alakhov V;  
XX  
DR WPI; 2002-089806/12.  
XX  
PT New multidimensional library useful for screening molecules that  
PT potentially interact with a target molecule, e.g. multidimensional

PT peptides useful in any industrial or pharmaceutical application.  
XX  
PS Example 1; Page 57; 77pp; English.  
XX  
CC The invention relates to a multidimensional library (MDL) for screening  
CC molecules that potentially interact with a target molecule. A MDL may be  
CC represented by various natural or artificial polymeric compounds  
CC including oligonucleotides, proteins, polypeptides, peptides,  
CC polycarbohydrates etc., where the library comprises at least one molecule  
CC comprising a general formula (X<sub>Yn</sub>)<sub>m</sub>, where: (X<sub>Yn</sub>) is a repeating unit of  
CC the at least one molecule; X = a functional unit that interacts with the  
CC target molecule; Y = a structural unit; n = the number of the structural  
CC units in the repeating unit; and m = a number of repeating units in the  
CC at least one molecule. The MDL is useful for screening molecules that  
CC potentially interact with a target molecule, particularly for screening  
CC proteins, polypeptides or peptides for binding specificity and desired  
CC affinity for target molecule. The multidimensional peptide products can  
CC be used in any industrial or pharmaceutical application that uses a  
CC peptide binding moiety specific for any given target. These are also  
CC useful in a wide variety of in vivo applications in the fields of  
CC biomedicine, bioregulation and control. Other in vivo uses include  
CC administration of multidimensional peptides (MDP) and MDP compositions as  
CC immunogens for vaccines, which useful for active immunisation procedures.  
CC The present sequence is that of an oligonucleotide useful in the  
CC construction of the MDL  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCT 9  
Db ||||| |||||  
10 GGTGCGCT 2  
  
RESULT 263  
AAS19821  
ID AAS19821 standard; DNA; 10 BP.  
XX  
AC AAS19821;  
XX  
DT 08-MAY-2002 (first entry)  
XX  
DE Oligonucleotide #1 to detect human RANGAP1 gene polymorphisms.  
XX  
KW Human; single nucleotide polymorphism; SNP; RANGAP1;  
KW haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1;  
KW genotyping; cancer; irregular cell cycle associated disorder; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200179240-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 17-APR-2001; 2001WO-US012455.  
XX  
PR 17-APR-2000; 2000US-0198072P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Chew A, Choi JY, Koshy B;  
XX  
DR WPI; 2002-075068/10.  
XX  
PT Genotyping human Ran GTPase activating protein 1 gene of individual for  
PT determining haplotype of individual, involves determining identity of  
PT nucleotide pair at specific polymorphic sites for two copies of the gene.  
XX  
PS Claim 17; Page 15; 148pp; English.  
XX



CC The present invention relates to novel single nucleotide polymorphisms  
CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene  
CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or  
CC genotyping the RANGAP1 gene. The methods of the invention make use of  
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or  
CC primer-extension oligonucleotides for detecting the RANGAP1 gene  
CC polymorphisms. The polynucleotides and screened compounds are useful for  
CC treatment of diseases associated with RANGAP1 activity, such as cancer  
CC and other disorders associated with an irregular cell cycle. AAS19821-  
CC AAS19898 represent primer-extension oligonucleotides for detecting human  
CC RANGAP1 gene polymorphisms  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 CGCGCTGTG 12  
Db 2 CGCGCGTG 10  
  
RESULT 264  
ABA93366  
ID ABA93366 standard; DNA; 10 BP.  
XX  
AC ABA93366;  
XX  
DT 22-APR-2002 (first entry)  
XX  
DE Human ACAA1 gene polymorphism detection primer SEQ ID NO:81.  
XX  
KW Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;  
KW peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;  
KW single nucleotide polymorphism; polymorphic variant; enzyme; probe;  
KW primer; allele specific oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200187903-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 03-MAY-2001; 2001WO-US014330.  
XX  
PR 18-MAY-2000; 2000US-0205022P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
PA (DUDA/) DUDA A E.  
XX  
PI Chew A, Koshy B;  
XX  
DR WPI; 2002-164134/21.  
XX  
PT Isolated polynucleotide, comprising a polymorphic variant of the acetyl-  
PT Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)  
PT gene useful for providing haplotype information and in therapy for  
PT treating related disorders.  
XX  
PS Claim 17; Page 14; 93pp; English.  
XX  
CC The present invention describes a polypeptide (I) which is a polymorphic  
CC variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal 3-  
CC oxoacyl-Coenzyme A thiolase) ACAA1 protein (ABB05516). ACAA1 is located  
CC on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)  
CC where the sequence comprises one of the haplotypes shown in Table 4 or  
CC one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are  
CC given in the specification. The polynucleotide encoding ACAA1 can be used  
CC for providing haplotype and genotype information of an individual.  
CC Furthermore, the polynucleotide is useful for the treatment of disorders  
CC related to its abnormal expression or function. ABA93289 to ABA93383  
CC represent allele specific oligonucleotides (ASOs) which are used in the

CC detection of polymorphisms in the human ACAA1 gene  
XX  
SQ Sequence 10 BP; 4 A; 0 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAGG 19  
Db 1 TGGAGAAGG 9  
  
RESULT 265  
AAS19954/c  
ID AAS19954 standard; DNA; 10 BP.  
XX  
AC AAS19954;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Primer-extension oligonucleotide #6 to detect human DNAL4 polymorphisms.  
XX  
KW Human; single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;  
KW dynein axonemal light polypeptide chain 4; haplotyping; genotyping;  
KW neuroprotective; neurological disorder; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200179235-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 16-APR-2001; 2001WO-US012304.  
XX  
PR 17-APR-2000; 2000US-0197460P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Chew A, Choi JY, Koshy B;  
XX  
DR WPI; 2002-075065/10.  
XX  
PT Genotyping human dynein, axonemal light polypeptide chain 4 gene of  
PT individual, useful for determining haplotype of individual, comprises  
PT determining identity of nucleotide pair at specific polymorphic sites for  
PT two copies of gene.  
XX  
PS Claim 18; Page 13; 79pp; English.  
XX  
CC The present invention relates to novel single nucleotide polymorphisms  
CC (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4)  
CC gene located on chromosome 22q13.1, and methods for haplotyping and/or  
CC genotyping the DNAL4 gene. The methods of the invention make use of  
CC allele-specific oligonucleotides (ASOs) as probes and primers and/or  
CC primer-extension oligonucleotides for detecting the DNAL4 gene  
CC polymorphisms. The polynucleotides and screened compounds are useful for  
CC the treatment of diseases associated with DNAL4 activity, such as  
CC neurological disorders. AAS19949-AAS19976 represent primer-extension  
CC oligonucleotides for detecting human DNAL4 gene polymorphisms  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGCGAAG 18  
Db 10 GTGGCTAAG 2  
  
RESULT 266

ABL45924/c  
ID ABL45924 standard; DNA; 10 BP.  
XX  
AC ABL45924;  
XX  
DT 26-APR-2002 (first entry)  
XX  
DE Human EDG6 gene allele specific primer extension oligo SEQ ID NO: 118.  
XX  
KW Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;  
KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;  
KW cytostatic; antiinflammatory; gene therapy; SNP;  
KW single nucleotide polymorphism; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200206446-A2.  
XX  
PD 24-JAN-2002.  
XX  
PF 17-JUL-2001; 2001WO-US022523.  
XX  
PR 17-JUL-2000; 2000US-0218727P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Kliem SE, Koshy B;  
XX  
DR WPI; 2002-171804/22.  
XX  
PT New genetic variants of endothelial differentiation, G-protein coupled  
PT receptor-6 gene for studying expression, function of the gene and  
PT expressing EDG6 protein for use in screening drugs to treat cancer,  
PT inflammation.  
XX  
PS Claim 18; Page 14; 111pp; English.  
XX  
CC The present invention provides the gene, protein and cDNA sequences of  
CC the human endothelial differentiation, G-protein coupled receptor 6  
CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found  
CC within the sequences. The sequences can be used in the identification of  
CC the haplotype of an individual, and in the treatment of cancer,  
CC angiogenesis and inflammation. The present sequence is an allele specific  
CC primer extension oligonucleotide for the EDG6 gene, which is found on  
CC Chromosome 19p13.3  
XX  
SQ Sequence 10 BP; 2 A; 7 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGG 13  
Db | |||||  
9 GGGCTGTGG 1  
  
RESULT 267  
ABK81557/c  
ID ABK81557 standard; DNA; 10 BP.  
XX  
AC ABK81557;  
XX  
DT 13-AUG-2002 (first entry)  
XX  
DE Human CASP5 gene allele-specific oligonucleotide PCR primer #38.  
XX  
KW Human; caspase 5; apoptosis-related cysteine protease; CASP5; primer; ss;  
KW haplotyping; haplotype pair; cancer; single nucleotide polymorphism;  
KW hereditary nonpolypoidis colorectal cancer; gastrointestinal tumour;  
KW endometrial tumour; chromosome 11q22.2-q22.3; PCR.  
XX  
OS Homo sapiens.

XX  
PN WO200226769-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 01-OCT-2001; 2001WO-US030878.  
XX  
PR 29-SEP-2000; 2000US-0236568P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Choi JY, Kliem SE, Russo DP;  
XX  
DR WPI; 2002-435191/46.  
XX  
PT Novel caspase 5 apoptosis-related cysteine protease, useful  
PT therapeutically and in screening for drugs targeting protease  
PT polypeptide.  
XX  
PS Claim 16; Page 15; 115pp; English.  
XX  
CC The invention relates to single nucleotide polymorphisms in the gene  
CC encoding the human caspase 5, apoptosis-related cysteine protease (CASP5)  
CC polypeptide. A method for haplotyping the CASP5 gene in an individual  
CC comprises identifying the nucleotide at one or more polymorphic sites and  
CC determining whether one of the copies of the gene is defined by one of  
CC the CASP5 haplotypes given in the specification or whether both copies  
CC are defined by a haplotype pair. This method is useful in genotyping,  
CC whereby all possible haplotype pairs can be assigned to specific  
CC genotypes. An association between a trait and a haplotype or haplotype  
CC pair of the CASP5 gene can be identified by comparing the frequency of  
CC the haplotype or haplotype pair in a population exhibiting the trait with  
CC the frequency of the haplotype or haplotype pair in a reference  
CC population, where a higher haplotype frequency in the trait population  
CC indicates the trait is associated with the haplotype or haplotype pair.  
CC CASP5 and its corresponding DNA are used for studying the expression and  
CC function of CASP5, for use in screening for candidate drugs to treat  
CC diseases related to CASP5 activity, such as cancer (e.g. hereditary  
CC nonpolypoidis colorectal cancer, gastrointestinal tumours and endometrial  
CC tumours). Sequences ABK81520-ABK81559 represent allele-specific  
CC oligonucleotide PCR primers used to detect CASP5 gene polymorphisms  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAG 18  
Db |||||  
10 GTGGTGAAG 2  
  
RESULT 268  
ABK96167/c  
ID ABK96167 standard; DNA; 10 BP.  
XX  
AC ABK96167;  
XX  
DT 24-SEP-2002 (first entry)  
XX  
DE Human CYP1A2 allele specific primer extension primer #30.  
XX  
KW Human; ss; PCR; Cytochrome P450 subfamily 1 polypeptide 2; primer;  
KW CYP1A2; cancer; tardive dyskinesia; TD; porphyria cutanea tarda; PCT;  
KW chromosome 15q22-qter; haplotype; genotype; cytotstatic; muscular-gen;  
KW hepatotropic; primer extension.  
XX  
OS Homo sapiens.  
XX  
PN WO200236608-A2.  
XX  
PD 10-MAY-2002.

XX 11-OCT-2001; 2001WO-US042637.  
PF  
XX  
PR 11-OCT-2000; 2000US-0239740P.  
XX  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
XX Bentivegna SC, Kazemi A, Koshy B, Parks KE, Rounds E, Sausker EA;  
PI  
XX WPI; 2002-519230/55.  
DR  
XX  
XX Novel genetic variants of Cytochrome P450, Subfamily I (Aromatic Compound  
PT -Inducible) isogenes, useful for improving efficiency and reliability in  
PT drug development for treating cancers.  
XX  
XX Claim 16; Page 15; 93pp; English.  
PS  
XX The invention relates to an isolated polynucleotide comprising a first  
CC nucleotide sequence which comprises cytochrome P450, subfamily I  
CC (aromatic compound-inducible) (CYP1A2), selected from isogenes 1-8 and 10  
CC -16 given in the specification, where the isogenes comprise the regions  
CC of a CYP1A2 gene sequence (ABK87391) or the cDNA (ABK87392). Also  
CC included are haplotyping or genotyping CYP1A2 gene of an individual,  
CC predicting a haplotype pair for CYP1A2 gene of an individual, identifying  
CC an association between a trait and at least one haplotype or haplotype  
CC pair of CYP1A2 gene, primers and probes for performing the  
CC genotyping/haplotyping, a recombinant non-human organism transformed or  
CC transfected with the CYP1A2 polynucleotide, where the organism expresses  
CC a CYP1A2 protein or variant, a fragment of a CYP1A2 isogene comprising at  
CC least 10 nucleotides and a polymorphism selected from the 18 identified  
CC polymorphisms, polymorphic variants of the CYP1A2 polypeptide, an anti-  
CC CYP1A2 monoclonal antibody, a computer system for storing and analysing  
CC polymorphism data for the CYP1A2 gene, and a genome anthology for CYP1A2  
CC gene. The polymorphic variants, haplotyping/genotyping methods and  
CC antibodies are useful in diagnostic, prognostic and therapeutic methods  
CC and in screening for drugs that are useful for treating cancers, tardive  
CC dyskinesia (TD) and porphyria cutanea tarda (PCT). The gene for CYP1A2 is  
CC located on chromosome 15q22-qter. The present sequence is the 3' end of  
CC an allele specific primer extension PCR primer used to detect the  
CC polymorphisms  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 CGCGCTGTG 12  
| | | | | | | |  
Db 9 CCCGCTGTG 1  
  
RESULT 269  
AAS94665/c  
ID AAS94665 standard; DNA; 10 BP.  
XX  
AC AAS94665;  
XX  
XX 14-FEB-2002 (first entry)  
DT  
XX Human PLTP gene allele-specific oligonucleotide PCR primer #24.  
DE  
XX Human; phospholipid transfer protein; PLTP; haplotyping; haplotype pair;  
KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;  
KW binding affinity; atherosclerosis; ss; sequencing primer; PCR primer;  
KW probe.  
XX Homo sapiens.  
OS  
XX WO200172966-A2.  
PN  
XX 04-OCT-2001.  
PD  
XX

PF 26-MAR-2001; 2001WO-US009776.  
XX  
PR 24-MAR-2000; 2000US-0192127P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Chew A, Choi JY, Koshy B;  
XX WPI; 2002-010724/01.  
DR  
XX  
XX New isolated polynucleotide which is polymorphic variant of phospholipid  
PT transfer protein (PLTP) gene, having any one of polymorphic sites PS1-  
PT PS25, for studying function of PLTP, and expressing PLTP protein.  
XX  
PS Claim 17; Page 85; 99pp; English.  
XX  
CC The invention relates to single nucleotide polymorphisms in the gene  
CC encoding the human phospholipid transfer protein (PLTP). A method for  
CC haplotyping the PLTP gene in an individual comprises identifying the  
CC nucleotide at one or more polymorphic sites and determining whether one  
CC of the copies of the gene is defined by one of the PLTP haplotypes given  
CC in the specification or whether both copies are defined by a haplotype  
CC pair. This method is useful in genotyping, whereby all possible haplotype  
CC pairs can be assigned to specific genotypes. An association between a  
CC trait and a haplotype or haplotype pair of the PLTP gene can be  
CC identified by comparing the frequency of the haplotype or haplotype pair  
CC in a population exhibiting the trait with the frequency of the haplotype  
CC or haplotype pair in a reference population, where a higher haplotype  
CC frequency in the trait population indicates the trait is associated with  
CC the haplotype or haplotype pair. PLTP and its corresponding DNA are used  
CC for studying the expression and function of PLTP, for use in screening  
CC for candidate drugs to treat diseases related to PLTP activity. The  
CC sequences are also useful for studying the effect of variation on the  
CC biological activity of PLTP as well as on the binding affinity of  
CC candidate drugs targeting PLTP for treating atherosclerosis. Sequences  
CC AAS94566-AAS94691 represent allele-specific oligonucleotide probes,  
CC sequencing primers and PCR primers used for detecting PLTP gene  
CC polymorphisms  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAG 18  
| | | | | | | |  
Db 10 GTGGCCAAG 2  
  
RESULT 270  
AAD25031/c  
ID AAD25031 standard; DNA; 10 BP.  
XX  
AC AAD25031;  
XX  
XX 12-MAR-2002 (first entry)  
DT  
XX Human AANAT gene polymorphism detecting primer #21.  
DE  
XX Human; genetic variant; arylalkylamine N-acetyltransferase; AANAT gene;  
KW haplotyping; genotyping; pineal gland disorder; melatonin synthesis;  
KW gene therapy; antisense therapy; primer; polymorphism; ss.  
XX Homo sapiens.  
OS  
XX WO200187909-A2.  
PN  
XX 22-NOV-2001.  
PD  
XX 18-MAY-2001; 2001WO-US016279.  
PF  
XX 18-MAY-2000; 2000US-0205068P.  
PR

XX (GENA-) GENAISSANCE PHARM INC.

PA Choi JY, Kazemi A, Nandabalan K;

PI WPI; 2002-055682/07.

XX

DR

XX New genetic variants of human arylalkylamine N-acetyltransferase (AANAT)

PT gene for studying expression, function of the gene and expressing AANAT

PT protein for use in screening for drugs to treat disorders of pineal

PT gland.

XX

XX Claim 18; Page 13; 67pp; English.

PS

XX The patent discloses novel genetic variants of the arylalkylamine N-

CC acetyltransferase (AANAT) gene. The invention also relates to

CC compositions and methods for haplotyping and/or genotyping the AANAT

CC gene. Polymorphic variants of AANAT protein are useful for screening for

CC drugs targeting the polypeptide. AANAT polynucleotides are useful for

CC studying the expression and function of AANAT and for expressing AANAT

CC protein for use in screening for candidate drugs to treat diseases

CC related to AANAT activity. The methods are used to develop diagnostic

CC tests and therapeutic treatment for disorders of pineal gland that derive

CC from defects in melatonin synthesis. It is useful for determining whether

CC an individual has one of the haplotypes 1-4 or the haplotype pairs. The

CC haplotyping method is useful to validate AANAT as a candidate target for

CC treating a specific condition or disease predicted to be associated with

CC AANAT activity. AANAT sequences of the invention are also used in gene

CC therapy and antisense therapy. The present DNA sequence is a primer which

CC is used for detecting human AANAT gene polymorphisms

XX

SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19

Db | | | | |

9 TGGCGCAGG 1

RESULT 271

ABK30052

ID ABK30052 standard; DNA; 10 BP.

XX

AC ABK30052;

XX

DT 23-APR-2002 (first entry)

XX

DE Vancomycin-resistant enterococci, VanH promoter mutant M10.

XX

KW Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;

KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;

KW vanH promoter; androgen receptor promoter; AR promoter;

KW human epidermal growth factor receptor 2 promoter; her2 promoter;

KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;

KW colon cancer; immunological disorder; prostate cancer; cytostatic;

KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;

KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;

KW Gene expression modulator; multiple sclerosis; MS;

KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;

KW systemic lupus erythematosus; SLE; graft-vs-host disease; GVHD;

KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;

KW mutant; transgenic; ds.

XX

OS Enterococcus sp.

XX

XX WO200194600-A2.

XX

PD 13-DEC-2001.

XX

PF 06-JUN-2001; 2001WO-US018343.

XX 06-JUN-2000; 2000US-0209549P.

PR (GENE-) GENELABS TECHNOLOGIES INC.

PA

XX Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;

PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;

PI Lim MY, Bruce TW;

XX WPI; 2002-130595/17.

DR

XX

PT New nucleic acid regulatory sequences, which are able to regulate

PT expression of a gene operably linked to a promoter, useful for regulating

PT the expression of transgenes and for treating e.g., cancer and

PT immunological diseases.

XX

PS Example 4; Page 50; 95pp; English.

XX

CC The invention describes an isolated nucleic acid regulatory sequence for

CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci

CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human

CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase

CC (Bla) promoter. Transcription regulatory sequences may be used to

CC regulate expression of the endogenous, autologous or heterologous genes

CC operably linked to the promoter, and may be incorporated into

CC heterologous nucleic acid constructs for use in regulated expression of

CC transgenes. Regulated expression of cyclin D1 can be used in cancer

CC therapies, such as breast, colon or pancreatic cancers and familial

CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter

CC may be used in the treatment of immunological disorders, such as

CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus

CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid

CC arthritis. Regulated expression of genes under the control of the HBV

CC (hepatitis B)-specific core, pre-S and X promoters can be used in the

CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,

CC hepatocellular carcinoma, and in the regulated expression of liver cell-

CC specific genes. Regulated expression of the vanH gene promoter can be

CC used in treatment of Enterococcus infection, while regulated expression

CC of the androgen receptor gene can be used in the treatment of prostate

CC cancer. This sequence represents a mutated promoter region used in the

CC invention to determine the regulatory regions involved in gene

CC expression, described in the method of the invention

XX

SQ Sequence 10 BP; 0 A; 4 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1.7e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTG 10

Db | | | | |

1 GGCGCGCTG 9

RESULT 272

ABL36392

ID ABL36392 standard; DNA; 10 BP.

XX

AC ABL36392;

XX

DT 22-APR-2002 (first entry)

XX

DE Human lysosomal acid phosphatase 2 primer-extension oligonucleotide 28.

XX

KW Human; ss; lysosomal acid phosphatase 2; ACP2; gene; chromosome 11;

KW lysosome-specific enzyme; orthophosphoric monoester hydrolysis;

KW Hodgkin's disease; HD; acid phosphatase deficiency;

KW novel polymorphic site; ACP2 haplotype; ACP2 genotype; polymorphism;

KW transgenic animal; primer; probe; primer-extension oligonucleotide; SNP;

KW single nucleotide polymorphism.

XX

OS Homo sapiens.

XX



PN WO200194362-A2.  
XX 13-DEC-2001.  
PD 07-JUN-2001; 2001WO-US018457.  
XX 07-JUN-2000; 2000US-0210047P.  
PF (GENA-) GENAISSANCE PHARM INC.  
XX Kliem SE, Messer C, Tanguay DA;  
PI WPI; 2002-154563/20.  
XX Novel genetic variants of acid phosphatase 2, lysosomal polypeptide gene  
PT useful in studying expression and function of the protein, and for  
PT screening drugs to treat diseases e.g. Hodgkin's disease.  
XX Claim 19; Page 15; 109pp; English.  
PS  
XX The invention comprises the human lysosomal acid phosphatase 2 (ACP2)  
CC nucleic acid and protein sequences. Specifically, the invention relates  
CC to the discovery of 22 novel polymorphic sites within the APC2 gene. The  
CC invention also comprises methods for haplotyping and genotyping the ACP2  
CC gene in an individual. The ACP2 gene (located on chromosome 11) encodes a  
CC lysosomal-specific enzyme that catalyses the hydrolysis of  
CC orthophosphoric monoesters to alcohol and phosphate. The ACP2 gene and  
CC protein are pharmaceutically important in the treatment of Hodgkin's  
CC disease (HD) and acid phosphatase deficiency. The novel ACP2 gene  
CC polymorphisms of the invention are useful in haplotyping the ACP2 gene.  
CC ACP2 haplotyping is useful in validating ACP2 as a target (and designing  
CC drugs) for treating an ACP2-related disease or condition (e.g. Hodgkin's  
CC disease and acid phosphatase deficiency). The ACP2 gene polymorphisms are  
CC useful for ACP2 genotyping, which can also be used to develop diagnostic  
CC tests and therapeutic treatments. The ACP2 protein and nucleic acids of  
CC the invention are useful in the production of a transgenic animal which  
CC expresses ACP2 protein. The ACP2 nucleic acids of the invention are  
CC useful in the production of allele-specific oligonucleotides designed to  
CC genotype each of the ACP2 polymorphisms. Nucleic acids ABL36299-ABL36320  
CC represent claimed ACP2 allele-specific probes. Nucleic acids ABL36321-  
CC ABL36364 represent claimed ACP2 allele-specific PCR primers. Nucleic  
CC acids ABL36365-ABL36408 represent claimed ACP2 primer-extension  
CC oligonucleotides  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GTCGCGCTG 10  
Db |||||  
2 GTCGTGCTG 10  
RESULT 273  
AAL48136  
ID AAL48136 standard; DNA; 10 BP.  
XX AAL48136;  
AC  
XX 27-SEP-2002 (first entry)  
DT Human neuropeptide Y primer extension oligo SEQ ID NO: 60.  
XX Human; neuropeptide Y; NPY; isogene; SNP; atherosclerosis; obesity;  
KW psychological disorder; single nucleotide polymorphism; alcoholism;  
KW antiarteriosclerotic; anorectic; PCR; primer extension oligonucleotide;  
KW ss.  
XX Homo sapiens.  
OS  
XX WO200251857-A1.  
PN

XX 04-JUL-2002.  
PD 21-DEC-2000; 2000WO-US034758.  
XX 21-DEC-2000; 2000WO-US034758.  
PF (GENA-) GENAISSANCE PHARM INC.  
XX Chew A, Denton RR, Lanz EM, Nandabalan K, Stephens JC;  
PI WPI; 2002-566671/60.  
XX New genetic variants of the human Neuropeptide Y (NPY) gene useful for  
PT treating disorders affected by abnormal expression or function of NPY  
PT isogene e.g., atherosclerosis or obesity.  
XX Disclosure; Page 17; 80pp; English.  
PS  
XX The present invention provides the human neuropeptide Y (NPY) gene and  
CC single nucleotide polymorphisms (SNPs) identified therein. The sequence  
CC can be used in the treatment of disorders associated with NPY, including  
CC atherosclerosis, obesity, psychological disorders and alcoholism. The  
CC present sequence is an allele specific primer extension oligonucleotide  
CC used to isolate the human NPY coding sequence  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5 GCGCTGTGG 13  
Db |||||  
1 GCTCTGTGG 9  
RESULT 274  
AAS95999/c  
ID AAS95999 standard; DNA; 10 BP.  
XX AAS95999;  
AC  
XX 26-FEB-2002 (first entry)  
DT Human CALM1 gene allele-specific oligonucleotide #108.  
XX Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;  
KW haplotyping; SCYA3; Alzheimer's disease; drug screening;  
KW calcium-dependent signal transduction; PCR primer; ss.  
XX Homo sapiens.  
OS  
XX WO200179218-A2.  
PN 25-OCT-2001.  
PD 09-APR-2001; 2001WO-US011509.  
XX 12-APR-2000; 2000US-0196340P.  
PF (GENA-) GENAISSANCE PHARM INC.  
XX Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;  
PI WPI; 2002-049190/06.  
XX New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in  
PT expressing CALM1 protein for use in screening for candidate drugs to  
PT treat diseases related to CALM1 activity such as Alzheimer's disease.  
XX Claim 17; Page 14; 82pp; English.  
PS  
XX



CC The invention relates to an isolated polynucleotide comprising a sequence  
CC selected from a polymorphic variant of calmodulin 1 (CALM1). The  
CC polymorphic variant comprises an CALM1 isogene defined by a haplotype  
CC selected from haplotypes 1-21 given in the specification. The  
CC polymorphisms are useful for studying the biological function of CALM1 as  
CC well as in identifying drugs targeting this protein for the treatment of  
CC a disorder related to its abnormal expression or function. The  
CC polymorphic variants may also be used in screening for compounds  
CC targeting CALM1 to treat a specific condition or disease predicted to be  
CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype  
CC pair of an individual is useful for improving the efficiency and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with SCYA3 activity, e.g. Alzheimer's  
CC disease and diseases involving defects in calcium-dependent signal  
CC transduction. Haplotyping the CALM1 gene in an individual is also useful  
CC in the design of clinical trials of candidate drugs for treating a  
CC specific condition or disease predicted to be associated with CALM1  
CC activity. AAS95892-AAS96018 represent human CALM1 allele- specific  
CC oligonucleotides and PCR primers of the invention  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
||||| |||  
Db 10 CGTGC GGC 2

RESULT 275  
AAS96001/C  
ID AAS96001 standard; DNA; 10 BP.  
XX  
AC AAS96001;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE Human CALM1 gene allele-specific oligonucleotide #110.  
XX  
KW Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;  
KW haplotyping; SCYA3; Alzheimer's disease; drug screening;  
KW calcium-dependent signal transduction; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200179218-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 09-APR-2001; 2001WO-US011509.  
XX  
PR 12-APR-2000; 2000US-0196340P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;  
XX  
DR WPI; 2002-049190/06.  
XX

New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in  
PT expressing CALM1 protein for use in screening for candidate drugs to  
PT treat diseases related to CALM1 activity such as Alzheimer's disease.  
XX  
PS Claim 17; Page 14; 82pp; English.  
XX

The invention relates to an isolated polynucleotide comprising a sequence  
CC selected from a polymorphic variant of calmodulin 1 (CALM1). The  
CC polymorphic variant comprises an CALM1 isogene defined by a haplotype  
CC selected from haplotypes 1-21 given in the specification. The  
CC polymorphisms are useful for studying the biological function of CALM1 as  
CC well as in identifying drugs targeting this protein for the treatment of

CC a disorder related to its abnormal expression or function. The  
CC polymorphic variants may also be used in screening for compounds  
CC targeting CALM1 to treat a specific condition or disease predicted to be  
CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype  
CC pair of an individual is useful for improving the efficiency and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with SCYA3 activity, e.g. Alzheimer's  
CC disease and diseases involving defects in calcium-dependent signal  
CC transduction. Haplotyping the CALM1 gene in an individual is also useful  
CC in the design of clinical trials of candidate drugs for treating a  
CC specific condition or disease predicted to be associated with CALM1  
CC activity. AAS95892-AAS96018 represent human CALM1 allele- specific  
CC oligonucleotides and PCR primers of the invention  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13  
||||| ||  
Db 9 GCGCTGCGG 1

RESULT 276  
ABK81811  
ID ABK81811 standard; DNA; 10 BP.  
XX  
AC ABK81811;  
XX  
DT 13-AUG-2002 (first entry)  
XX  
DE Human CHRM5 gene polymorphism detection oligonucleotide primer #17.  
XX  
KW Human; cholinergic receptor muscarinic 5; CHRM5; genotyping; haplotyping;  
KW single nucleotide polymorphism; SNP; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200232924-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 11-OCT-2001; 2001WO-US032022.  
XX  
PR 19-OCT-2000; 2000WO-US029071.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bieglecki KM, Chew A, Choi JY, Denton RR, Nandabalan K;  
PI Sausker EA, Stephens JC;  
XX  
DR WPI; 2002-435523/46.  
XX  
XX

Novel cholinergic receptor, muscarinic 5 polynucleotide useful  
PT therapeutically and in screening for candidate drug to treat diseases  
PT related to the receptor activity.  
XX  
PS Claim 16; Page 14; 72pp; English.  
XX

The present invention relates to a new cholinergic receptor, muscarinic 5  
CC (CHRM5) polynucleotide comprising a sequence which is a polymorphic  
CC variant for a reference sequence for the CHRM5 gene or its fragment, or a  
CC polymorphic variant of a reference sequence for a CHRM5 cDNA or its  
CC fragment. The invention is useful in drug screening assays. The molecules  
CC of the invention are useful in studying the expression and function of  
CC CHRM5, and in expressing CHRM5 protein for use in screening for candidate  
CC drugs to treat diseases related to CHRM5 activity. The methods of the  
CC invention are useful in developing diagnostic tests and therapeutic  
CC treatments. The method is also useful in the design of clinical trials of  
CC candidate drugs for treating specific condition or disease associated  
CC with CHRM5 activity and is useful in determining whether an individual

CC has one of the haplotypes or one of the haplotype pairs. The invention is  
CC useful in a variety of diagnostic and prognostic formats and therapeutic  
CC methods. The invention is also useful in genotyping and/or haplotyping  
CC the CHRM5 gene in an individual. The present nucleic acid sequence  
CC represents one of a collection of oligonucleotide primers (ABK81795-  
CC ABK81814) that were used in the invention to detect polymorphisms in the  
CC human CHRM5 gene  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 10 GTGGCGAAG 18  
Db ||||| ||||  
2 GTGGCCAAG 10  
  
RESULT 277  
ACA94410  
ID ACA94410 standard; DNA; 10 BP.  
XX  
AC ACA94410;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DE DNA tag from human transcript repressed in adenomas/cancers #5.  
XX  
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;  
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;  
KW kidney proximal tubule.  
XX  
OS Homo sapiens.  
XX  
PN WO2003022863-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028518.  
XX  
PR 07-SEP-2001; 2001US-0317494P.  
PR 30-MAY-2002; 2002US-0383805P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Buckhaults P, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2003-313220/30.  
XX  
PT Detecting colorectal cancer in a subject, involves detecting macrophage  
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood  
PT of the subject.  
XX  
PS Example 1; Page 18; 59pp; English.  
XX  
CC The invention relates to detecting CC (colorectal cancer e.g. colorectal  
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)  
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing  
CC amount of MIC or RDP detected to that in normal subjects, where an  
CC elevated amount of MIC or RDP in the subject is an indicator of CC in  
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting  
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP  
CC mRNA detected to that in normal subjects, where an elevated amount of MIC  
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)  
CC isolating epithelial cells from blood of a subject, isolating an mRNA  
CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP  
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in  
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where  
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative  
CC of CC in the subject; (d) contacting blood or faeces of a subject, with  
CC an RDP substrate, detecting activity of RDP in the blood or faeces by  
CC detection of increased reaction product or decreased RDP substrate, and

CC comparing the amount of activity of RDP in blood or faeces of the subject  
CC to that in normal subjects, where an elevated amount of activity of RDP  
CC in the blood or faeces of the subject is an indicator of CC in the  
CC subject; (e) administering to a subject an antibody which specifically  
CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is  
CC labeled with a moiety which is detectable from outside of the subject and  
CC detecting the moiety in the subject from outside of the subject, where an  
CC area of localisation of the moiety within the subject but outside the  
CC proximal tubules of the kidney identifies CC; or (f) administering to a  
CC subject a substrate for RDP, the substrate being labeled with a  
CC detectable moiety, isolating faeces or blood from the subject, and  
CC detecting in the faeces or blood RDP reaction product or RDP substrate  
CC with the detectable moiety, where increased product or decreased  
CC substrate in the faeces or blood indicates CC in the subject. The methods  
CC are useful for detecting colorectal cancer in a subject. The present  
CC sequence is a DNA tag derived from a human transcript whose expression is  
CC repressed in colorectal cancer or colorectal adenoma  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAG 19  
Db ||||| ||||  
2 TGGCAAAG 10  
  
RESULT 278  
ACA94519/c  
ID ACA94519 standard; DNA; 10 BP.  
XX  
AC ACA94519;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DE DNA tag from human transcript repressed in adenomas/cancers #52.  
XX  
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;  
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;  
KW kidney proximal tubule.  
XX  
OS Homo sapiens.  
XX  
PN WO2003022863-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028518.  
XX  
PR 07-SEP-2001; 2001US-0317494P.  
PR 30-MAY-2002; 2002US-0383805P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Buckhaults P, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2003-313220/30.  
XX  
PT Detecting colorectal cancer in a subject, involves detecting macrophage  
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood  
PT of the subject.  
XX  
PS Disclosure; Page 27; 59pp; English.  
XX  
CC The invention relates to detecting CC (colorectal cancer e.g. colorectal  
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)  
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing  
CC amount of MIC or RDP detected to that in normal subjects, where an  
CC elevated amount of MIC or RDP in the subject is an indicator of CC in  
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting  
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP

CC mRNA detected to that in normal subjects, where an elevated amount of MIC  
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)  
CC isolating epithelial cells from blood of a subject, isolating an mRNA  
CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP  
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in  
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where  
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative  
CC of CC in the subject; (d) contacting blood or faeces of a subject, with  
CC an RDP substrate, detecting activity of RDP in the blood or faeces, by  
CC detection of increased reaction product or decreased RDP substrate, and  
CC comparing the amount of activity of RDP in blood or faeces of the subject  
CC to that in normal subjects, where an elevated amount of activity of RDP  
CC in the blood or faeces of the subject is an indicator of CC in the  
CC subject; (e) administering to a subject an antibody which specifically  
CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is  
CC labeled with a moiety which is detectable from outside of the subject and  
CC detecting the moiety in the subject from outside of the subject, where an  
CC area of localisation of the moiety within the subject but outside the  
CC proximal tubules of the kidney identifies CC; or (f) administering to a  
CC subject a substrate for RDP, the substrate being labeled with a  
CC detectable moiety, isolating faeces or blood from the subject, and  
CC detecting in the faeces or blood RDP reaction product or RDP substrate  
CC with the detectable moiety, where increased product or decreased  
CC substrate in the faeces or blood indicates CC in the subject. The methods  
CC are useful for detecting colorectal cancer in a subject. The present  
CC sequence is a DNA tag derived from a human transcript whose expression is  
CC repressed in colorectal cancer or colorectal adenoma  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGGCGCT 9  
||||| ||||  
Db 9 GGTCGGGGCT 1

RESULT 279  
ACA94580  
ID ACA94580 standard; DNA; 10 BP.  
XX  
AC ACA94580;  
XX  
DT 18-JUL-2003 (first entry)  
XX  
DE DNA tag from human transcript repressed in adenomas/cancers #113.  
XX  
KW Colorectal cancer; colorectal adenoma; ss; human; renal dipeptidase;  
KW macrophage inhibitory cytokine; MIC; RDP; faeces; blood;  
KW kidney proximal tubule.

XX Homo sapiens.  
XX  
PN WO2003022863-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028518.  
XX  
PR 07-SEP-2001; 2001US-0317494P.  
PR 30-MAY-2002; 2002US-0383805P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Buckhaults P, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2003-313220/30.  
XX  
PT Detecting colorectal cancer in a subject, involves detecting macrophage  
PT inhibitory cytokine or renal dipeptidase or their mRNA in feces or blood  
PT of the subject.

XX Disclosure; Page 29; 59pp; English.  
PS  
XX  
CC The invention relates to detecting CC (colorectal cancer e.g. colorectal  
CC adenoma), comprising: (a) detecting macrophage inhibitory cytokine (MIC)  
CC or renal dipeptidase (RDP) in faeces or blood of a subject and comparing  
CC amount of MIC or RDP detected to that in normal subjects, where an  
CC elevated amount of MIC or RDP in the subject is an indicator of CC in  
CC subject; (b) isolating mRNA sample from faeces of a subject, detecting  
CC MIC or RDP mRNA in the mRNA sample, and comparing amount of MIC or RDP  
CC mRNA detected to that in normal subjects, where an elevated amount of MIC  
CC or RDP mRNA in the subject is an indicator of CC in subject; (c)  
CC isolating epithelial cells from blood of a subject, isolating an mRNA  
CC sample from faeces of a subject or epithelial cells, detecting MIC or RDP  
CC mRNA in the mRNA sample, and comparing the amount of MIC or RDP mRNA in  
CC the mRNA sample to amounts of MIC or RDP mRNA in normal subjects, where  
CC an elevated amount of MIC or RDP mRNA in the mRNA sample is an indicative  
CC of CC in the subject; (d) contacting blood or faeces of a subject, with  
CC an RDP substrate, detecting activity of RDP in the blood or faeces, by  
CC detection of increased reaction product or decreased RDP substrate, and  
CC comparing the amount of activity of RDP in blood or faeces of the subject  
CC to that in normal subjects, where an elevated amount of activity of RDP  
CC in the blood or faeces of the subject is an indicator of CC in the  
CC subject; (e) administering to a subject an antibody which specifically  
CC binds to RDP or an inhibitor of RDP, where the antibody or inhibitor is  
CC labeled with a moiety which is detectable from outside of the subject and  
CC detecting the moiety in the subject from outside of the subject, where an  
CC area of localisation of the moiety within the subject but outside the  
CC proximal tubules of the kidney identifies CC; or (f) administering to a  
CC subject a substrate for RDP, the substrate being labeled with a  
CC detectable moiety, isolating faeces or blood from the subject, and  
CC detecting in the faeces or blood RDP reaction product or RDP substrate  
CC with the detectable moiety, where increased product or decreased  
CC substrate in the faeces or blood indicates CC in the subject. The methods  
CC are useful for detecting colorectal cancer in a subject. The present  
CC sequence is a DNA tag derived from a human transcript whose expression is  
CC repressed in colorectal cancer or colorectal adenoma  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
||||| ||||  
Db 2 TGGCAAAGG 10

RESULT 280  
ADC15526/c  
ID ADC15526 standard; DNA; 10 BP.  
XX  
AC ADC15526;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Biological molecule delivery ligand related DNA seq id 9.  
XX  
KW small intestine barrier; blood brain barrier;  
KW central nervous system disorder; ss.  
XX  
OS Synthetic.  
XX  
PN US2002137684-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 03-MAY-2001; 2001US-00848537.  
XX  
PR 03-MAY-2000; 2000US-0201981P.  
XX  
PA (TCHI/) TCHISTIAKOVA L.

PA (LISS/) LI S.  
PA (PIET/) PIETRZYNSKI G.  
PA (ALAK/) ALAKHOV V.  
XX  
PI Tchistiakova L, Li S, Pietrzynski G, Alakhov V;  
XX  
XX WPI; 2003-719970/68.  
XX  
XX New peptides capable of crossing the small intestine or blood brain  
PT barrier are useful as a ligand to increase bioavailability in the  
PT treatment of disease associated with central nervous system pathologies.  
XX  
PS Example 3; Page 21; 33pp; English.  
XX  
CC The invention describes a polypeptide capable of crossing the small  
CC intestine or blood brain barrier. The polypeptide is used to treat a  
CC disease associated with central nervous system pathologies. This sequence  
CC represents an oligonucleotide used in the creation of a phage capable of  
CC producing peptide that can deliver a biological agent across the small  
CC intestine or blood brain barrier.  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GGTCGCGCT 9  
Db |||||  
10 GGTGGCGCT 2  
  
RESULT 281  
ADJ93954/c  
ID ADJ93954 standard; DNA; 10 BP.  
XX  
AC ADJ93954;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Azotobacter bacteria RAPD-PCR primer, Azr4.  
XX  
KW edaphic; bacterial biomass; aqueous soil suspension; biofilm; fertilizer;  
KW bacterisation; soil; agricultural waste; cereal; maize; primer; ss.  
XX  
OS Azotobacter chroococcum.  
XX  
PN FR2833016-A1.  
XX  
PD 06-JUN-2003.  
XX  
PF 30-NOV-2001; 2001FR-00015542.  
XX  
PR 30-NOV-2001; 2001FR-00015542.  
XX  
PA (VALB-) VALBIOS SA.  
XX  
PI Claude PP;  
XX  
XX WPI; 2003-560903/53.  
DR  
XX Production of bacterial biomasses useful for bacterization of soil and  
PT agricultural waste comprises contacting soil suspension with substrate,  
PT maturing biofilm and recovering and culturing most prolific strains.  
XX  
XX Disclosure; Page 18; 50pp; French.  
PS  
XX The invention relates to the novel method for production of edaphic  
CC bacterial biomasses. The method comprises contacting an aqueous soil  
CC suspension with a substrate to form a biofilm, maturing the biofilm to  
CC allow dominant strains to migrate into the supernatant liquid, and  
CC recovering and culturing the most prolific strains in liquid media. The  
CC biomasses can be used as a fertilizer. The biomasses are useful for

CC bacterisation of the soil and agricultural waste, especially cereal  
CC (including maize) waste. This polynucleotide sequence represents a primer  
CC used in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 CGCGCTGTG 12  
Db |||||  
10 CGCGCTGGG 2  
  
RESULT 282  
ADG65513/c  
ID ADG65513 standard; DNA; 10 BP.  
XX  
AC ADG65513;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE UCP2 primer extension primer seq id 109.  
XX  
KW anorectic; antidiabetic; immunomodulator; gene therapy; haplotyping;  
KW uncoupling protein 2; mitochondrial; proton carrier; UCP2;  
KW polymorphic site; haplotype; haplotype pair; obesity; diabetes;  
KW immunological disorder; body mass defect; thermoregulation defect; human;  
KW primer extension; PCR; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003207284-A1.  
XX  
PD 06-NOV-2003.  
XX  
PF 16-JUL-2002; 2002US-00197019.  
XX  
PR 25-JAN-2001; 2001WO-US002485.  
XX  
PA (CHEW/) CHEW A.  
PA (DENT/) DENTON R R.  
PA (GILS/) GILSON C R.  
PA (NAND/) NANDABALAN K.  
PA (PARK/) PARKS K E.  
XX  
PI Chew A, Denton RR, Gilson CR, Nandabalan K, Parks KE;  
XX  
DR WPI; 2004-051505/05.  
XX  
XX Haplotyping Uncoupling Protein 2 gene of an individual comprises  
PT identifying the phased sequence of nucleotides at polymorphic sites of  
PT the gene and assigning a haplotype or haplotype pair consistent with the  
PT phased sequence.  
XX  
PS Disclosure; SEQ ID NO 109; 64pp; English.  
XX  
XX The invention describes haplotyping the uncoupling protein 2  
CC (mitochondrial, proton carrier) (UCP2) gene of an individual comprising  
CC identifying the phased sequence of nucleotides at polymorphic sites (PS)1  
CC -23 for at least one copy of the individual's UCP2 gene and assigning to  
CC the individual a UCP2 haplotype or haplotype pair that is consistent with  
CC the phased sequence. The composition and methods are useful in  
CC haplotyping and/or genotyping the UCP2 gene in an individual to e.g.  
CC screen for drugs targeting the UCP2 protein to treat a condition or  
CC disease predicted to be associated with UCP2 activity. The disease or  
CC condition may include obesity, diabetes, immunological disorders and  
CC other diseases associated with defects in body mass and thermoregulation.  
CC This sequence represents a primer extension primer used for detecting  
CC human uncoupling protein 2 (UCP2) gene polymorphisms.  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;



Query Match		38.9%;	Score 7.4;	DB 1;	Length 10;
Best Local Similarity		88.9%;	Pred. No. 1.7e+02;		
Matches	8;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	2	GTGCGGCTG	10		
Db	9	GTAGCGCTG	1		
RESULT 283					
ADN89094/c					
ID	ADN89094 standard; DNA; 10 BP.				
XX					
AC	ADN89094;				
XX					
DT	15-JUL-2004 (first entry)				
XX					
DE	Hyperlipidemia treatment associated human ITGB3 haplotype probe #159.				
XX					
KW	ss; probe; antilipemic; gene therapy; allele; polymorphic site;				
KW	integrin beta 3; ITGB3; statin response marker; hyperlipidemia.				
XX					
OS	Homo sapiens.				
XX					
PN	WO2004033710-A2.				
XX					
PD	22-APR-2004.				
XX					
PF	09-OCT-2003; 2003WO-US032361.				
XX					
PR	09-OCT-2002; 2002US-0417743P.				
XX					
PA	(GENA-) GENAISSANCE PHARM INC.				
XX					
PI	Bentivegna SC, Bieglecki KM, Brain CD, Dain BJ, Cappola G;				
PI	Judson RS, Lachowicz M, Lee HH, Litvyn L, Messer C, Petersen N;				
PI	Reed CR, Rounds EM, Russo DP, Windemuth AK;				
XX					
DR	WPI; 2004-340942/31.				
XX					
PT	New kit comprising a set of oligonucleotides, useful for determining				
PT	whether an individual has a statin response marker I or II for preparing				
PT	a composition for treating hyperlipidemia.				
XX					
PS	Disclosure; SEQ ID NO 162; 202pp; English.				
XX					
CC	A kit comprising a set of oligonucleotides designed for identifying at				
CC	least one of the alleles at each polymorphic site (PS) in a set of 129				
CC	polymorphic sites (PSs) given in the specification, is new. The kit				
CC	identifies at least one of the alleles at each polymorphic site (PS) in a				
CC	set of 129 polymorphic sites (PSs) given in the specification, for				
CC	example: PSI and PS42; PS19 and PS42; PS3, PS12, and PS42; a set of				
CC	polymorphic sites comprising a linked haplotype to any one of haplotypes				
CC	101-194, 201-463 or 501-515 given in the specification; or a set of				
CC	polymorphic sites comprising a substitute haplotype for any one of				
CC	haplotypes 101-194, 201-463 or haplotypes 501-515 given in the				
CC	specification; where the nucleotide position of each polymorphic site				
CC	corresponds to the following nucleotide position in the 32577-bp				
CC	sequence: 1118 (PS1), 1773 (PS3), 1875 (PS4), 1911 (PS5), 1957 (PS6),				
CC	2087 (PS10), 2157 (PS12), 13384 (PS15), 13405 (PS16), 16200 (PS19), 17194				
CC	(PS20), 17273 (PS21), 20035 (PS26), 20047 (PS28), 20615 (PS30), 21944				
CC	(PS33), 22155 (PS35), 25705 (PS37), 25921 (PS38), 27882 (PS39), and 30618				
CC	(PS42). INDEPENDENT CLAIMS are also included for: determining whether an				
CC	individual has a statin response marker I or a statin response marker II;				
CC	selecting a statin therapy to provide an optimal High Density Lipoprotein				
CC	Cholesterol (HDLc) response in an individual; predicting an individual's				
CC	High Density Lipoprotein Cholesterol (HDLc) response to treatment with a				
CC	statin; predicting an individual's High Density Lipoprotein Cholesterol				
CC	(HDLc) response to treatment with a statin; manufacturing a drug product;				
CC	seeking regulatory approval for marketing a pharmaceutical formulation				
CC	for treating a disease or condition in a population partially or wholly				
CC	defined by having a statin response marker I; marketing a drug product				

comprising a statin as at least one active ingredient for treating a disease or condition in a population partially or wholly defined by having a statin response marker 1; an isolated polynucleotide comprising a first nucleotide sequence which comprises an integrin, beta 3 (ITGB3) isogene encoding a ITGB3 polypeptide, where the ITGB3 isogene consisting of isogenes 1-38 and 40-98 defined by a correspondingly numbered haplotype, where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 1317913723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 25559-26029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence, except where substituted by the sequence of alleles for the correspondingly numbered haplotype at the polymorphic sites whose nucleotide positions in the 32577-bp sequence and a second nucleotide sequence which is complementary to the first nucleotide sequence; a recombinant nonhuman organism transformed or transfected with the isolated polynucleotide, where the organism expresses an ITGB3 polypeptide encoded by the selected ITGB3 isogene; an isolated fragment of an integrin, beta 3 (ITGB3) isogene, where the fragment comprises one or more polymorphisms consisting of thymine at PS 1, guanine at PS2, cytosine at PS3, thymine at PS4, cytosine at PS5, adenine at PS6, thymine at PS7, thymine at PS8, guanine at PS9, adenine at PS10, adenine at PS11, thymine at PS12, adenine at PS13, guanine at PS 16, adenine at PS 18, thymine at PS 19, guanine at PS2 I, guanine at PS22, cytosine at PS23, cytosine at PS24, thymine at PS25: adenine at PS26, adenine at PS27, thymine at PS29, adenine at PS30, cytosine at PS31, guanine at PS32, adenine at PS33, adenine at PS35, cytosine at PS37, thymine at PS38, cytosine at PS39, adenine at PS40, thymine at PS41, thymine at PS42, guanine at PS43 and guanine at PS44; a genome anthology for the integrin, beta 3 (ITGB3) gene which comprises two or more ITGB3 isogenes consisting of isogenes 1-98, where each of the selected isogenes is defined by a correspondingly numbered haplotype given in the specification, and where each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-13723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 2555926029, 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence except where substituted by the sequence of alleles for the correspondingly numbered haplotype at each of file polymorphic sites; haplotyping the integrin, beta 3 (ITGB3) gene of an individual; assigning a haplotype pair for the integrin, beta 3 (ITGB3) gene to an individual; reducing the potential for bias in a clinical trial of a candidate drug for treating a disease or condition predicted to be associated with ITGB3 activity; an isolated polypeptide comprising a ITGB3 protein variant consisting of protein variants A, B, C, D, E, F and G and comprising 788-amino acid sequence, except where substituted by the corresponding sequence of amino acids whose positions and alleles are given in the specification; an isolated monoclonal antibody specific for and immunoreactive with the selected ITGB3 protein variant comprising the isolated polypeptide; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; an isolated fragment of an ITGB3 protein variant, where the fragment is at least 6 amino acids in length and comprises one or more variant amino acids consisting of methionine at a position corresponding to amino acid position 14, arginine at a position corresponding to amino acid position 66, methionine at a position corresponding to amino acid position 445, and glutamine at a position corresponding to amino acid position 515 the 788-amino acid sequence; screening for drugs targeting the selected ITGB3 protein variant comprising the isolated polypeptide; screening for compounds targeting the ITGB3 protein to treat a condition or disease predicted to be associated with ITGB3 activity; validating the ITGB3 protein as a candidate target for treating a medical condition predicted to be associated with ITGB3 activity; and an isolated oligonucleotide designed for detecting a polymorphism in the integrin, beta 3 (ITGB3) gene at a polymorphic site (PS) consisting of PS1-PS44, where the oligonucleotide contains or is located one to several nucleotides downstream of the selected PS, where the oligonucleotide has a length of about 15 to about 100 nucleotides. Preferred Kit: The kit further comprises a manual with instructions for performing one or more reactions on a human nucleic acid sample to identify the allele(s) present in the individual at each polymorphic site in the set of polymorphic sites and determining if the individual has a statin response marker I or a statin response marker II based on the identified allele(s). The set of oligonucleotides is designated for identifying both alleles at each polymorphic site of the selected set of polymorphic sites. The set of PSs comprises PS3, PS12 and PS42; PS 1, PS12 and PS42;



PS3 and PS42; PS1 and PS42; PS1, PS3, PS12 and PS42; or PS39. The set of PS is PS3, PS12 or PS42. The individual is Caucasian. The linkage disequilibrium between the linked haplotype and any one of haplotypes 101-194, 201-463 or 501-515 has <math>\delta G\_r/2</math> consisting of at least 0.75, at least 0.80, at least 0.85, at least 0.90, at least 0.95 or 1.0. At least one of the oligonucleotides in the set of oligonucleotides is an allele-specific oligonucleotide comprising a nucleotide sequence consisting of 10-15 bp. The set of polymorphic sites is PS3, PS12, and PS42 and the set of oligonucleotides comprises first, second and third allele-specific oligonucleotide (ASO) probes, where the first ASO probe comprises 15-bp sequence, or its complement, and S in the 15-bp sequence is guanine; the second ASO probe comprises 15-bp sequence, or its complement, and Y in the 15-bp sequence is cytosine, and the third ASO probe comprises 15 bp, or its complement, and Y in the 15-bp sequence is cytosine. Preferred Article: The article of manufacture comprises a pharmaceutical formulation and at least one indicium identifying a population for whom the pharmaceutical formulation is indicated, where the pharmaceutical formulation comprises a statin as at least one active ingredient and the identified population is partially or wholly defined by having a statin response marker I, where a trial population having the statin response marker I exhibits a better HDLC response to the pharmaceutical formulation than to treatment with atorvastatin or a salt of atorvastatin acid. Preferred Oligonucleotide: The isolated oligonucleotide is an allele-specific oligonucleotide that specifically hybridizes to an allele of the ITGB3 gene at a region containing the polymorphic site. The isolated oligonucleotide is a primer-extension oligonucleotide. The kit is for haplotyping the integrin, beta 3 (ITGB3) gene of all individual, comprises a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (PS) in a set of two or more polymorphic sites. Preferred Method: Determining whether an individual has a statin response marker I or a statin response marker II comprises determining the copy number in the individual of the haplotype, where if the selected haplotype is one of haplotypes given in the specification, then the individual has a statin response marker I if the individual has at least one copy of the selected haplotype and a statin response marker II if the individual has zero copy of the selected haplotype; and the individual has a statin response marker I if the individual has zero or one copy of the selected haplotype and a statin response marker II if the individual has two copies of the selected haplotype. The individual is a candidate for treatment with a statin. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites comprising the selected haplotype and using the results of the genotyping step to identify, for the set of polymorphic sites the haplotype pair present in the individual. The determining step comprises consulting a data repository, that provides information on the copy number present in the individual for the selected haplotype. The data repository is the individual's medical records or a medical data card. Assigning an individual to a first or second statin response marker group comprises determining the copy number in the individual or a haplotype and assigning the individual to the first statin response marker group if the individual has at least one copy of the selected haplotype and to the second statin response marker group if the individual has zero copy of the selected haplotype; and assigning the individual to the first statin response marker group if the individual has zero or one copy of the selected haplotype and to the second statin response marker group if the individual has two copies of the selected haplotype. The determining step comprises genotyping each polymorphic site in a set of polymorphic sites

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 16  
||| |||||

Db 10 CTATGGCGA 2  
RESULT 284  
ADN89098  
ID ADN89098 standard; DNA; 10 BP.  
XX  
AC ADN89098;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Hyperlipidemia treatment associated human ITGB3 haplotype probe #163.  
XX  
KW ss; probe; antilipemic; gene therapy; allele; polymorphic site;  
KW integrin beta 3; ITGB3; statin response marker; hyperlipidemia.  
XX  
OS Homo sapiens.  
XX  
PN WO2004033710-A2.  
XX  
PD 22-APR-2004.  
XX  
PF 09-OCT-2003; 2003WO-US032361.  
XX  
PR 09-OCT-2002; 2002US-0417743P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Bieglecki KM, Brain CD, Dain BJ, Cappola G;  
PI Judson RS, Lachowicz M, Lee HH, Litvyn L, Messer C, Petersen N;  
PI Reed CR, Rounds EM, Russo DP, Windemuth AK;  
XX  
XX WPI; 2004-340942/31.  
XX  
PT New kit comprising a set of oligonucleotides, useful for determining whether an individual has a statin response marker I or II for preparing a composition for treating hyperlipidemia.  
XX  
PS Claim 13; SEQ ID NO 166; 202pp; English.  
XX  
CC A kit comprising a set of oligonucleotides designed for identifying at least one of the alleles at each polymorphic site (PS) in a set of 129 polymorphic sites (PSs) given in the specification, is new. The kit identifies at least one of the alleles at each polymorphic site (PS) in a set of 129 polymorphic sites (PSs) given in the specification, for example: PSI and PS42; PS19 and PS42; PS3, PS12, and PS42; a set of polymorphic sites comprising a linked haplotype to any one of haplotypes 101-194, 201-463 or 501-515 given in the specification; or a set of polymorphic sites comprising a substitute haplotype for any one of haplotypes 101-194, 201-463 or haplotypes 501-515 given in the specification; where the nucleotide position of each polymorphic site corresponds to the following nucleotide position in the 32577-bp sequence: 1118 (PS1), 1773 (PS3), 1875 (PS4), 1911 (PS5), 1957 (PS6), 2087 (PS10), 2157 (PS12), 13384 (PS15), 13405 (PS16), 16200 (PS19), 17194 (PS20), 17273 (PS21), 20035 (PS26), 20047 (PS28), 20615 (PS30), 21944 (PS33), 22155 (PS35), 25705 (PS37), 25921 (PS38), 27882 (PS39), and 30618 (PS42). INDEPENDENT CLAIMS are also included for: determining whether an individual has a statin response marker I or a statin response marker II; selecting a statin therapy to provide an optimal High Density Lipoprotein Cholesterol (HDLc) response in an individual; predicting an individual's High Density Lipoprotein Cholesterol (HDLc) response to treatment with a statin; predicting an individual's High Density Lipoprotein Cholesterol (HDLc) response to treatment with a statin; manufacturing a drug product; seeking regulatory approval for marketing a pharmaceutical formulation for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; marketing a drug product comprising a statin as at least one active ingredient for treating a disease or condition in a population partially or wholly defined by having a statin response marker I; an isolated polynucleotide comprising a first nucleotide sequence which comprises an integrin, beta 3 (ITGB3) isogene encoding a ITGB3 polypeptide, where the ITGB3 isogene consisting of isogenes 1-38 and 40-98 defined by a correspondingly numbered haplotype, where each of the isogenes comprises nucleotides 1000-2235,

CC 4256-4716, 1317913723, 14235-14858, 16126-16619, 16930-17414, 19241-  
CC 19644, 19748-20177, 2053721009, 21731-22412, 24385-24930, 25559-26029,  
CC 27822-28255, 30265-30754, and 31300-31718 of the 32577-bp sequence,  
CC except where substituted by the sequence of alleles for the  
CC correspondingly numbered haplotype at the polymorphic sites whose  
CC nucleotide positions in the 32577-bp sequence and a second nucleotide  
CC sequence which is complementary to the first nucleotide sequence; a  
CC recombinant nonhuman organism transformed or transfected with the  
CC isolated polynucleotide, where the organism expresses an ITGB3  
CC polypeptide encoded by the selected ITGB3 isogene; an isolated fragment  
CC of an integrin, beta 3 (ITGB3) isogene, where the fragment comprises one  
CC or mom polymorphisms consisting of thymine at PS 1, guanine at PS2,  
CC cytosine at PS3, thymine at PS4, cytosine at PS5, adenine at PS6, thymine  
CC at PS7, thymine at PS8, guanine at PS9, adenine at PS10, adenine at PS11,  
CC thymine at PS12, adenine at PS13, guanine at PS 16, adenine at PS 18,  
CC thymine at PS 19, guanine at PS2 I, guanine at PS22, cytosine at PS23,  
CC cytosine at PS24, thymine at PS25: adenine at PS26, adenine at PS27,  
CC thymine at PS29, adenine at PS30, cytosine at PS31, guanine at PS32,  
CC adenine at PS33, adenine at PS35, cytosine at PS37, thymine at PS38,  
CC cytosine at PS39, adenine at PS40, thymine at PS41, thymine at PS42,  
CC guanine at PS43 and guanine at PS44; a genome anthology for the integrin,  
CC beta 3 (ITGB3) gene which comprises two or more ITGB3 isogenes consisting  
CC of isogenes 1-98, where each of the selected isogenes is defined by a  
CC correspondingly numbered haplotype given in the specification, and where  
CC each of the isogenes comprises nucleotides 1000-2235, 4256-4716, 13179-  
CC 13723, 14235-14858, 16126-16619, 16930-17414, 19241-19644, 19748-20177,  
CC 2053721009, 21731-22412, 24385-24930, 2555926029, 27822-28255, 30265-  
CC 30754, and 31300-31718 of the 32577-bp sequence except where substituted  
CC by the sequence of alleles for the correspondingly numbered haplotype at  
CC each of file polymorphic sites; haplotyping the integrin, beta 3 (ITGB3)  
CC gene of an individual; assigning a haplotype pair for the integrin, beta  
CC 3 (ITGB3) gene to an individual; reducing the potential for bias in a  
CC clinical trial of a candidate drug for treating a disease or condition  
CC predicted to be associated with ITGB3 activity; an isolated polypeptide  
CC comprising a ITGB3 protein variant consisting of protein variants A, B,  
CC C, D, E, F and G and comprising 788-amino acid sequence, except where  
CC substituted by the corresponding sequence of amino acids whose positions  
CC and alleles are given in the specification; an isolated monoclonal  
CC antibody specific for and immunoreactive with the selected ITGB3 protein  
CC variant comprising the isolated polypeptide; screening for drugs  
CC targeting the selected ITGB3 protein variant comprising the isolated  
CC polypeptide; an isolated fragment of an ITGB3 protein variant, where the  
CC fragment is at least 6 amino acids in length and comprises one or more  
CC variant amino acids consisting of methionine at a position corresponding  
CC to amino acid position 14, arginine at a position corresponding to amino  
CC acid position 66, methionine at a position corresponding to amino acid  
CC position 445, and glutamine at a position corresponding to amino acid  
CC position 515 the 788-amino acid sequence; screening for drugs targeting  
CC the selected ITGB3 protein variant comprising the isolated polypeptide;  
CC screening for compounds targeting the ITGB3 protein to treat a condition  
CC or disease predicted to be associated with ITGB3 activity; validating the  
CC ITGB3 protein as a candidate target for treating a medical condition  
CC predicted to be associated with ITGB3 activity; and an isolated  
CC oligonucleotide designed for detecting a polymorphism in the integrin,  
CC beta 3 (ITGB3) gene at a polymorphic site (PS) consisting of PS1-PS44,  
CC where the oligonucleotide contains or is located one to several  
CC nucleotides downstream of the selected PS, where the oligonucleotide has  
CC a length of about 15 to about 100 nucleotides. Preferred Kit: The kit  
CC further comprises a manual with instructions for performing one or more  
CC reactions on a human nucleic acid sample to identify the allele(s)  
CC present in the individual at each polymorphic site in the set of  
CC polymorphic sites and determining if the individual has a statin response  
CC marker I or a statin response marker II based on the identified  
CC allele(s). The set of oligonucleotides is designated for identifying both  
CC alleles at each polymorphic site of the selected set of polymorphic  
CC sites. The set of PSs comprises PS3, PS12 and PS42; PS 1, PS12 and PS42;  
CC PS3 and PS42; PS1 and PS42; PS1, PS3, PS12 and PS42; or PS39. The set of  
CC PS is PS3, PS12 or PS42. The individual is Caucasian. The linkage  
CC disequilibrium between the linked haplotype and any one of haplotypes 101  
CC -194, 201-463 or 501-515 has <Dgr;2 consisting of at least 0.75, at least  
CC 0.80, at least 0.85, at least 0.90, at least 0.95 or 1.0. At least one of  
CC the oligonucleotides in the set of oligonucleotides is an allele-specific  
CC oligonucleotide comprising a nucleotide sequence consisting of 10-15 bp.

CC The set of polymorphic sites is PS3, PS12, and PS42 and the set of  
CC oligonucleotides comprises first, second and third allele-specific  
CC oligonucleotide (ASO) probes, where the first ASO probe comprises 15-bp  
CC sequence, or its complement, and S in the 15-bp sequence is guanine; the  
CC second ASO probe comprises 15-bp sequence, or its complement, and Y in  
CC the 15-bp sequence is cytosine, and the third ASO probe comprises 15 bp,  
CC or its complement, and Y in the 15-bp sequence is cytosine. Preferred  
CC Article: The article of manufacture comprises a pharmaceutical  
CC formulation and at least one indicium identifying a population for whom  
CC the pharmaceutical formulation is indicated, where the pharmaceutical  
CC formulation comprises a statin as at least one active ingredient and the  
CC identified population is partially or wholly defined by having a statin  
CC response marker I, where a trial population having the statin response  
CC marker I exhibits a better HDLC response to the pharmaceutical  
CC formulation than to treatment with atorvastatin or salt of atorvastatin  
CC acid. It also comprises packaging material and a pharmaceutical  
CC formulation contained within the packaging material, where the  
CC pharmaceutical formulation comprises a statin as at least one separate  
CC active ingredient, and the packaging material comprises an approved label  
CC which states that the pharmaceutical formulation is indicated for a  
CC population partly or wholly defined by having a statin response marker I,  
CC where a trial population having the statin response marker exhibits a  
CC better HDLC response to the pharmaceutical formulation than to treatment  
CC with atorvastatin or a salt of atorvastatin acid. Preferred  
CC Oligonucleotide: The isolated oligonucleotide is an allele-specific  
CC oligonucleotide that specifically hybridizes to an allele of the ITGB3  
CC gene at a region containing the polymorphic site. The isolated  
CC oligonucleotide is a primer-extension oligonucleotide. The kit is for  
CC haplotyping the integrin, beta 3 (ITGB3) gene of all individual,  
CC comprises a set of oligonucleotides designed for identifying at least one  
CC of the alleles at each polymorphic site (PS) in a set of two or more  
CC polymorphic sites. Preferred Method: Determining whether an individual  
CC has a statin response marker I or a statin response marker II comprises  
CC determining the copy number in the individual of the haplotype, where if  
CC the selected haplotype is one of haplotypes given in the specification,  
CC then the individual has a statin response marker I if the individual has  
CC at least one copy of the selected haplotype and a statin response marker  
CC II if the individual has zero copy of the selected haplotype; and the  
CC individual has a statin response marker I if the individual has zero or  
CC one copy of the selected haplotype and a statin response marker II if the  
CC individual has two copies of the selected haplotype. The individual is a  
CC candidate for treatment with a statin. The determining step comprises  
CC genotyping each polymorphic site in a set of polymorphic sites comprising  
CC the selected haplotype and using the results of the genotyping step to  
CC identify, for the set of polymorphic sites the haplotype pair present in  
CC the individual. The determining step comprises consulting a data  
CC repository, that provides information on the copy number present in the  
CC individual for the selected haplotype. The data repository is the  
CC individual's medical records or a medical data card. Assigning an  
CC individual to a first or second statin response marker group comprises  
CC determining the copy number in the individual or a haplotype and  
CC assigning the individual to the first statin response marker group if the  
CC individual has at least one copy of the selected haplotype and to the  
CC second statin response marker group if the individual has zero copy of  
CC the selected haplotype; and assigning the individual to the first statin  
CC response marker group if the individual has zero or one copy of the  
CC selected haplotype and to the second statin response marker group if the  
CC individual has two copies of the selected haplotype. The determining step  
CC comprises genotyping each polymorphic site in a set of polymorphic sites

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 6 CGCTGTGGC 14  
| | | | | | | |  
Db 1 CGCTGTGAC 9  
  
RESULT 285  
ADQ82166  
ID ADQ82166 standard; DNA; 10 BP.  
XX

AC ADQ82166;  
DT 21-OCT-2004 (first entry)  
XX  
DE Human Short stature homeobox-containing DNA binding site #3.  
XX  
KW cardiovascular; endocrine; SHOX; PCR; binding site; ds;  
KW natriuretic peptide; short stature; growth protein;  
XX cardiovascular disease; short stature homeobox-containing gene.  
OS Homo sapiens.  
XX  
PN WO2004062555-A2.  
XX  
PD 29-JUL-2004.  
XX  
PF 12-JAN-2004; 2004WO-EP000134.  
XX  
PR 13-JAN-2003; 2003EP-00000728.  
XX  
PA (RAPP/) RAPPOLD-HOERBRAND G.  
XX  
PI Rappold-Hoerbrand G, Haecker B;  
XX  
DR WPI; 2004-544028/52.  
XX  
XX  
PT Use of natriuretic peptide in combination with a growth protein, e.g.  
PT Short Stature Homeobox-containing gene (SHOX) protein for preparing  
PT pharmaceutical compositions for treating short stature in a subject or  
PT cardiovascular diseases.  
XX  
PS Disclosure; Fig 2B; 36pp; English.  
XX  
CC The present invention relates to the use of a natriuretic peptide (atrial  
CC natriuretic peptide, ANP or brain natriuretic peptide, BNP) in  
CC combination with a growth protein, e.g. Short Stature Homeobox-containing  
CC gene (SHOX) protein for the preparation of pharmaceutical compositions  
CC for the treatment of short stature in a subject being suspected of having  
CC a genetic defect in the SHOX gene or for treatment of patients with  
CC cardiovascular diseases. The natriuretic peptide (ANP or BNP) in  
CC combination with a growth protein, e.g. SHOX protein is useful for the  
CC preparation of pharmaceutical compositions for the treatment of short  
CC stature in a subject being suspected of having a genetic defect in the  
CC SHOX gene or for treatment of patients with cardiovascular diseases. It  
CC is also useful for the preparation of pharmaceutical compositions for  
CC stimulating or increasing human growth or for treating patients with  
CC idiopathic short stature, patients with Turner syndrome, or patients with  
CC Leri-Weill syndrome. The present sequence is a SHOX DNA binding site used  
CC in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 7 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAGG 19  
Db 1 TGGGGAAGG 9  
  
RESULT 286  
ADR27907/c  
ID ADR27907 standard; DNA; 10 BP.  
XX  
AC ADR27907;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Human VE-statin exon 2 3' oligonucleotide.  
XX  
KW Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;  
KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;

KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; human;  
KW ds.  
XX  
OS Homo sapiens.  
XX  
PN FR2851249-A1.  
XX  
PD 20-AUG-2004.  
XX  
PF 17-FEB-2003; 2003FR-00001875.  
XX  
PR 17-FEB-2003; 2003FR-00001875.  
XX  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
XX  
PI Soncin F, Mattot V;  
XX  
DR WPI; 2004-618122/60.  
XX  
PT Using VE-statins to inhibit recruitment of perivascular smooth muscle  
PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,  
PT related nucleic acids and antibodies.  
XX  
PS Example 3; Page 11; 63pp; French.  
XX  
CC The present invention relates to a method for preparing a composition for  
CC inhibiting recruitment of perivascular cells of smooth muscle type using  
CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,  
CC soluble factors secreted by endothelial cells of the blood vessels, block  
CC recruitment of perivascular smooth muscle cells (but do not affect their  
CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide  
CC fragments, nucleic acids encoding them and vectors containing this  
CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis  
CC and restenosis, including in gene therapy. The VE-statin nucleic acids  
CC can also be used to produce transgenic animals (for studying the VE-  
CC statin proteins and genes); the VE-statins are used to screen for  
CC specific (ant)agonists, and antibodies specific for VE-statins can be  
CC used to determine expression profiles, particularly for diagnosis of  
CC diseases associated with VE-statins. The present sequence was used to  
CC illustrate the structure of the human VE-statin gene.  
XX  
SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAGG 19  
Db 9 TGGCGGAGG 1  
  
RESULT 287  
ADR27977/c  
ID ADR27977 standard; DNA; 10 BP.  
XX  
AC ADR27977;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Murine VE-statin intron acceptor site.  
XX  
KW Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;  
KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;  
KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; mouse;  
KW ds.  
XX  
OS Mus musculus.  
XX  
PN FR2851249-A1.  
XX  
PD 20-AUG-2004.  
XX



PF 17-FEB-2003; 2003FR-00001875.  
XX  
PR 17-FEB-2003; 2003FR-00001875.  
XX  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
XX  
PI Soncin F, Mattot V;  
XX  
DR WPI; 2004-618122/60.  
XX  
PT Using VE-statins to inhibit recruitment of perivascular smooth muscle  
PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,  
PT related nucleic acids and antibodies.  
XX  
PS Example 3; Page 11; 63pp; French.  
XX  
CC The present invention relates to a method for preparing a composition for  
CC inhibiting recruitment of perivascular cells of smooth muscle type using  
CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,  
CC soluble factors secreted by endothelial cells of the blood vessels, block  
CC recruitment of perivascular smooth muscle cells (but do not affect their  
CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide  
CC fragments, nucleic acids encoding them and vectors containing this  
CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis  
CC and restenosis, including in gene therapy. The VE-statin nucleic acids  
CC can also be used to produce transgenic animals (for studying the VE-  
CC statin proteins and genes); the VE-statins are used to screen for  
CC specific (ant)agonists, and antibodies specific for VE-statins can be  
CC used to determine expression profiles, particularly for diagnosis of  
CC diseases associated with VE-statins. The present sequence was used to  
CC illustrate the structure of the murine VE-statin gene.  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGA 16  
Db ||||| ||  
10 CTGTGGTGA 2  
  
RESULT 288  
ADR88561/c  
ID ADR88561 standard; DNA; 10 BP.  
XX  
AC ADR88561;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Alpha 7 nicotinic ACh receptor exon-intron boundary DNA seqid 92.  
XX  
KW schizophrenia; alpha7 allele; polymorphism;  
KW alpha 7 nicotinic ACh receptor; human; CHRNA7; intron-exon boundary; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2004185468-A1.  
XX  
PD 23-SEP-2004.  
XX  
PF 26-NOV-2003; 2003US-00723940.  
XX  
PR 23-OCT-1997; 97US-00956518.  
XX  
PA (USGO ) USA DEPT VETERANS AFFAIRS.  
XX  
PI Leonard S, Freedman R;  
XX  
DR WPI; 2004-689185/67.  
XX  
PT Identifying individuals predisposed to schizophrenia, by providing

PT nucleic acid comprising alpha7 allele from subject, detecting  
PT polymorphism within alpha7 allele, and correlating polymorphism with  
PT predisposition to schizophrenia.  
XX  
PS Example 3; SEQ ID NO 92; 105pp; English.  
XX  
CC The invention describes a method of identifying (M1) individuals  
CC predisposed to schizophrenia, involving providing a nucleic acid from a  
CC human subject, where the nucleic acid comprises an alpha7 allele,  
CC detecting the presence of a polymorphism within the alpha7 allele, and  
CC correlating the presence of the polymorphism with a predisposition to  
CC schizophrenia. Also described are: a kit for determining if a subject is  
CC predisposed to schizophrenia, comprising a reagent suitable for use in  
CC specifically detecting a polymorphism in an alpha7 allele, and  
CC instructions for determining whether a subject is predisposed to  
CC schizophrenia; and screening (M2) compounds, involving providing a cell  
CC comprising an alpha7 allele with the polymorphism, and one or more test  
CC compounds, contacting the cell with the test compound, and detecting a  
CC change in alpha7 expression in the cell in the presence of the test  
CC compound relative to the absence of the test compound. (M1) is useful for  
CC identifying individuals predisposed to schizophrenia. This sequence  
CC represents an exon-intron boundary sequence of the human alpha 7  
CC nicotinic ACh receptor (CHRNA7) DNA.  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CTGTGGCGA 16  
Db ||||| ||  
10 CTGTGGAGA 2  
  
RESULT 289  
ADS76954/c  
ID ADS76954 standard; DNA; 10 BP.  
XX  
AC ADS76954;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #736.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Polyak K, Porter D, Allinen M;  
XX  
DR WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 2; SEQ ID NO 736; 149pp; English.

XX The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.

SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
Db |||||  
10 CGCGGTGGC 2

RESULT 290  
ADS77992/c  
ID ADS77992 standard; DNA; 10 BP.  
XX  
AC ADS77992;  
XX  
DT 30-DEC-2004. (first entry)  
XX  
DE Breast cancer detection oligonucleotide #1774.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF Breast cancer detection oligonucleotide #1774.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Polyak K, Porter D, Allinen M;  
XX  
DR WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 6; SEQ ID NO 1774; 149pp; English.

XX The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.

SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
Db |||||  
10 CGCGGTGGC 2

RESULT 291  
ADS77023/c  
ID ADS77023 standard; DNA; 10 BP.  
XX  
AC ADS77023;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #805.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Polyak K, Porter D, Allinen M;  
XX  
DR WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 2; SEQ ID NO 805; 149pp; English.

XX The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.

SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14  
Db |||||  
10 CGCAGTGGC 2

RESULT 292  
ADS76564  
ID ADS76564 standard; DNA; 10 BP.  
XX



AC ADS76564;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #346.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
PI Polyak K, Porter D, Allinen M;  
XX  
DR WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 2; SEQ ID NO 346; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
XX  
PS Example 2; SEQ ID NO 346; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
XX  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 11 TGGCGAAGG 19  
Db 2 TGGTGAAGG 10  
||| |||||  
RESULT 293  
ADS76953/c  
ID ADS76953 standard; DNA; 10 BP.  
XX  
AC ADS76953;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #735.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.

XX WO2004085621-A2.  
PN  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Polyak K, Porter D, Allinen M;  
XX  
DR WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 2; SEQ ID NO 735; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;  
XX  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
XX  
QY 6 CGCTGTGGC 14  
Db 10 CGCGGTGGC 2  
||| |||||  
RESULT 294  
ADS77055  
ID ADS77055 standard; DNA; 10 BP.  
XX  
AC ADS77055;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #837.  
XX  
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Polyak K, Porter D, Allinen M;  
XX

DR WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 2; SEQ ID NO 837; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 7 GCTGTGGCG 15  
Db ||||| |||  
1 GCTGTGGCG 9  
  
RESULT 295  
ADS78162/c  
ID ADS78162 standard; DNA; 10 BP.  
XX  
AC ADS78162;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #1944.  
XX  
KW ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
DE Breast cancer detection oligonucleotide #1944.  
XX  
KW ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
PI Polyak K, Porter D, Allinen M;  
XX WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 6; SEQ ID NO 1944; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the

CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 CGCTGTGGC 14  
Db ||||| |||||  
10 CGCGGTGGC 2  
  
RESULT 296  
ADS76565  
ID ADS76565 standard; DNA; 10 BP.  
XX  
AC ADS76565;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Breast cancer detection oligonucleotide #347.  
XX  
KW ss; primer; cytosstatic; RNA interference; RNAi; gene silencing;  
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW cathepsin L inhibitor; cathepsin F inhibitor;  
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW collagen antagonist; diagnosis; breast tissue; cancer.  
XX  
OS Homo sapiens.  
XX  
PN WO2004085621-A2.  
XX  
PD 07-OCT-2004.  
XX  
PF 22-MAR-2004; 2004WO-US008866.  
XX  
PR 20-MAR-2003; 2003US-0456735P.  
XX  
PA (DAND ) DANA FARBER CANCER INST INC.  
PI Polyak K, Porter D, Allinen M;  
XX WPI; 2004-728732/71.  
XX  
PT Diagnosing breast cancer comprises determining expression levels of a  
PT gene selected from those differentially expressed in normal or cancerous  
PT cells of a breast tissue sample including interleukin 1, thrombospondin 1  
PT and cystatin C.  
XX  
PS Example 2; SEQ ID NO 347; 149pp; English.  
XX  
CC The invention relates to a method of diagnosis (M1) comprising: (a)  
CC providing a test sample of breast tissue; (b) determining the level of  
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide  
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
CC specification, and (c) if the gene is expressed in the test sample at a  
CC lower level than in a control normal breast tissue sample, diagnosing the  
CC test sample as containing cancer cells. The method is used for diagnosing  
CC breast cancer. This sequence corresponds to an oligonucleotide primer  
CC used in the method of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 11 TGGCGAAGG 19

Db                   ||| |||||  
                  2 TGGTGAAG 10

RESULT 297  
ADS77022/c  
ID   ADS77022 standard; DNA; 10 BP.  
XX  
AC   ADS77022;  
XX  
DT   30-DEC-2004   (first entry)  
XX  
DE   Breast cancer detection oligonucleotide #804.  
XX  
KW   ss; primer; cytostatic; RNA interference; RNAi; gene silencing;  
KW   antisense oligonucleotide inhibitor; cathepsin K inhibitor;  
KW   cathepsin L inhibitor; cathepsin F inhibitor;  
KW   metalloprotease 2 inhibitor; thrombospondin-2 antagonist;  
KW   collagen antagonist; diagnosis; breast tissue; cancer.  
XX

OS   Homo sapiens.  
XX  
PN   WO2004085621-A2.  
XX  
PD   07-OCT-2004.  
XX  
PF   22-MAR-2004; 2004WO-US008866.  
XX  
PR   20-MAR-2003; 2003US-0456735P.  
XX  
PA   (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI   Polyak K,   Porter D,   Allinen M;  
XX  
DR   WPI; 2004-728732/71.  
XX

Diagnosing breast cancer comprises determining expression levels of a  
gene selected from those differentially expressed in normal or cancerous  
cells of a breast tissue sample including interleukin 1, thrombospondin 1  
and cystatin C.

XX   Example 2; SEQ ID NO 804; 149pp; English.  
PS  
XX

The invention relates to a method of diagnosis (M1) comprising: (a)  
providing a test sample of breast tissue; (b) determining the level of  
expression in the test sample of a gene (e.g. interleukin-8, superoxide  
dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the  
specification, and (c) if the gene is expressed in the test sample at a  
lower level than in a control normal breast tissue sample, diagnosing the  
test sample as containing cancer cells. The method is used for diagnosing  
breast cancer. This sequence corresponds to an oligonucleotide primer  
used in the method of the invention.

XX  
SQ   Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;  
                  38.9%;   Score 7.4;   DB 1;   Length 10;  
Best Local Similarity 88.9%;   Pred. No. 1.7e+02;  
Matches   8;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

QY                   6 CGCTGTGGC 14  
                  ||| |||||  
Db                   10 CGCAGTGGC 2

RESULT 298  
ADU19103/c  
ID   ADU19103 standard; DNA; 10 BP.  
XX  
AC   ADU19103;  
XX  
DT   13-JAN-2005   (first entry)  
XX  
DE   Hypoxia-related tumorigenesis-related SAGE tag #894.

XX  
KW   screening; hypoxia-related tumorigenesis;  
KW   hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS   Unidentified.  
XX  
PN   WO2004092198-A2.  
XX  
PD   28-OCT-2004.  
XX  
PF   09-APR-2004; 2004WO-US011087.  
XX  
PR   09-APR-2003; 2003US-0461712P.  
XX   (GENZ ) GENZYME CORP.  
PA   Nacht M;  
XX  
PI   WPI; 2004-758333/74.  
XX

Identifying agents that alter biological activity of a polypeptide  
encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
comprises contacting an agent with a target cell and monitoring activity  
of expressed product.

XX  
PS   Disclosure; Page 73; 100pp; English.  
XX

The invention comprises a method of screening for candidate agents  
capable of altering the biological activity of a protein encoded by a  
nucleotide involved in hypoxia-related tumorigenesis. The method of the  
invention involves: contacting a test agent with a target cell expressing  
the nucleotide, and monitoring the activity of the expressed protein  
product; if the test agent modifies the activity of the expressed protein  
then this is a candidate agent. The method of the invention is useful for  
modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
or treating tumours. The present DNA sequence represents a SAGE tag that  
was used in the exemplification of the invention.

XX  
SQ   Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;  
                  38.9%;   Score 7.4;   DB 1;   Length 10;  
Best Local Similarity 88.9%;   Pred. No. 1.7e+02;  
Matches   8;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

QY                   5 GCGCTGTGG 13  
                  |||| |||||  
Db                   9 GCGCAGTGG 1

RESULT 299  
ADU18946  
ID   ADU18946 standard; DNA; 10 BP.  
XX  
AC   ADU18946;  
XX  
DT   13-JAN-2005   (first entry)  
XX  
DE   Hypoxia-related tumorigenesis-related SAGE tag #737.  
XX  
KW   screening; hypoxia-related tumorigenesis;  
KW   hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS   Unidentified.  
XX  
PN   WO2004092198-A2.  
XX  
PD   28-OCT-2004.  
XX  
PF   09-APR-2004; 2004WO-US011087.  
XX  
PR   09-APR-2003; 2003US-0461712P.  
XX   (GENZ ) GENZYME CORP.  
PA

XX Nacht M;  
PI WPI; 2004-758333/74.  
XX  
XX Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX  
XX Disclosure; Page 70; 100pp; English.  
PS  
XX The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGG 13  
Db 2 GGGCTGTGG 10  
| | | | |  
| | | | |  
  
RESULT 300  
ADU18864  
ID ADU18864 standard; DNA; 10 BP.  
XX  
AC ADU18864;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Hypoxia-related tumorigenesis-related SAGE tag #655.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004092198-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 09-APR-2004; 2004WO-US011087.  
XX  
PR 09-APR-2003; 2003US-0461712P.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Nacht M;  
XX  
DR WPI; 2004-758333/74.  
XX  
PT Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX  
PS Disclosure; Page 68; 100pp; English.  
XX  
CC The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the

CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 9 TGTGGCGAA 17  
Db 1 TGTGGCGTA 9  
| | | | |  
| | | | |  
  
RESULT 301  
ADZ24419  
ID ADZ24419 standard; DNA; 10 BP.  
XX  
AC ADZ24419;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human SNP detection related oligonucleotide #1386.  
XX  
KW ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;  
KW immune disorder; cardiovascular disease; metabolic disorder;  
KW respiratory disease; musculoskeletal disease; renal disease;  
KW nephrotropic; endocrine disease; genitourinary disease.  
XX  
OS Homo sapiens.  
XX  
PN WO2005030952-A1.  
XX  
PD 07-APR-2005.  
XX  
PF 30-SEP-2004; 2004WO-JP014784.  
XX  
PR 30-SEP-2003; 2003JP-00342519.  
PR 28-MAY-2004; 2004JP-00158717.  
XX  
XX (RIKE ) RIKEN KK.  
PA (STAG-) STAGEN CO LTD.  
PA (SEKI/) SEKINE A.  
PA (IIDA/) IIDA A.  
PA (SAIT/) SAITO S.  
XX  
PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;  
XX  
DR WPI; 2005-305936/31.  
XX  
PT Analyzing haplotype, by detecting polymorphism in drug-related genes,  
PT electing common polymorphism (CP), building haplotype block using CP,  
PT specifying CP within block, specifying tag polymorphism from CP within  
PT block.  
XX  
PS Disclosure; SEQ ID NO 1386; 1290pp; Japanese.  
XX  
CC The invention relates to a method of analyzing haplotype, by detecting  
CC gene polymorphism in drug-related genes such as aryl acetamide  
CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,  
CC sub-family A (ABC1), member 1. The method is useful for analyzing  
CC haplotype. The method is useful for estimating the sensitivity or disease  
CC of a medicine or a foreign material, for selecting medicine for  
CC preventing or treating diseases, for determining appropriate dosage of  
CC medicine for preventing or treating a disease, for analyzing a drug  
CC interaction, and for determining the related polymorphism relative to the  
CC sensitivity of the medicine, foreign material or disease. The diseases  
CC include malignant tumor, immune disorder circulatory disease, metabolic



CC disease, kidney disease, respiratory disease and muscle associated  
CC disease. The method enables analysis of the individual differences  
CC related to the sensitivity of a medicine, using a haplotype, without  
CC using each single nucleotide polymorphism. The present sequence  
CC represents a human SNP detection related oligonucleotide.  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 5 G; 3 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGG 13  
||| |||||  
Db 1 GCGATGTGG 9  
  
RESULT 302  
ADZ24430  
ID ADZ24430 standard; DNA; 10 BP.  
XX  
AC ADZ24430;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human SNP detection related oligonucleotide #1397.  
XX  
KW ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;  
KW immune disorder; cardiovascular disease; metabolic disorder;  
KW respiratory disease; musculoskeletal disease; renal disease;  
KW nephrotropic; endocrine disease; genitourinary disease.  
XX  
OS Homo sapiens.  
XX  
PN WO2005030952-A1.  
XX  
PD 07-APR-2005.  
XX  
PF 30-SEP-2004; 2004WO-JP014784.  
XX  
PR 30-SEP-2003; 2003JP-00342519.  
PR 28-MAY-2004; 2004JP-00158717.  
XX  
PA (RIKE ) RIKEN KK.  
PA (STAG-) STAGEN CO LTD.  
PA (SEKI/) SEKINE A.  
PA (IIDA/) IIDA A.  
PA (SAIT/) SAITO S.  
XX  
PI Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;  
XX WPI; 2005-305936/31.  
DR  
XX Analyzing haplotype, by detecting polymorphism in drug-related genes,  
PT electing common polymorphism (CP), building haplotype block using CP,  
PT specifying CP within block, specifying tag polymorphism from CP within  
PT block.  
XX  
PS Disclosure; SEQ ID NO 1397; 1290pp; Japanese.  
XX  
CC The invention relates to a method of analyzing haplotype, by detecting  
CC gene polymorphism in drug-related genes such as aryl acetylamide  
CC deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,  
CC sub-family A (ABCI), member 1. The method is useful for analyzing  
CC haplotype. The method is useful for estimating the sensitivity or disease  
CC of a medicine or a foreign material, for selecting medicine for  
CC preventing or treating diseases, for determining appropriate dosage of  
CC medicine for preventing or treating a disease, for analyzing a drug  
CC interaction, and for determining the related polymorphism relative to the  
CC sensitivity of the medicine, foreign material or disease. The diseases  
CC include malignant tumor, immune disorder circulatory disease, metabolic  
CC disease, kidney disease, respiratory disease and muscle associated  
CC disease. The method enables analysis of the individual differences

CC related to the sensitivity of a medicine, using a haplotype, without  
CC using each single nucleotide polymorphism. The present sequence  
CC represents a human SNP detection related oligonucleotide.  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 GCGCTGTGG 13  
||| |||||  
Db 1 GCGATGTGG 9  
  
RESULT 303  
AEA37223  
ID AEA37223 standard; DNA; 10 BP.  
XX  
AC AEA37223;  
XX  
DT 25-AUG-2005 (first entry)  
XX  
DE MoMLV derived vector associated polynucleotide #2.  
XX  
KW expression; drug screening; diagnosis; protein purification;  
KW protein interaction; gene tagging; ds.  
XX  
OS Unidentified.  
XX  
PN WO2005054476-A1.  
XX  
PD 16-JUN-2005.  
XX  
PF 13-SEP-2004; 2004WO-US029658.  
XX  
PR 12-SEP-2003; 2003US-00660893.  
XX  
PA (NEWL-) NEWLINK GENETICS INC.  
XX  
PI Link CJ, Seregina T, Vahanian NN, Higginbotham JN, Ramsey WJ;  
PI Powers BJ, Shukla SA, Young WB, Dicolandrea T, Mautino MR;  
XX  
DR WPI; 2005-425418/43.  
XX  
PT Elucidating protein expression profile of test cell line, by randomly  
PT introducing promoterless polynucleotide construct into genome of cells,  
PT identifying cells expressing marker peptide fused to protein and  
PT determining proteins.  
XX  
PS Disclosure; Fig 2K; 141pp; English.  
XX  
CC The invention describes a method of elucidating (M1) a protein expression  
CC profile of a test cell line or group of cells. The method involves  
CC randomly introducing into the genome of a cell or group of cells a  
CC promoterless polynucleotide construct (I), comprising in a 5'-3'  
CC orientation: a splice acceptor consensus sequence, a complementary  
CC sequence of a first type IIS restriction enzyme recognition sequence, an  
CC oligonucleotide sequence encoding an assayable marker peptide, a splice  
CC of a second type IIS restriction enzyme recognition sequence, a splice  
CC donor consensus sequence, where the promoterless polynucleotide construct  
CC when introduced into an actively expressed gene results in the generation  
CC of a fusion protein, containing the assayable marker peptide inserted at  
CC a random position within two exons coding for the cellular protein  
CC encoded by the gene, identifying those cells expressing the marker  
CC peptide fused to the cellular protein, and determining the identity of  
CC the proteins to which the marker peptide is fused in each group of cells.  
CC Also described are: identifying (M2) differentially expressed proteins in  
CC two different populations of cells; and identifying (M3) protein/protein  
CC interactions. (M1) is useful for elucidating a protein expression profile  
CC of a test cell line or group of cells and for identifying differentially  
CC expressed proteins in two different populations of cells. (M1) and (M2)  
CC are useful for screening small molecule drugs, which involves generating



CC cells using (M1) or (M2), selecting cells which have integrated the  
CC marker peptide into a locus coding a protein for which a small molecule  
CC drug is to be identified, establishing a monoclonal cell line from the  
CC cells, and screening the cell line against libraries of drug compounds to  
CC identify compounds which decrease expression of the marker polypeptide by  
CC inhibiting expression of the protein to which the marker polypeptide is  
CC fused, where the screening is performed in cells generated by (M1) or  
CC (M3). This sequence represents a polynucleotide associated with the  
CC creation of a MoMLV derived vector associated with determining the  
CC protein expression profile of a cell line.

XX SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 1.7e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCCGCGT 9  
|||||  
Db 2 GGTCCGCGT 10

RESULT 304  
AAT29313  
ID AAT29313 standard; DNA; 10 BP.

XX AC AAT29313;  
XX DT 25-MAR-2003 (revised)  
DT 28-JUN-1996 (first entry)  
XX DE 5'-primer for mammalian G-protein coupled receptor coding sequences.  
XX KW 5'-primer; mammalian; G-protein coupled receptor; PCR primer kit;  
KW characterisation; biological samples; PCR amplification; indexing;  
KW identification; cloning; analysis; genes; genome mapping;  
KW disease diagnosis; ss.

OS Synthetic.

XX WO9531574-A1.

XX PD 23-NOV-1995.

PF 12-MAY-1995; 95WO-US006032.

XX PR 16-MAY-1994; 94US-00242887.

XX PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.

XX PI Lopeznieto CE, Nigam SK;

XX DR WPI; 1996-010958/01.

XX PT Characterisation of nucleotide sequences using primer pairs - by PCR  
PT amplification and indexing of amplification prods. w.r.t. primers used  
PT for genome mapping and disease diagnosis.

PS Claim 46; Page 55; 72pp; English.

XX CC The 5'-primers AAT29262-382, and the complementary 3'-primers derived  
CC from them, which target mammalian G-protein coupled receptor coding  
CC sequences, together comprise a PCR primer kit. The kit is used in a new  
CC method for the characterisation of nucleic acid sequences obtd. from  
CC mammalian biological samples, which comprises PCR amplification and  
CC indexing of the prods. w.r.t. the primer pair that hybridised to its  
CC delineating subsequences. The method may be used in the identification,  
CC cloning and analysis of genes, e.g. in genome mapping, and disease  
CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGG 13  
|||||  
Db 4 GCTGTGG 10

RESULT 305  
AAV09238/c  
ID AAV09238 standard; DNA; 10 BP.

XX AC AAV09238;

XX DT 07-JUL-1998 (first entry)

XX DE Degenerate RT-PCR primer 2.

XX KW Degenerate peptide; RT-PCR; amplification; cytochrome P450 gene;  
KW oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.

OS Synthetic.

XX PN WO9749832-A2.

XX PD 31-DEC-1997.

XX PF 23-JUN-1997; 97WO-CA000488.

XX PR 21-JUN-1996; 96US-00667546.

XX PR 01-OCT-1996; 96US-00724466.

XX PA (TOOH ) UNIV QUEENS KINGSTON.

XX PI Petkovich PM;

XX DR WPI; 1998-077193/07.

XX PT Identifying DNA encoding inducible or suppressible cytochrome P450 - by  
PT screening for drugs which reduce the catabolism of retinoic acid, useful  
PT in cancer chemotherapy and the treatment of acne and psoriasis.

PS Example 1; Page 52; 113pp; English.

XX CC This is a degenerate RT-PCR primer used in combination with a 3' poly(T)  
CC primer (AAV09225-V09236) for the amplification of the inducible  
CC cytochrome P450RAI gene which specifically metabolises a derivative of  
CC the retinoic acid (RA). The cytochrome P450 gene in general produces  
CC enzymes involved in the oxidative metabolism of endogenous and exogenous  
CC compounds. The cytochrome P450 nucleotide sequence can be used to induce  
CC or suppress the expression of its protein. P450RAI is highly induced by  
CC RA in cell lines and tissues. This allows for development of a drug  
CC screen using promoters and nucleotide sequences to identify drugs which  
CC are useful for reducing the catabolism of RA

XX SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCGAA 17  
|||||  
Db 9 TGGCGAA 3

RESULT 306  
AAV12230/c  
ID AAV12230 standard; DNA; 10 BP.

XX AC AAV12230;

XX DT 22-JUN-1998 (first entry)

XX Differential display 5' PCR primer.  
DE  
XX  
KW Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid;  
KW zebrafish; inhibitor; antisense; cancer; actinic keratosis;  
KW oral leukoplakia; head tumour; neck tumour;  
KW non-small cell lung carcinoma; basal cell carcinoma;  
KW acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;  
KW therapy; diagnosis; screening; differential display; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO9749815-A1.  
XX  
PD 31-DEC-1997.  
XX  
PF 23-JUN-1997; 97WO-CA000440.  
XX  
PR 21-JUN-1996; 96US-00667546.  
PR 01-OCT-1996; 96US-00724466.  
XX  
PA (TOOH ) UNIV QUEENS KINGSTON.  
XX  
PI Petkovich PM, White JA, Beckett BR, Jones G;  
XX  
DR WPI; 1998-077178/07.  
XX  
PT Retinoid metabolising protein - useful to develop products to treat, e.g.  
PT cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or  
PT ichthyosis.  
XX  
PS Disclosure; Page 14; 110pp; English.  
XX  
CC 5' PCR primers (see AAV12229-33) were used in various combinations with  
CC polyT primers (see AAV12217-28) in a differential display PCR of cDNA  
CC derived from mRNA of control or retinoic acid-treated zebrafish (Danio  
CC rerio). Bands demonstrating reproducible differential amplifications were  
CC found using the primers given in AAV12221 and AAV12231. This PCR product  
CC was reamplified (see AAV12234-35). A differential display product (see  
CC AAV12213) which exhibited a dependence on the presence of retinoic acid  
CC for its expression was isolated, and was used to isolate a full-length  
CC clone (see AAV12203) coding for a novel retinoid metabolising protein  
CC (see AAW44159), designated zP450RAI  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 TGGCGAA 17  
Db 9 TGGCGAA 3  
  
RESULT 307  
AAV34959  
ID AAV34959 standard; DNA; 10 BP.  
XX  
AC AAV34959;  
XX  
DT 13-OCT-1998 (first entry)  
XX  
DE Synthetic Agaricus bisporus RAPD primer.  
XX  
KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.  
XX  
OS Synthetic.  
XX  
PN WO9821975-A1.  
XX  
PD 28-MAY-1998.  
XX

PF 19-NOV-1996; 96WO-US018686.  
XX  
PR 19-NOV-1996; 96WO-US018686.  
XX  
PA (AMYC-) AMYCEL INC.  
XX  
PI Loftus MG, Lodder SC, Legg EJ;  
XX  
DR WPI; 1998-312054/27.  
XX  
PT New strains of Agaricus bisporus with improved cap whiteness - compared  
PT with the U1 strain but retaining other desirable features of this strain.  
XX  
PS Disclosure; Page 10; 26pp; English.  
XX  
CC The sequence is that of an RAPD (random amplified DNA) primer which was  
CC used in the isolation of an Agaricus bisporus mushroom strain which has  
CC whiter caps, less scaling than known strains, particularly for mushrooms  
CC produced in the first break, so it is more valuable (suitable for  
CC marketing fresh rather than canning). It also retains the desirable  
CC characteristics (good cap shape and shelf life, thick stem and veil) of  
CC the U1 strain  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 GCGAAGG 19  
Db 4 GCGAAGG 10  
  
RESULT 308  
AAV50187  
ID AAV50187 standard; DNA; 10 BP.  
XX  
AC AAV50187;  
XX  
DT 21-OCT-1998 (first entry)  
XX  
DE Yeast tag for additional NORF chromosome 5 tag position 118089.  
XX  
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;  
KW eukaryotic cell; antifungal; SAGE tag; gene expression;  
KW serial analysis of gene expression; probe; ss.  
XX  
OS Saccharomyces cerevisiae.  
OS Synthetic.  
XX  
PN WO9832847-A2.  
XX  
PD 30-JUL-1998.  
XX  
PF 22-JAN-1998; 98WO-US001216.  
XX  
PR 23-JAN-1997; 97US-0035917P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1998-427943/36.  
XX  
PT Yeast transcriptome - useful for modulating eukaryotic cell, for  
PT screening antifungal agents, and for identifying genes in cell cycle  
PT progression.  
XX  
PS Claim 1; Page 24; 44pp; English.  
XX  
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene  
CC involved in cell cycle progression selected from the group of

CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)  
CC tags for highly expressed genes and NORF genes are given in AAV50051 to  
CC AAV50345. The present invention describes: (1) a method of using yeast  
CC genes to modulate the cell cycle which comprises administering to a cell  
CC an isolated DNA molecule comprising a yeast gene which is involved in  
CC cell cycle progression selected from differentially expressed genes (SAGE  
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate  
CC antifungal drugs which comprises contacting a test substance with a yeast  
CC cell and monitoring expression of a yeast gene which is involved in cell  
CC cycle progression; (3) a method of identifying human genes which are  
CC involved in cell cycle progression which comprises hybridizing a probe  
CC comprising at least 10 contiguous nucleotides of a yeast gene which is  
CC differentially expressed between at least 2 phases selected from the log  
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining  
CC the phase in the cell cycle, where the probe comprises at least 14  
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to  
CC AAV50345), or as an array of probes on a solid support  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12  
|||||||  
Db 4 CGCTGTG 10

RESULT 309  
AAV35966  
ID AAV35966 standard; DNA; 10 BP.

XX AAV35966;

DT 26-AUG-1998 (first entry)

XX Primer used in RAPD assay of the invention.

DE Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.

XX Synthetic.  
OS Sus sp.

XX WO9815837-A1.

PN 16-APR-1998.

PD 07-OCT-1997; 97WO-GB002741.

XX 07-OCT-1996; 96GB-00020904.

PR 18-FEB-1997; 97GB-00003350.

PR 20-MAR-1997; 97GB-00005796.

PR 09-SEP-1997; 97GB-00019002.

XX (MEAT-) MEAT & LIVESTOCK COMMISSION.

PA Maltin CA, Steven J, Warkup CC;

XX WPI; 1998-240968/21.

XX Assay for alleles or muscle fibre composition characteristic of Duroc  
PT type pigs - comprises determination of genotype or muscle fibre  
PT properties, used to identify animals for breeding programs and to assess  
PT meat quality.

XX Example 3; Page 33; 56pp; English.

PS PCR primers AAV35877-996 were used in a rapid amplification of  
XX polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
CC is used to determine if an animal has an allele for, or muscle fibre  
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce

CC meat of superior quality (particularly tenderness) but are normally less  
CC efficient feed converters and fatter than other types. The assay  
CC comprises analysing a tissue sample to determine if the genotype  
CC comprises the allele, and genetic features typical of animals with Duroc-  
CC type MFC are present. The method is used to select animals that have  
CC Duroc characteristics for use in breeding programmes (to develop the  
CC animals with Duroc pig characteristics), and to assess meat quality  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7  
|||||||  
Db 4 GGTCGCG 10

RESULT 310  
AAX77467/c  
ID AAX77467 standard; DNA; 10 BP.

XX AAX77467;

DT 05-AUG-1999 (first entry)

DE US5912147 primer 11.

XX Primer; quantitation; genetic instability; tumour cell; detection;  
KW neoplastic transformation; carcinogenesis; ss.

XX Synthetic.

PN US5912147-A.

PD 15-JUN-1999.

XX 22-OCT-1996; 96US-00734973.

PR 22-OCT-1996; 96US-00734973.

XX (HEAL-) HEALTH RES INC.

XX Anderson G, Stoler D, Basik M;

XX WPI; 1999-357197/30.

XX Quantitating genetic instability.

PS Claim 4; Col 19-20; 27pp; English.

XX This invention describes a novel method for quantitating genetic  
CC instability independent of microsatellite alterations by treating a  
CC comparison pair comprising genomic DNA from tumour cells and genomic DNA  
CC from normal cells. The method involves the cells from the same individual  
CC with oligonucleotide primers selected from (i) a nucleotide sequence  
CC (CG)xRG, where R is a purine selected from adenine and guanine and x = 3-  
CC 7, (ii) a nucleotide sequence (CG)xRY, where R is as in (i) and Y is a  
CC pyrimidine selected from cytosine, thymine, and uracil and x = 3-7, (iii)  
CC a nucleotide sequence (CG)xRR, where R is as in (i) and x = 3-7, (iv) a  
CC nucleotide sequence (CG)xYY, where Y is a pyrimidine selected from  
CC cytosine, thymine, and uracil and x = 3-7, (v) a nucleotide sequence  
CC (CA)xRG, where R is a purine selected from adenine and guanine and x = 6-  
CC 16, (vi) a nucleotide sequence (CA)xRY, where R is a purine selected from  
CC adenine and guanine and Y is a pyrimidine selected from cytosine,  
CC thymine, and uracil, and x = 6-16, (vii) a nucleotide sequence (CA)xRR,  
CC where R is a purine selected from adenine and guanine and x = 6-16,  
CC (viii) a nucleotide sequence (CA)xYY, where Y is a pyrimidine selected  
CC from cytosine, thymine, and uracil and x = 6-16, and (ix) a combination  
CC of the primers. The method is useful for detecting genomic instability  
CC which are commonly associated with the various stages of neoplastic  
CC transformation and carcinogenesis. The method is rapid and simple

```
XX
SQ      Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

      Query Match      36.8%; Score 7; DB 1; Length 10;
      Best Local Similarity 100.0%; Pred. No. 2.1e+02;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTCGCGC 8
Db      10 GTCGCGC 4

RESULT 311
AAZ28347/c
ID      AAZ28347 standard; cDNA; 10 BP.
XX
AC      AAZ28347;
XX
DT      20-DEC-1999 (first entry)
XX
DE      Lung cancer indicator polynucleotide #27.
XX
KW      Lung cancer; tumour; primary squamous cell; gene expression pattern; ss;
KW      antibody; detect; diagnosis; transgenic animal; expressed sequence tag.
XX
OS      Homo sapiens.
XX
PN      WO9950278-A1.
XX
PD      07-OCT-1999.
XX
PF      30-MAR-1999; 99WO-US006938.
XX
PR      31-MAR-1998; 98US-0080037P.
XX
PA      (GENZ ) GENZYME CORP.
XX
PI      Beaudry GA, Madden SL, Bertelsen AH;
XX
DR      WPI; 1999-591271/50.
XX
PT      Polynucleotides which are differentially expressed in lung cancer, used
PT      for diagnosis and screening for therapeutic agents.
XX
PS      Claim 1; Page 51; 69pp; English.
XX
CC      Sequences Z28321-Z28360 are polynucleotides isolated from primary
CC      squamous cell lung cancers of two patients. These sequences represent a
CC      profile of gene expression patterns in lung cancer. Sequences Z28321-
CC      Z28360 correspond to previously characterised genes. Sequences Z28341-
CC      Z28360 do not correspond to known genes, although some do correspond to
CC      reported Expressed Sequence Tags (ESTs). This sequence does correspond to
CC      an EST (Genbank Accession No. AAL1142). The presence of these
CC      polynucleotide sequences in lung cells is indicative of lung cancer. The
CC      sequences can be used to generate antibodies for the detection of tumour
CC      cells. Detection of the overexpression of the polynucleotides and their
CC      gene products can be used in the diagnosis of lung cancer or the
CC      susceptibility to the disease. The sequences can also be used to screen
CC      for agents potentially useful for treating lung cancer and to generate
CC      transgenic animals (for studying gene function and for drug screening)
XX
SQ      Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;

      Query Match      36.8%; Score 7; DB 1; Length 10;
      Best Local Similarity 100.0%; Pred. No. 2.1e+02;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
Db      9 CTGTGGC 3

RESULT 312
```

```
AAZ61441/c
ID      AAZ61441 standard; DNA; 10 BP.
XX
AC      AAZ61441;
XX
DT      19-JUN-2000 (first entry)
XX
DE      Primer SP4A5 for genetic mapping and cloning of the Pi-ta region.
XX
KW      Disease resistance protein; rice; Pi-ta gene; resistance gene;
KW      Pi-ta resistance gene-mediated defence response; fungal pathogen;
KW      rice blast fungus; PCR primer; ss.
XX
OS      Oryza sativa.
XX
PN      WO200008162-A1.
XX
PD      17-FEB-2000.
XX
PF      03-AUG-1999; 99WO-US017706.
XX
PR      04-AUG-1998; 98US-0095229P.
PR      21-JUN-1999; 99US-00336946.
XX
PA      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI      Valent BS, Bryan GT;
XX
DR      WPI; 2000-205715/18.
XX
PT      Novel nucleic acid fragments conferring Pi-ta resistance gene-mediated
PT      defense response for producing transgenic plants resistant to fungal
PT      pathogens, especially rice blast fungus.
XX
PS      Example 3; Page 29; 96pp; English.
XX
CC      AAZ61437-52 represent random amplified polymorphic DNA (RAPD) primers
CC      which were used for genetic mapping and cloning of the Pa-ti disease
CC      resistance region of rice. The rice Pi-ta gene was cloned by a map-based
CC      cloning strategy. The Pi-ta protein has a novel structure, compared to
CC      all known classes of resistance gene products. The polynucleotide
CC      sequence confers a Pi-ta resistance gene-mediated defence response
CC      against diseases caused by fungal pathogens, particularly the rice blast
CC      fungus. Introduction of the cloned Pi-ta gene into susceptible rice
CC      confers resistance to pathogen strains
XX
SQ      Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

      Query Match      36.8%; Score 7; DB 1; Length 10;
      Best Local Similarity 100.0%; Pred. No. 2.1e+02;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCTGT 11
Db      7 GCGCTGT 1

RESULT 313
AAZ79591
ID      AAZ79591 standard; DNA; 10 BP.
XX
AC      AAZ79591;
XX
DT      10-APR-2000 (first entry)
XX
DE      Human dendritic cell SAGE tag, SEQ ID NO:2019.
XX
KW      SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW      APC; monocyte-derived dendritic cell; differential gene expression;
KW      immunostimulatory cofactor; costimulatory factor; CTL;
KW      cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS      Homo sapiens.
```



XX WO9965924-A2.  
XX 23-DEC-1999.  
XX 18-JUN-1999; 99WO-US013800.  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX WPI; 2000-106077/09.  
XX  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 122; 130pp; English.  
XX  
CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify

CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db 1 GCTGTGG 7  
  
RESULT 314  
AAZ77871  
ID AAZ77871 standard; DNA; 10 BP.  
XX  
AC AAZ77871;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:299.  
XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.  
PR 08-DEC-1998; 98US-0111715P.  
PR



XX	(GENZ ) GENZYME CORP.	
PA	(ROBE/) ROBERTS B L.	
PA	(SHAN/) SHANKARA S.	
XX		
PI	Roberts BL, Shankara S;	
XX		
DR	WPI; 2000-106077/09.	
XX		
PT	Isolated polynucleotides differentially expressed in antigen-presenting	
PT	cells, useful in gene vaccines against cancer.	
XX		
PS	Claim 1; Page 72; 130pp; English.	
XX		
CC	Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene	
CC	expression) tags used to identify mRNA transcripts encoding	
CC	immunostimulatory cofactor proteins which are preferentially or	
CC	differentially expressed in monocyte-derived dendritic cells compared	
CC	with monocytes. Some of the transcripts correspond to known genes or ESTs	
CC	(expressed sequence tags) which were previously unknown to be	
CC	preferentially or differentially expressed in dendritic cells, while	
CC	other transcripts correspond to novel genes. Antigen-presenting cell	
CC	(APC)-associated costimulatory factors play an important role in the	
CC	activation of the cytotoxic immune response, particularly against tumour	
CC	cells. Tumour antigen presentation via the MHC (major histocompatibility	
CC	complex) and subsequent recognition by T-cell receptors is alone	
CC	insufficient to activate a robust cytotoxic immune response that can lyse	
CC	the tumour cells, immunostimulatory cofactors also being required for	
CC	efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid	
CC	sequences identified using the SAGE tags have several potential uses.	
CC	They may be used in vaccines to induce an immune response, particularly	
CC	against a tumour antigen; to modulate the genotype of an APC; to screen	
CC	for agents that modulate expression of differentially expressed genes in	
CC	an APC; and as hybridisation probes/amplification primers for the	
CC	diagnosis, prognosis and monitoring of diseases related to abnormal	
CC	expression of these genes. Detection of the dendritic cell differentially	
CC	expressed genes, or of their encoded proteins, can be used to identify	
CC	cells as belonging to the monocyte lineage. Cells containing these genes	
CC	can be used in active immunotherapy (or to stimulate production of a	
CC	population of antigen-specific effector cells) and vectors containing	
CC	them are used in gene therapy. Co-administration of tumour antigens and	
CC	APC-associated costimulatory factors ensures adequate antigen	
CC	presentation to endogenous APCs and upregulates the APCs for the	
CC	presentation of co-stimulatory signals, migration to T cell-rich sites,	
CC	secretion of T cell growth factors and secretion of chemokines for	
CC	recruitment of immune effector cells	
XX		
SQ	Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;	
Query Match 36.8%; Score 7; DB 1; Length 10;		
Best Local Similarity 100.0%; Pred. No. 2.1e+02;		
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	6 CGCTGTG 12	
Db	1 CGCTGTG 7	
RESULT 315		
AAZ79427/c		
ID	AAZ79427 standard; DNA; 10 BP.	
XX		
AC	AAZ79427;	
XX		
DT	10-APR-2000 (first entry)	
XX		
DE	Human dendritic cell SAGE tag, SEQ ID NO:1855.	
XX		
KW	SAGE tag; serial analysis of gene expression; antigen-presenting cell;	
KW	APC; monocyte-derived dendritic cell; differential gene expression;	
KW	immunostimulatory cofactor; costimulatory factor; CTL;	
KW	cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.	
XX		

OS	Homo sapiens.	
XX		
PN	WO9965924-A2.	
XX		
PD	23-DEC-1999.	
XX		
PF	18-JUN-1999; 99WO-US013800.	
XX		
PR	19-JUN-1998; 98US-0089833P.	
PR	19-JUN-1998; 98US-0089844P.	
PR	19-JUN-1998; 98US-0089853P.	
PR	19-JUN-1998; 98US-0089878P.	
PR	19-JUN-1998; 98US-0089991P.	
PR	19-JUN-1998; 98US-0089992P.	
PR	19-JUN-1998; 98US-0089993P.	
PR	19-JUN-1998; 98US-0089994P.	
PR	19-JUN-1998; 98US-0089997P.	
PR	19-JUN-1998; 98US-0089999P.	
PR	19-JUN-1998; 98US-0090000P.	
PR	19-JUN-1998; 98US-0090035P.	
PR	19-JUN-1998; 98US-0090036P.	
PR	19-JUN-1998; 98US-0090039P.	
PR	19-JUN-1998; 98US-0090040P.	
PR	19-JUN-1998; 98US-0090041P.	
PR	19-JUN-1998; 98US-0090042P.	
PR	19-JUN-1998; 98US-0090043P.	
PR	19-JUN-1998; 98US-0090044P.	
PR	19-JUN-1998; 98US-0090045P.	
PR	19-JUN-1998; 98US-0090047P.	
PR	19-JUN-1998; 98US-0090048P.	
PR	19-JUN-1998; 98US-0090072P.	
PR	19-JUN-1998; 98US-0090076P.	
PR	19-JUN-1998; 98US-0090077P.	
PR	19-JUN-1998; 98US-0090078P.	
PR	19-JUN-1998; 98US-0090079P.	
PR	19-JUN-1998; 98US-0090080P.	
PR	08-DEC-1998; 98US-0111715P.	
XX		
PA	(GENZ ) GENZYME CORP.	
PA	(ROBE/) ROBERTS B L.	
PA	(SHAN/) SHANKARA S.	
XX		
PI	Roberts BL, Shankara S;	
XX		
DR	WPI; 2000-106077/09.	
XX		
PT	Isolated polynucleotides differentially expressed in antigen-presenting	
PT	cells, useful in gene vaccines against cancer.	
XX		
PS	Claim 1; Page 118; 130pp; English.	
XX		
CC	Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene	
CC	expression) tags used to identify mRNA transcripts encoding	
CC	immunostimulatory cofactor proteins which are preferentially or	
CC	differentially expressed in monocyte-derived dendritic cells compared	
CC	with monocytes. Some of the transcripts correspond to known genes or ESTs	
CC	(expressed sequence tags) which were previously unknown to be	
CC	preferentially or differentially expressed in dendritic cells, while	
CC	other transcripts correspond to novel genes. Antigen-presenting cell	
CC	(APC)-associated costimulatory factors play an important role in the	
CC	activation of the cytotoxic immune response, particularly against tumour	
CC	cells. Tumour antigen presentation via the MHC (major histocompatibility	
CC	complex) and subsequent recognition by T-cell receptors is alone	
CC	insufficient to activate a robust cytotoxic immune response that can lyse	
CC	the tumour cells, immunostimulatory cofactors also being required for	
CC	efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid	
CC	sequences identified using the SAGE tags have several potential uses.	
CC	They may be used in vaccines to induce an immune response, particularly	
CC	against a tumour antigen; to modulate the genotype of an APC; to screen	
CC	for agents that modulate expression of differentially expressed genes in	
CC	an APC; and as hybridisation probes/amplification primers for the	
CC	diagnosis, prognosis and monitoring of diseases related to abnormal	
CC	expression of these genes. Detection of the dendritic cell differentially	
CC	expressed genes, or of their encoded proteins, can be used to identify	
CC	cells as belonging to the monocyte lineage. Cells containing these genes	
CC	can be used in active immunotherapy (or to stimulate production of a	
CC	population of antigen-specific effector cells) and vectors containing	
CC	them are used in gene therapy. Co-administration of tumour antigens and	
CC	APC-associated costimulatory factors ensures adequate antigen	
CC	presentation to endogenous APCs and upregulates the APCs for the	
CC	presentation of co-stimulatory signals, migration to T cell-rich sites,	
CC	secretion of T cell growth factors and secretion of chemokines for	
CC	recruitment of immune effector cells	
XX		

CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db |||||  
9 GCTGTGG 3  
  
RESULT 316  
AAZ78099/c  
ID AAZ78099 standard; DNA; 10 BP.  
XX  
AC AAZ78099;  
XX  
DT 10-APR-2000 (first entry)  
XX  
DE Human dendritic cell SAGE tag, SEQ ID NO:527.  
XX  
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;  
KW APC; monocyte-derived dendritic cell; differential gene expression;  
KW immunostimulatory cofactor; costimulatory factor; CTL;  
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965924-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013800.  
XX  
PR 19-JUN-1998; 98US-0089833P.  
PR 19-JUN-1998; 98US-0089844P.  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089878P.  
PR 19-JUN-1998; 98US-0089991P.  
PR 19-JUN-1998; 98US-0089992P.  
PR 19-JUN-1998; 98US-0089993P.  
PR 19-JUN-1998; 98US-0089994P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0089999P.  
PR 19-JUN-1998; 98US-0090000P.  
PR 19-JUN-1998; 98US-0090035P.  
PR 19-JUN-1998; 98US-0090036P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
PR 19-JUN-1998; 98US-0090042P.  
PR 19-JUN-1998; 98US-0090043P.  
PR 19-JUN-1998; 98US-0090044P.  
PR 19-JUN-1998; 98US-0090045P.  
PR 19-JUN-1998; 98US-0090047P.  
PR 19-JUN-1998; 98US-0090048P.  
PR 19-JUN-1998; 98US-0090072P.  
PR 19-JUN-1998; 98US-0090076P.  
PR 19-JUN-1998; 98US-0090077P.  
PR 19-JUN-1998; 98US-0090078P.  
PR 19-JUN-1998; 98US-0090079P.  
PR 19-JUN-1998; 98US-0090080P.

PR 08-DEC-1998; 98US-0111715P.  
XX (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX WPI; 2000-106077/09.  
PT Isolated polynucleotides differentially expressed in antigen-presenting  
PT cells, useful in gene vaccines against cancer.  
XX  
PS Claim 1; Page 80; 130pp; English.  
XX  
CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene  
CC expression) tags used to identify mRNA transcripts encoding  
CC immunostimulatory cofactor proteins which are preferentially or  
CC differentially expressed in monocyte-derived dendritic cells compared  
CC with monocytes. Some of the transcripts correspond to known genes or ESTs  
CC (expressed sequence tags) which were previously unknown to be  
CC preferentially or differentially expressed in dendritic cells, while  
CC other transcripts correspond to novel genes. Antigen-presenting cell  
CC (APC)-associated costimulatory factors play an important role in the  
CC activation of the cytotoxic immune response, particularly against tumour  
CC cells. Tumour antigen presentation via the MHC (major histocompatibility  
CC complex) and subsequent recognition by T-cell receptors is alone  
CC insufficient to activate a robust cytotoxic immune response that can lyse  
CC the tumour cells, immunostimulatory cofactors also being required for  
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid  
CC sequences identified using the SAGE tags have several potential uses.  
CC They may be used in vaccines to induce an immune response, particularly  
CC against a tumour antigen; to modulate the genotype of an APC; to screen  
CC for agents that modulate expression of differentially expressed genes in  
CC an APC; and as hybridisation probes/amplification primers for the  
CC diagnosis, prognosis and monitoring of diseases related to abnormal  
CC expression of these genes. Detection of the dendritic cell differentially  
CC expressed genes, or of their encoded proteins, can be used to identify  
CC cells as belonging to the monocyte lineage. Cells containing these genes  
CC can be used in active immunotherapy (or to stimulate production of a  
CC population of antigen-specific effector cells) and vectors containing  
CC them are used in gene therapy. Co-administration of tumour antigens and  
CC APC-associated costimulatory factors ensures adequate antigen  
CC presentation to endogenous APCs and upregulates the APCs for the  
CC presentation of co-stimulatory signals, migration to T cell-rich sites,  
CC secretion of T cell growth factors and secretion of chemokines for  
CC recruitment of immune effector cells  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CTGTGGC 14  
Db |||||  
9 CTGTGGC 3  
  
RESULT 317  
AAZ82030  
ID AAZ82030 standard; DNA; 10 BP.  
XX  
AC AAZ82030;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1264.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX



KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
XX antimetastatic; vaccine; diagnosis; ss.  
OS Homo sapiens.  
XX WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX WPI; 2000-106079/09.  
XX  
DR Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 160; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db 7 GCTGTGG 1  
|||||||  
GCTGTGG 1  
  
RESULT 320  
AAZ82784  
ID AAZ82784 standard; DNA; 10 BP.  
XX  
AC AAZ82784;  
XX  
DT 07-APR-2000 (first entry)  
XX

DE Metastatic breast tumour cell upregulated transcript tag #2018.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX WO9965928-A2.  
PN  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 113; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 GCGAAGG 19  
Db 1 GCGAAGG 7  
|||||||  
GCGAAGG 7  
  
RESULT 321  
AAZ84917  
ID AAZ84917 standard; DNA; 10 BP.  
XX  
AC AAZ84917;  
XX



DT 07-APR-2000 (first entry)  
XX Metastatic breast tumour cell downregulated transcript tag #4151.  
DE  
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
PI WPI; 2000-106079/09.  
DR  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 169; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CGCTGTG 12  
Db 1 CGCTGTG 7  
  
RESULT 322  
AAZ86247/c  
ID AAZ86247 standard; DNA; 10 BP.  
XX

AC AAZ86247;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #5481.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
PI WPI; 2000-106079/09.  
DR  
XX Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 203; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 5 A; 4 C; 1 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db 8 GCTGTGG 2  
  
RESULT 323  
AAZ81792

ID AAZ81792 standard; DNA; 10 BP.  
XX AAZ81792;  
AC  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1026.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 86; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 TGGCGAA 17  
Db 3 TGGCGAA 9  
|||||

RESULT 324  
AAZ81334  
ID AAZ81334 standard; DNA; 10 BP.  
XX  
AC AAZ81334;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #568.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 73; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 GCGAAGG 19  
Db 1 GCGAAGG 7  
|||||

RESULT 325  
AAZ85903  
ID AAZ85903 standard; DNA; 10 BP.  
XX  
AC AAZ85903;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell downregulated transcript tag #5137.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 195; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 GTGGCGA 16

|||||  
1 GTGGCGA 7  
  
Db  
  
RESULT 326  
AAZ82560  
ID AAZ82560 standard; DNA; 10 BP.  
XX  
AC AAZ82560;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #1794.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 106; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGGC 14  
| | | | |  
Db 4 CTGTGGC 10

RESULT 327  
AAZ82992/c  
ID AAZ82992 standard; DNA; 10 BP.  
XX  
AC AAZ82992;  
XX  
DT 07-APR-2000 (first entry)  
XX  
DE Metastatic breast tumour cell upregulated transcript tag #2226.  
XX  
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;  
KW non-metastatic breast tumour tissue; gene therapy; anticancer;  
KW antimetastatic; vaccine; diagnosis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9965928-A2.  
XX  
PD 23-DEC-1999.  
XX  
PF 18-JUN-1999; 99WO-US013647.  
XX  
PR 19-JUN-1998; 98US-0089853P.  
PR 19-JUN-1998; 98US-0089997P.  
PR 19-JUN-1998; 98US-0090039P.  
PR 19-JUN-1998; 98US-0090040P.  
PR 19-JUN-1998; 98US-0090041P.  
XX  
PA (GENZ ) GENZYME CORP.  
PA (ROBE/) ROBERTS B L.  
PA (SHAN/) SHANKARA S.  
XX  
PI Roberts BL, Shankara S;  
XX  
DR WPI; 2000-106079/09.  
XX  
PT Isolated polynucleotides differentially expressed between metastatic and  
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and  
PT treatment of cancer.  
XX  
PS Claim 1; Page 119; 219pp; English.  
XX  
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts  
CC that are preferentially transcribed in the metastatic breast tumour  
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942  
CC to AAZ86677 represent tags corresponding to distinct transcripts that are  
CC preferentially transcribed in the primary or non-metastatic breast tumour  
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These  
CC transcripts can be used for diagnosis, prognosis, monitoring and  
CC treatment of breast cancer, particularly where metastatic. Diagnosis is  
CC by standard immunoassays or hybridisation/amplification reactions.  
CC Compounds that modulate expression of the transcripts are potentially  
CC useful for treatment of (metastatic) breast cancer, while promoters from  
CC the transcripts are used to direct expression, in selected cell types, of  
CC e.g. therapeutic genes (also ribozymes or antisense sequences),  
CC particularly an antigen-encoding sequence for use in gene or cell-based  
CC vaccines. Polypeptides encoded by the transcripts are also useful in  
CC vaccines; for diagnosing breast cancer and for raising specific  
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic  
CC agents. Host cells that produce the polypeptides can be used to expand  
CC and isolate populations of educated, antigen-specific immune effector  
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive  
CC immunotherapy  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CTGTGGC 14  
| | | | |  
Db 10 CTGTGGC 4

RESULT 328  
AAA99863  
ID AAA99863 standard; DNA; 10 BP.  
XX  
AC AAA99863;  
XX  
DT 06-AUG-2003 (revised)  
DT 26-JAN-2001 (first entry)  
XX  
DE Prokaryote RT-PCR primer PCR5.  
XX  
KW Prokaryote; gene identification; environmental stimulus; gene regulation;  
KW bioprocess fermentation; PCR primer; ss.  
XX  
OS Bacteria.  
XX  
PN WO200056936-A1.  
XX  
PD 28-SEP-2000.  
XX  
PF 24-MAR-2000; 2000WO-US007912.  
XX  
PR 25-MAR-1999; 99US-0126038P.  
XX  
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.  
XX  
PI Bentley WE, Gill RT;  
XX  
DR WPI; 2000-587669/55.  
XX  
PT Performing differential display of prokaryotic mRNA by a RT (reverse  
PT transcriptase)/RAP (random arbitrary-primed) PCR based technique comprises  
PT using a unique combination of random primers in a single amplification  
PT step.  
XX  
PS Claim 1; Page 19; 63pp; English.  
XX  
CC The present invention is concerned with a method of differential display  
CC of prokaryotic mRNA by RT-PCR. This involves the amplification of the  
CC mRNA once, and the further amplification of the cDNA, rather than the  
CC repeated amplification of the mRNA sample. It also eliminates the need  
CC for sequencing gels, using Northern and total RNA dot blots to confirm  
CC differentially displayed transcript levels. The primers AAA99849-A99868  
CC were used in a reverse transcription PCR amplification, and primers  
CC AAA99869-A99876 were used to prepare probes for a Northern blot analysis.  
CC The method can be used to rapidly identify genes with increased or  
CC decreased transcription following environmental stimuli, in bioprocess  
CC fermentations, and to analyse gene regulation. (Updated on 06-AUG-2003 to  
CC correct OS field.)  
XX  
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 TGGCGAA 17  
| | | | |  
Db 4 TGGCGAA 10

RESULT 329  
AAA73648/c  
ID AAA73648 standard; DNA; 10 BP.  
XX





XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GCTGTGG 13  
Db 7 GCTGTGG 1  
RESULT 332  
AAS04437/C  
ID AAS04437 standard; DNA; 10 BP.  
XX  
AC AAS04437;  
XX  
DT 07-SEP-2001 (first entry)  
XX Human DAXX DNA primer-extension oligonucleotide #24.  
DE  
XX Death-associated protein 6; DAXX; polymorphism; haplotype pair; human;  
KW immune disorder; autoimmune disease; population diversity; ss;  
KW paternity testing; anthropological lineage; forensic application;  
KW primer-extension oligonucleotide.  
XX  
OS Homo sapiens.  
XX  
PN WO200125245-A2.  
XX  
PD 12-APR-2001.  
XX  
PF 05-OCT-2000; 2000WO-US027487.  
XX  
PR 06-OCT-1999; 99US-0157909P.  
XX (GENA-) GENAISSANCE PHARM INC.  
PA  
PI Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;  
XX WPI; 2001-308220/32.  
DR  
XX New human death-associated protein 6 (DAXX) gene variants comprising 19  
PT polymorphic sites useful in studying the effect of variation on the  
PT biological activity of DAXX and in developing drugs targeting the  
PT protein.  
XX  
PS Disclosure; Page 21; 97pp; English.  
XX  
CC Sequences AAS04414-AAS04451 represent primer-extension oligonucleotides  
CC specific for a DNA encoding human death-associated protein 6 (DAXX). This  
CC DNA may comprise one or more polymorphisms at specific nucleotide  
CC positions to form one of nineteen possible polymorphic variants.  
CC Associations between a trait and a genotype or a haplotype of the DAXX  
CC gene can be identified by comparing the frequency of the genotype or  
CC haplotype in a population exhibiting the trait with that of a reference  
CC population. A higher frequency in the trait population indicates an  
CC association. Methods involving genotyping or haplotyping of the DAXX gene  
CC of an individual can lead to prediction of haplotype pairs for the DAXX  
CC gene of related individuals, and may be useful in studying the expression  
CC and biological function of DAXX, as well as in developing drugs targeting  
CC this protein. Polymorphic variants of DAXX are useful in studying the  
CC effect of the variation on the biological activity of DAXX as well as on  
CC the binding affinity of candidate drugs targeting DAXX for the treatment  
CC of autoimmune diseases and other immune disorders. Polymorphism is also  
CC useful for studying population diversity, anthropological lineage,  
CC paternity testing, forensic applications, and for identifying  
CC associations between the DAXX genetic variation and a trait such as level  
CC of drug response or susceptibility to disease. DAXX proteins may be used  
CC to measure binding affinities of one or more candidate drugs targeting  
CC the DAXX protein  
XX

SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GCTGTGG 13  
Db 10 GCTGTGG 4  
RESULT 333  
AAH63684  
ID AAH63684 standard; cDNA; 10 BP.  
XX  
AC AAH63684;  
XX  
DT 20-SEP-2001 (first entry)  
XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 524.  
DE  
XX Human; transcriptome; gene expression pattern; cancer; drug screening;  
KW cancer diagnosis; cell specific gene expression; ss.  
KW Homo sapiens.  
XX  
PN WO200138577-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 21-NOV-2000; 2000WO-US031922.  
XX  
PR 24-NOV-1999; 99US-00448480.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX WPI; 2001-367706/38.  
DR  
XX New isolated polynucleotides, useful for identifying specific cell type,  
PT such as cancer cell, comprises transcriptomes expressed in particular  
PT cell types.  
XX  
PS Claim 13; Page 51; 94pp; English.  
XX  
CC The present invention describes a method of identifying the type of cell  
CC in a sample, involving determining which of the sequences AAH63161-  
CC AAH64724 is expressed by the cell. The transcriptomes described in the  
CC invention are cell-type specific, cancer specific or ubiquitously  
CC expressed in humans. They can also be used to screen for drugs, reduce  
CC cancer specific gene expression, standardise expression and restore the  
CC function of a diseased cell or tissue. The present sequence is one of the  
CC transcriptomes described in the exemplification of the invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CTGTGGC 14  
Db 4 CTGTGGC 10  
RESULT 334  
AAS57302  
ID AAS57302 standard; DNA; 10 BP.  
XX  
AC AAS57302;  
XX  
DT 16-JAN-2002 (first entry)

XX Human CHRNA2 allele specific oligonucleotide PCR primer terminus #27.  
DE Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;  
XX CHRNA2; memory disorder; Alzheimer's disease; epilepsy; learning;  
KW Chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;  
KW ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADFLE; ss;  
KW allele specific oligonucleotide; ASO; PCR primer.  
XX  
OS Homo sapiens.  
XX WO200174833-A2.  
PN  
XX  
PD 11-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010666.  
XX  
PR 03-APR-2000; 2000US-0194155P.  
PR 13-JUL-2000; 2000US-0217952P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Choi JY, Kliem SE, Koshy B, Lee HH, Sanchis A;  
PI WPI; 2001-626374/72.  
XX  
DR Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of an  
XX individual involves determining for two copies of the gene, the identity  
PT of nucleotide pair at polymorphic sites selected from PS1-24.  
PT  
XX  
PS Claim 17; Page 15; 82pp; English.  
XX  
CC The invention relates to genotyping/haplotyping the cholinergic receptor,  
CC nicotinic, beta-polypeptide 2 (neuronal) (CHRNA2) gene of an individual,  
CC comprising determining for the two copies of the CHRNA2 gene present in  
CC the individual, the identity of the nucleotide pair at one or more  
CC polymorphic sites selected from PS1-24. Also include are oligonucleotides  
CC for performing the method and the nucleotide sequence of the polymorphic  
CC variants of CHRNA2. The method is useful for detecting novel CHRNA2  
CC polymorphisms and for determining if an individual has a haplotype or  
CC haplotype pairs defined in the specification and to validate CHRNA2 as a  
CC candidate agent for treating a specific condition or disease predicted to  
CC be associated with CHRNA2 activity (e.g. a memory disorder, Alzheimer's  
CC disease, epilepsy, a learning disorder, schizophrenia, attention  
CC deficit/hyperactivity disorder, (ADHD) and autosomal dominant nocturnal  
CC frontal lobe epilepsy (ADFLE)), and in the design of clinical trials of  
CC candidate drugs for treating a specific condition or disease predicted to  
CC be associated with CHRNA2 activity. The method is useful to screen for  
CC compounds targeting CHRNA2 to treat a specific condition or disease  
CC associated with CHRNA2 activity. The polymorphic nucleic acids are useful  
CC in studying the expression and function of CHRNA2, and in expressing  
CC CHRNA2 protein for use in screening for candidate drugs to treat diseases  
CC related to CHRNA2 activity and are useful for therapeutic purposes. The  
CC CHRNA2 gene is located on chromosome 1q21. The present sequence is an  
CC allele specific oligonucleotide (ASO) PCR primer (3' terminus) for  
CC performing the method of the invention  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db |||||  
1 GCTGTGG 7  
  
RESULT 335  
AAF31259  
ID AAF31259 standard; DNA; 10 BP.  
XX  
AC AAF31259;

XX 09-APR-2001 (first entry)  
DT GC-rich template cycle sequencing mixture related sequence #3.  
XX  
DE GC-rich template cycle sequencing mixture related sequence #3.  
XX  
KW GC-rich template; cycle sequencing; 7-deaza dGTP; dTTP;  
KW DNA amplification; ds.  
XX  
OS Synthetic.  
XX  
XX WO200102602-A2.  
PN  
XX 11-JAN-2001.  
PD  
XX  
PF 05-JUL-2000; 2000WO-EP006349.  
XX  
PR 05-JUL-1999; 99EP-00112943.  
XX  
PA (LION-) LION BIOSCIENCE AG.  
XX  
PI Motz M, Voss H;  
XX  
XX WPI; 2001-138153/14.  
DR  
XX  
XX  
PT Use of a mixture comprising 7-deaza dGTP and dTTP for direct exponential  
PT amplification and sequencing of nucleic acids, particularly guanosine  
PT cytosine rich templates.  
XX  
PS Disclosure; Fig 2; 18pp; English.  
XX  
CC The present invention describes a mixture comprising 7-deaza dGTP and  
CC dTTP, which can be used in the cycle sequencing of GC-rich templates. In  
CC addition, the mixture can be used in DNA amplification. Sequences  
CC AAF31257-AAF31267 are examples of compression prone sequences  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 GCGAAGG 19  
Db |||||  
1 GCGAAGG 7  
  
RESULT 336  
AAH41713/C  
ID AAH41713 standard; DNA; 10 BP.  
XX  
AC AAH41713;  
XX  
DT 28-AUG-2001 (first entry)  
XX  
DE Anti-PEP gene construction related oligonucleotide S18.  
XX  
KW Phosphoenolpyruvate carboxylase; PEPCase; seed; acetyl-CoA carboxylase;  
KW oilseed; PEP; plant breeding; soya bean; sunflower; rapeseed; peanut;  
KW sesame; crop plant; protein content; fatty acid content; anti-PEP; ss.  
XX  
OS Synthetic.  
XX  
XX WO200134812-A1.  
PN  
XX 17-MAY-2001.  
PD  
XX  
XX 06-NOV-2000; 2000WO-CN000418.  
PF  
XX  
PR 09-NOV-1999; 99CN-00124511.  
XX  
PA (ZHEJ-) ZHEJIANG AGRIC SCI ACAD.  
XX  
PI Chen J, Lang C, Huang R, Hu Z, Liu Z;

XX WPI; 2001-335934/35.  
XX Altering protein/fatty acid composition of seeds, useful for producing  
PT e.g. soya bean or sesame seed with high protein/fatty acid content,  
PT comprises introducing antisense gene.  
XX  
PS Example 8; Page 9; 25pp; Chinese.  
XX  
CC The present invention describes a method for altering the protein/fatty  
CC acid composition of seeds. The method comprises: (1) cloning  
CC phosphoenopyruvate carboxylase (PEP) or acetyl-CoA carboxylase (ACC)  
CC genes or their fragments; (2) constructing the corresponding antisense  
CC gene of anti-PEP or anti-ACC; and (3) introducing the antisense gene into  
CC the plant cell of a crop. The method is applicable in plant breeding to  
CC give oilseed crops with high oil or protein content like soya bean,  
CC sunflower, rapeseed, peanut and sesame. The produced crop plants have  
CC high yield of oil or protein. The present sequence represents an  
CC oligonucleotide which is used in the construction of an anti-PEP gene in  
CC an example from the present invention  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db 7 GCTGTGG 1  
  
RESULT 337  
ABA06097/c  
ID ABA06097 standard; cDNA; 10 BP.  
XX  
AC ABA06097;  
XX  
DT 10-JAN-2002 (first entry)  
XX  
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 74.  
XX  
KW Human; hepatocyte; gene expression; hepatopathy; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2001211883-A.  
XX  
PD 07-AUG-2001.  
XX  
PF 31-JAN-2000; 2000JP-00023170.  
XX  
PR 31-JAN-2000; 2000JP-00023170.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2001-629566/73.  
XX  
PT Human normal hepatocyte expression gene group.  
XX  
PS Claim 1; Page 7; 26pp; Japanese.  
XX  
CC The invention relates to a human normal hepatocyte expression gene group  
CC comprising 200 genes in the human normal hepatocyte. The cDNA of each  
CC gene comprises one of 200 fully defined nucleotide sequences as given in  
CC the specification. The gene group and the cDNAs corresponding to each of  
CC the genes in the group are useful in the diagnosis and treatment of human  
CC hepatopathy. The present sequence is a cDNA corresponding to a gene  
CC expressed by normal human hepatocytes  
XX  
SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 TGTGGCG 15  
Db 7 TGTGGCG 1  
  
RESULT 338  
AAF36769/c  
ID AAF36769 standard; DNA; 10 BP.  
XX  
AC AAF36769;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3508.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 125; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX



SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 GTGGCGA 16  
Db 7 GTGGCGA 1  
RESULT 339  
AAF37041  
ID AAF37041 standard; DNA; 10 BP.  
XX  
AC AAF37041;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3780.  
XX  
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX Example; Page 135; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle. The  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 4 A; 1 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 TGGCGAA 17  
Db 4 TGGCGAA 10  
RESULT 340  
AAF33704  
ID AAF33704 standard; DNA; 10 BP.  
XX  
AC AAF33704;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:443.  
XX  
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX Claim 1; Page 391; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle. The  
CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CGCTGTG 12  
Db 4 CGCTGTG 10  
  
RESULT 341  
AAF36509/c  
ID AAF36509 standard; DNA; 10 BP.  
XX  
AC AAF36509;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3248.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 116; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 GCGCTGT 11  
Db 8 GCGCTGT 2  
  
RESULT 342  
AAF43548/c  
ID AAF43548 standard; DNA; 10 BP.  
XX  
AC AAF43548;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11687.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 367; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 1 G; 4 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 11 TGGCGAA 17  
Db 10 TGGCGAA 4  
  
RESULT 343  
AAAF33404  
ID AAF33404 standard; DNA; 10 BP.  
AC AAF33404;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:143.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Claim 1; Page 24; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CGCTGTG 12  
Db 4 CGCTGTG 10  
  
RESULT 344  
AAAF40064/C  
ID AAF40064 standard; DNA; 10 BP.  
XX  
AC AAF40064;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6803.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 243; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 10 GTGGCGA 16  
Db 8 GTGGCGA 2  
  
RESULT 345  
AAF40212  
ID AAF40212 standard; DNA; 10 BP.  
XX  
AC AAF40212;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6951.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velulescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 248; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 TGGCGAA 17  
Db 2 TGGCGAA 8  
  
RESULT 346  
AAF34364/c  
ID AAF34364 standard; DNA; 10 BP.  
XX  
AC AAF34364;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1103.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velulescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
DR  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 39; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log



CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCGAAG 18  
Db 9 GGCGAAG 3

RESULT 347  
AAF36295  
ID AAF36295 standard; DNA; 10 BP.

XX AAF36295;

AC AAF36295;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3034.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.

XX Example; Page 108; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCGCGCT 9  
Db 2 TCGCGCT 8

RESULT 348  
AAF42137/C  
ID AAF42137 standard; DNA; 10 BP.

XX AAF42137;

AC AAF42137;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8876.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO ) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.

PS Example; Page 317; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAAGG 19

Db 10 GCGAAGG 4

RESULT 349

AAF37397/c

ID AAF37397 standard; DNA; 10 BP.

XX

AC AAF37397;

XX

DT 23-MAR-2001 (first entry)

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4136.

XX

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

PD 21-DEC-2000.

XX

PF 14-JUN-2000; 2000WO-US016223.

XX

XX 16-JUN-1999; 99US-00335032.

PR

XX (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Velculescu V, Vogelstein B, Kinzler K;

XX

XX WPI; 2001-061874/07.

XX

PT Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

XX affecting phases of the cell cycle.

PS Example; Page 147; 419pp; English.

XX

CC The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10

Db 8 CGCGCTG 2

RESULT 350

AAF43249

ID AAF43249 standard; DNA; 10 BP.

XX

AC AAF43249;

XX

DT 23-MAR-2001 (first entry)

XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11388.

XX

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

PD 21-DEC-2000.

XX

XX 14-JUN-2000; 2000WO-US016223.

PF

XX 16-JUN-1999; 99US-00335032.

PR

XX (UYJO ) UNIV JOHNS HOPKINS.

XX

PI Velculescu V, Vogelstein B, Kinzler K;

XX

DR WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX Example; Page 356; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 5 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17

Db |||||

1 TGGCGAA 7

RESULT 351

AAAF40108

ID AAF40108 standard; DNA; 10 BP.

XX AAF40108;

AC AAF40108;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6847.

DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

XX nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO ) UNIV JOHNS HOPKINS.

XX PA

XX Velculescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

DR gene expression (SAGE) tags, useful for studying, monitoring and

XX affecting phases of the cell cycle.

PT Example; Page 244; 419pp; English.

PS The present invention describes an isolated DNA molecule comprising a

XX coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGTGGC 14

Db |||||

3 CTGTGGC 9

RESULT 352

AAAF43351

ID AAF43351 standard; DNA; 10 BP.

XX AAF43351;

AC AAF43351;

XX 23-MAR-2001 (first entry)

DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11490.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

DE nor previously assigned open reading frame; nonannotated ORF; SAGE;

XX serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

XX 21-DEC-2000.

PD 14-JUN-2000; 2000WO-US016223.

XX PF



PR 16-JUN-1999; 99US-00335032.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 360; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.le+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CGCTGTG 12  
Db |||||  
4 CGCTGTG 10  
  
RESULT 353  
AAF33705  
ID AAF33705 standard; DNA; 10 BP.  
XX  
AC AAF33705;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:444.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.  
XX  
XX 16-JUN-1999; 99US-00335032.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Claim 1; Page 391; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.le+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 CGCTGTG 12  
Db |||||  
4 CGCTGTG 10  
  
RESULT 354  
AAF41416/c  
ID AAF41416 standard; DNA; 10 BP.  
XX  
AC AAF41416;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8155.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX



PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 291; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 0 A; 5 C; 1 G; 4 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 GGCGAAG 18  
Db | | | | | | |  
9 GGCGAAG 3  
  
RESULT 355  
AAF41494  
ID AAF41494 standard; DNA; 10 BP.  
XX  
AC AAF41494;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8233.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.

XX OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 294; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 TGGCGAA 17  
Db | | | | | | |  
2 TGGCGAA 8  
  
RESULT 356  
AAF37535  
ID AAF37535 standard; DNA; 10 BP.  
XX  
AC AAF37535;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4274.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
XX linker; PCR primer; ds.  
OS Saccharomyces cerevisiae.  
XX WO200077214-A2.  
XX 21-DEC-2000.  
XX 14-JUN-2000; 2000WO-US016223.  
XX 16-JUN-1999; 99US-00335032.  
XX (UYJO ) UNIV JOHNS HOPKINS.  
XX Velculescu V, Vogelstein B, Kinzler K;  
PI WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 152; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGTCGCG 7  
Db ||||| 3 GGTCGCG 9  
  
RESULT 357  
AAF33686  
ID AAF33686 standard; DNA; 10 BP.  
XX  
AC AAF33686;  
XX  
XX 23-MAR-2001 (first entry)  
XX

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:425.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
XX linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Claim 1; Page 390; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGTCGCG 7  
Db ||||| 3 GGTCGCG 9  
  
RESULT 358  
AAF36000  
ID AAF36000 standard; DNA; 10 BP.  
XX  
AC AAF36000;

XX 23-MAR-2001 (first entry)  
DT  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2739.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
XX Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 97; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 6 CGCTGTG 12  
|||||||  
Db 4 CGCTGTG 10  
  
RESULT 359  
AAF42020/c

ID AAF42020 standard; DNA; 10 BP.  
XX  
AC AAF42020;  
XX  
DT 23-MAR-2001 (first entry)  
XX  
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8759.  
XX  
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;  
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;  
KW serial analysis of gene expression; antifungal; tag; identification;  
KW linker; PCR primer; ds.  
XX  
OS Saccharomyces cerevisiae.  
XX  
PN WO200077214-A2.  
XX  
PD 21-DEC-2000.  
XX  
PF 14-JUN-2000; 2000WO-US016223.  
XX  
PR 16-JUN-1999; 99US-00335032.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI Velculescu V, Vogelstein B, Kinzler K;  
XX  
DR WPI; 2001-061874/07.  
XX  
PT Yeast gene coding sequences comprising NORF genes with serial analysis of  
PT gene expression (SAGE) tags, useful for studying, monitoring and  
PT affecting phases of the cell cycle.  
XX  
PS Example; Page 312; 419pp; English.  
XX  
CC The present invention describes an isolated DNA molecule comprising a  
CC coding sequence of a yeast gene selected from a group of 745 NORF (not  
CC previously assigned open reading frame; or nonannotated ORF) genes  
CC comprising a SAGE (serial analysis of gene expression) tag. Also  
CC described are: (1) a method (M1) of using NORF genes to affect the cell  
CC cycle comprising administering a NORF gene whose expression varies by at  
CC least 10% between any two phases of the cell cycle selected from log  
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate  
CC antifungal drugs comprising: (a) contacting a test substance with a yeast  
CC cell; and (b) monitoring expression of a NORF gene whose expression  
CC varies as in M1, where a test substance which modifies the expression of  
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for  
CC identifying human genes which are involved in cell cycle progression  
CC comprising contacting human DNA with a probe which comprises at least 10  
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;  
CC and (4) a method (M4) for identifying a candidate drug as a member of a  
CC class of drugs having a characteristic effect on gene expression in a  
CC yeast cell comprising contacting a yeast cell with a candidate drug and  
CC monitoring expression in the yeast cell of at least 1 NORF gene whose  
CC expression is affected by the class of drugs. The NORF genes may be used  
CC to study, monitor and affect phases of the cell cycle, the differentially  
CC expressed genes may be used as markers of phases of the cell cycle. The  
CC methods may be used to identify candidate drugs which affect the cell  
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064  
CC represent SAGE tags used in the exemplification of the present invention.  
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE  
CC method, in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 TCGCGCT 9  
|||||||  
Db 8 TCGCGCT 2

RESULT 360  
AAS95650  
ID AAS95650 standard; DNA; 10 BP.  
XX  
AC AAS95650;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE Human NPY1R gene allele-specific oligonucleotide PCR primer #5.  
XX  
KW Human; neuropeptide Y receptor Y1; NPY1R; ss; antiarteriosclerotic;  
KW haplotyping; haplotype pair; single nucleotide polymorphism; genotyping;  
KW gene therapy; drug screening; cardiovascular disease; antidepressant;  
KW hypertension; cardiant; depression; probe; sequencing primer; PCR primer;  
KW PCR primer universal tail.  
XX  
OS Homo sapiens.  
XX  
PN WO200185742-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 07-MAY-2001; 2001WO-US014773.  
XX  
PR 05-MAY-2000; 2000US-0201950P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Choi JY, Kliem SE, Koshy B, Lee HH;  
XX WPI; 2002-055579/07.  
DR  
XX  
PT New isolated polynucleotide variant of neuropeptide Y receptor Y1 (NPY1R)  
PT for studying the function of NPY1R, and expressing NPY1R protein for use  
PT in screening candidate drugs to treat NPY1R-related diseases.  
XX  
PS Claim 17; Page 12; 48pp; English.  
XX  
CC The invention relates to single nucleotide polymorphisms in the human  
CC neuropeptide Y receptor Y1 (NPY1R) gene. A method for haplotyping the  
CC NPY1R gene in an individual comprises identifying the nucleotide at one  
CC or more polymorphic sites and determining whether one of the copies of  
CC the gene is defined by one of the NPY1R haplotypes given in the  
CC specification or whether both copies are defined by a haplotype pair.  
CC This method is useful in genotyping, whereby all possible haplotype pairs  
CC can be assigned to specific genotypes. An association between a trait and  
CC a haplotype or haplotype pair of the NPY1R gene can be identified by  
CC comparing the frequency of the haplotype or haplotype pair in a  
CC population exhibiting the trait with the frequency of the haplotype or  
CC haplotype pair in a reference population, where a higher haplotype  
CC frequency in the trait population indicates the trait is associated with  
CC the haplotype or haplotype pair. NPY1R and its corresponding DNA are used  
CC for studying the expression and function of NPY1R, for use in screening  
CC for candidate drugs to treat diseases related to NPY1R activity, such as  
CC cardiovascular diseases (e.g. hypertension) and depression. The sequences  
CC are also useful for studying the effect of variation on the biological  
CC activity of NPY1R as well as on the binding affinity of candidate drugs  
CC targeting NPY1R. Sequences AAS95637-AAS95659 represent allele-specific  
CC oligonucleotide probes, sequencing primers, PCR primers and PCR primer  
CC universal tails used to detect NPY1R gene polymorphisms  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CTGTGGC 14  
Db 1 CTGTGGC 7

RESULT 361  
AAD25081/C  
ID AAD25081 standard; DNA; 10 BP.  
XX  
AC AAD25081;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Primer #8 used to detect human OSM gene polymorphism.  
XX  
KW Human; oncostatin M; OSM gene; haplotyping; genotyping; cancer; primer;  
KW lung inflammation; polymorphism; rheumatoid arthritis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200187907-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 17-MAY-2001; 2001WO-US016157.  
XX  
PR 17-MAY-2000; 2000US-0204868P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Duda AE, Kazemi A, Koshy B;  
XX WPI; 2002-055680/07.  
DR  
XX  
PT New isolated human oncostatin M polynucleotide, useful for therapeutic  
PT purposes, for studying the expression and function of the polynucleotide  
PT and for expressing oncostatin protein.  
XX  
PS Claim 18; Page 13; 71pp; English.  
XX  
CC The invention relates to genetic variants of human oncostatin M (OSM)  
CC gene. The invention also relates to compositions and methods for  
CC haplotyping and/or genotyping OSM gene in an individual. Polynucleotides  
CC of the invention are useful in studying the expression and function of  
CC OSM, and in expressing OSM protein for use in screening candidate drugs  
CC to treat diseases related to OSM activity. They are also useful for  
CC therapeutic purposes. Methods of the invention are useful for determining  
CC whether an individual has a haplotype or haplotype pairs. The method is  
CC also useful for improving the efficacy and reliability of several steps  
CC in the discovery and development of drugs for treating diseases  
CC associated with OSM activity, e.g. cancer, diseases involving lung  
CC inflammation and rheumatoid arthritis. The present sequence is a primer  
CC used for detecting human OSM gene polymorphisms  
XX  
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CTGTGGC 14  
Db 9 CTGTGGC 3

RESULT 362  
AAD26712  
ID AAD26712 standard; DNA; 10 BP.  
XX  
AC AAD26712;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Human GPR31 gene polymorphism detecting primer #13.  
XX  
KW Human; G-protein coupled receptor 31; GPR31 protein; haplotyping;  
KW genotyping; gene therapy; cancer; polymorphism; primer; ss.  
XX



OS Homo sapiens.  
XX WO200190124-A2.  
PN  
XX  
PD 29-NOV-2001.  
XX  
PF 23-MAY-2001; 2001WO-US016908.  
XX  
PR 23-MAY-2000; 2000US-0206572P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bieglecki KM, Duda A, Kazemi A, Lee HH, Messer C;  
XX  
DR WPI; 2002-089915/12.  
XX  
PT Novel genetic variants of G-protein coupled receptor gene useful in  
PT studying expression and function of the protein, and for screening drugs  
PT to treat diseases e.g. cancer.  
XX  
PS Claim 18; Page 13; 75pp; English.  
XX  
CC The invention relates to genetic variants of human G-protein coupled  
CC receptor 31 (GPR31) gene. The invention also relates to compositions and  
CC methods for haplotyping and/or genotyping the GPR31 gene in an  
CC individual. Polynucleotides of the invention are useful in studying the  
CC expression and function of GPR31, and in expressing GPR31 protein for use  
CC in screening candidate drugs to treat diseases related to GPR31 activity of  
CC and in studying the effect of the variation on the biological activity of  
CC GPR31 as well as on the binding affinity of candidate drugs targetting  
CC GPR31 for the treatment of cancer. They are also used in gene therapy.  
CC The haplotyping method is useful for improving the efficiency and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with GPR31 activity e.g. cancer. This  
CC method is also useful for haplotyping GPR31 gene in an individual, which  
CC can also be used by the pharmaceutical research scientist to validate  
CC GPR31 as a candidate target for, and in design of clinical trials of  
CC candidate drugs, for treating a specific condition drugs or disease  
CC predicted to be associated with GPR31 activity. The present sequence is a  
CC primer used to detect human GPR31 gene polymorphisms  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 7 GCTGTGG 13  
Db |||||  
3 GCTGTGG 9  
  
RESULT 363  
AAS98814  
ID AAS98814 standard; DNA; 10 BP.  
XX  
AC AAS98814;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Colony stimulating factor 1 receptor (CSF1R) oligonucleotide #180.  
XX  
KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;  
KW cytostatic; gene therapy; malignant histiocytosis; isogene;  
KW myeloid malignancy; inflammatory disorder; transgenic animal; haplotype;  
KW genotype; human; allele specific oligonucleotide; ASO; primer;  
KW primer extension; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200179225-A2.  
XX  
PD 25-OCT-2001.

XX 12-APR-2001; 2001WO-US012044.  
PF  
XX  
PR 12-APR-2000; 2000US-0196411P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Chew A, Choi JY, Koshy B;  
XX  
DR WPI; 2002-075058/10.  
XX  
PT Novel polymorphic variants of colony stimulating factor 1 receptor useful  
PT in studying expression and function of the protein, useful for screening  
PT candidate drugs to treat diseases e.g. inflammatory disorders.  
XX  
PS Claim 17; Page 17; 164pp; English.  
XX  
CC The invention describes a novel isolated polynucleotide (I) comprising a  
CC sequence which is a polymorphic variant (PV) of a reference sequence for  
CC colony stimulating factor 1 receptor (CSF1R) gene, found on The  
CC polypeptide are useful for improving the discovery and development of  
CC drugs for treating diseases associated with CSF1R activity, e.g.,  
CC malignant histiocytosis, myeloid malignancies, and inflammatory disorders  
CC and the haplotypes can be used to validate CSF1R as a candidate target  
CC for treating a specific condition or disease predicted to be associated  
CC with CSF1R activity. Genotyping the CSF1R gene of an individual can also  
CC be used in developing diagnostic tests and therapeutic treatments. (I) is  
CC useful in studying the expression and function of CSF1R, and in  
CC expressing CSF1R protein for use in screening for candidate drugs to  
CC treat diseases related to CSF1R activity and in studying the effect of  
CC the variation on the biological activity of CSF1R as well as on the  
CC binding affinity of candidate drugs targeting CSF1R. Antibodies are  
CC useful in a variety of diagnostic and prognostic formats and therapeutic  
CC methods. A transgenic animal is useful in studying expression of the  
CC CSF1R isogenes in vivo, for in vivo screening and testing of drugs  
CC targeted against CSF1R protein, and for testing the efficacy of  
CC therapeutic agents and compounds. Allele specific oligonucleotides (ASO)  
CC are useful as probes and primers, and for assaying a polymorphism in the  
CC target region. Without requiring any a priori knowledge of the phenotypic  
CC effect of any particular CSF1R or haplotype the invention provides a  
CC method for identifying lead compounds that are more likely to show  
CC efficacy in clinical trials. This sequence is a primer used to detect  
CC CSF1R gene polymorphisms by primer extension, described in the method of  
CC the invention  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 8 CTGTGGC 14  
Db |||||  
2 CTGTGGC 8  
  
RESULT 364  
ABQ71544  
ID ABQ71544 standard; DNA; 10 BP.  
XX  
AC ABQ71544;  
XX  
DT 28-AUG-2002 (first entry)  
XX  
DE Zinc finger protein related oligonucleotide target SEQ ID NO:1278.  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200242459-A2.  
XX

PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
XX (SANG-) SANGAMO BIOSCIENCES INC.  
PA  
XX  
PI Liu Q;  
XX  
DR WPI; 2002-500284/53.  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
PS Example 1; Page 47; 81pp; English.  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
XX invention  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db |||||  
4 GCTGTGG 10  
  
RESULT 365  
ABQ71291  
ID ABQ71291 standard; DNA; 10 BP.  
XX  
AC ABQ71291;  
XX  
DT 28-AUG-2002 (first entry)  
XX  
DE Zinc finger protein related oligonucleotide target SEQ ID NO:92.  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200242459-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX

PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Liu Q;  
XX  
DR WPI; 2002-500284/53.  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
PS Example 1; Page 38; 81pp; English.  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
XX invention  
SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 GGCGAAG 18  
Db |||||  
4 GGCGAAG 10  
  
RESULT 366  
ABQ71292  
ID ABQ71292 standard; DNA; 10 BP.  
XX  
AC ABQ71292;  
XX  
DT 28-AUG-2002 (first entry)  
XX  
DE Zinc finger protein related oligonucleotide target SEQ ID NO:93.  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200242459-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX

PI Liu Q;  
XX  
DR WPI; 2002-500284/53.  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
PS Example 1; Page 38; 8lpp; English.  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 GGCGAAG 18  
Db 4 GGCGAAG 10  
  
RESULT 367  
ABQ71662  
ID ABQ71662 standard; DNA; 10 BP.  
XX  
AC ABQ71662;  
XX  
DT 28-AUG-2002 (first entry)  
XX  
DE Zinc finger protein related oligonucleotide target SEQ ID NO:1654.  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200242459-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Liu Q;  
XX  
DR WPI; 2002-500284/53.  
XX

PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX  
PS Example 1; Page 51; 8lpp; English.  
XX  
CC The present invention describes a zinc finger protein (I) that binds to a  
CC target site, comprising a first (F1), a second (F2), and a third (F3)  
CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the  
CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),  
CC and a third (S3) target subsite. Also described are: (1) a polypeptide  
CC (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and  
CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it  
CC binds to the S1 target subsite, selecting the F2 zinc finger such that it  
CC binds to the S2 target subsite, and selecting the F3 zinc finger such  
CC that it binds to the S3 target subsite, thus designing (I) that binds to  
CC a target site. (I) is useful for recognition of triplet target subsites  
CC having the nucleotide G in the 5'-most position of the subsite. (I) is  
CC useful in studying gene function, and for human therapeutics and plant  
CC engineering. (I), (II) or (III) is useful in therapeutic methods to  
CC modulate the expression of a target region within a subject, in  
CC diagnostic methods for sequence specific detection of target nucleic acid  
CC in a sample, and in assays to determined the phenotype and function of  
CC gene expression. (I) has improved affinity and specificity for their  
CC target sequences, as well as enhanced biological activity. ABQ71213 to  
CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc  
CC finger peptides which are given in the exemplification of the present  
CC invention  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGTCGCG 7  
Db 3 GGTCGCG 9  
  
RESULT 368  
ABQ71675  
ID ABQ71675 standard; DNA; 10 BP.  
XX  
AC ABQ71675;  
XX  
DT 28-AUG-2002 (first entry)  
XX  
DE Zinc finger protein related oligonucleotide target SEQ ID NO:1667.  
XX  
KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200242459-A2.  
XX  
PD 30-MAY-2002.  
XX  
PF 20-NOV-2001; 2001WO-US043438.  
XX  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (SANG-) SANGAMO BIOSCIENCES INC.  
XX  
PI Liu Q;  
XX  
DR WPI; 2002-500284/53.  
XX  
PT New zinc finger protein that binds to target site, useful in studying  
PT gene function and for human therapeutics and plant engineering, comprises  
PT first, second and third zinc fingers, ordered from N- to C-terminus.  
XX

PS Example 1; Page 51; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3) zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7  
Db 3 GGTCGCG 9

RESULT 369  
ABQ71661  
ID ABQ71661 standard; DNA; 10 BP.  
XX AC ABQ71661;  
XX DT 28-AUG-2002 (first entry)  
XX DE Zinc finger protein related oligonucleotide target SEQ ID NO:1653.  
XX KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200242459-A2.

XX PD 30-MAY-2002.

XX PF 20-NOV-2001; 2001WO-US043438.

XX PR 20-NOV-2000; 2000US-00716637.

XX PA (SANG-) SANGAMO BIOSCIENCES INC.

XX PI Liu Q;

XX DR WPI; 2002-500284/53.

XX PT New zinc finger protein that binds to target site, useful in studying gene function and for human therapeutics and plant engineering, comprises first, second and third zinc fingers, ordered from N- to C-terminus.

XX PS Example 1; Page 51; 81pp; English.

XX CC The present invention describes a zinc finger protein (I) that binds to a target site, comprising a first (F1), a second (F2), and a third (F3)

CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the target site comprises, in 3'-5' direction, a first (S1), a second (S2), and a third (S3) target subsite. Also described are: (1) a polypeptide (II) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and (3) designing (M) (I) involves selecting the F1 zinc finger such that it binds to the S1 target subsite, selecting the F2 zinc finger such that it binds to the S2 target subsite, and selecting the F3 zinc finger such that it binds to the S3 target subsite, thus designing (I) that binds to a target site. (I) is useful for recognition of triplet target subsites having the nucleotide G in the 5'-most position of the subsite. (I) is useful in studying gene function, and for human therapeutics and plant engineering. (I), (II) or (III) is useful in therapeutic methods to modulate the expression of a target region within a subject, in diagnostic methods for sequence specific detection of target nucleic acid in a sample, and in assays to determine the phenotype and function of gene expression. (I) has improved affinity and specificity for their target sequences, as well as enhanced biological activity. ABQ71213 to ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc finger peptides which are given in the exemplification of the present invention

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7  
Db 3 GGTCGCG 9

RESULT 370  
ABQ88698  
ID ABQ88698 standard; DNA; 10 BP.  
XX AC ABQ88698;

XX DT 23-SEP-2002 (first entry)

XX DE Human CFL1 primer extension oligonucleotide #21.

XX KW Human; cofilin 1; CFL1; gene therapy; antisense gene therapy;  
XX KW immunological disorder; primer extension; PCR; primer; probe; ss.

XX OS Homo sapiens.

XX PN WO200194376-A1.

XX PD 13-DEC-2001.

XX PF 11-JUN-2001; 2001WO-US018815.

XX PR 09-JUN-2000; 2000US-0210884P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Anastasio AE, Duda A, Kliem SE, Koshy B, Sausker EA;

XX DR WPI; 2002-566437/60.

XX PT Novel genetic variants of human cofilin 1, CFL1 gene for studying expression, function of the gene and expressing CFL1 protein useful in identifying drugs to treat immunological disorders.

XX PS Claim 19; Page 14; 84pp; English.

XX CC The invention relates to a novel polynucleotide sequence which is a polymorphic variant of a reference sequence for the cofilin 1 (non-muscle) (CFL1) gene or its fragment, or a polymorphic variant of a reference sequence for a CFL1 cDNA or its fragment. The polynucleotide of the invention may have a use in gene therapy, and in antisense gene therapy. The polynucleotide is useful for studying the expression and



CC function of CFL1 and expressing CFL1 protein for use in screening for  
CC candidate drugs to treat diseases related to CFL1 activity. The  
CC polymorphism and haplotype data are useful for validating whether CFL1 is  
CC a suitable target for drugs to treat immunological disorders, screening  
CC for such drugs and reducing bias in clinical trials of such drugs. The  
CC present sequence represents one of a set of primer extension  
CC oligonucleotide PCR primers used in the invention to detect polymorphisms  
CC in the CFL1 gene  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 3 G; 5 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CTGTGGC 14  
Db 1 CTGTGGC 7  
|||||  
  
RESULT 371  
ABAO3980  
ID ABA03980 standard; DNA; 10 BP.  
XX  
AC ABA03980;  
XX  
DT 19-FEB-2002 (first entry)  
XX  
DE Human STK11 gene polymorphism detection primer SEQ ID NO:47.  
XX  
KW Human; STK11; serine/threonine kinase 11; polymorphism; SNP;  
KW single nucleotide polymorphism; Peutz-Jeghers Syndrome; genotyping;  
KW haplotype; genetic variant; haplotyping; allele-specific oligonucleotide;  
KW primer; primer extension; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200187906-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 17-MAY-2001; 2001WO-US016045.  
XX  
PR 17-MAY-2000; 2000US-0204697P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bieglecki KM, Chew A, Choi JY, Nandabalan K, Sausker EA;  
XX WPI; 2002-055679/07.  
XX  
PT Novel genetic variants of serine/threonine kinase 11 (Peutz-Jeghers  
PT syndrome) useful in studying expression and function of the protein, and  
PT for screening candidate drugs to treat diseases e.g. Peutz-Jeghers  
PT syndrome.  
XX  
PS Claim 18; Page 14; 86pp; English.  
XX  
CC The present invention describes a method for haplotyping the  
CC serine/threonine kinase 11 (Peutz-Jeghers syndrome) (STK11) gene of an  
CC individual. STK11 gene sequences can be used in gene therapy. The STK11  
CC gene is useful for screening drug targeting comprising contacting STK11  
CC with a candidate agent and assaying for binding activity. STK11 is useful  
CC for improving the efficiency and reliability of several steps in the  
CC discovery and development of drugs for treating diseases associated with  
CC STK11 activity, e.g. Peutz-Jeghers syndrome. The method is useful for  
CC haplotyping the STK11 gene in an individual, which can also be used in  
CC pharmaceutical research to validate STK11 as a candidate target for, and  
CC in design of clinical trials of candidate drugs for, treating a specific  
CC condition drugs or disease predicted to be associated with STK11  
CC activity. Allele-specific oligonucleotides (ASOs) are useful as probes  
CC and primers for assaying a polymorphism in the target region. The present  
CC sequence represents a primer used for detecting STK11 gene polymorphisms,

CC which is used in the exemplification of the present invention  
XX  
SQ Sequence 10 BP; 3 A; 1 C; 4 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 GCGAAGG 19  
Db 2 GCGAAGG 8  
|||||  
  
RESULT 372  
ABN80659/C  
ID ABN80659 standard; DNA; 10 BP.  
XX  
AC ABN80659;  
XX  
DT 19-JUL-2002 (first entry)  
XX  
DE Human P450(cytochrome) oxidoreductase ASO primer extension oligo #47.  
XX  
KW Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;  
KW single nucleotide polymorphism; flavoprotein; enzyme;  
KW primer extension oligonucleotide; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200226768-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 01-OCT-2001; 2001WO-US030877.  
XX  
PR 29-SEP-2000; 2000US-0236449P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;  
XX WPI; 2002-394236/42.  
XX  
PT New genetic variants comprising haplotypes of the P450 (cytochrome)  
PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug  
PT screening protocols for compounds targeting POR.  
XX  
PS Claim 16; Page 15; 141pp; English.  
XX  
CC The present invention provides the protein, gene and cDNA sequences of  
CC human P450(cytochrome) oxidoreductase POR, and single nucleotide  
CC polymorphisms (SNPs) identified therein. The sequences can be used to  
CC haplotype the POR gene of an individual, and to establish whether POR is  
CC a suitable target for drugs to treat cancer and disorders associated with  
CC impaired protein synthesis in cells. The present sequence is an allele  
CC specific primer extension oligonucleotide for the coding sequences of the  
CC invention  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CTGTGGC 14  
Db 10 CTGTGGC 4  
|||||  
  
RESULT 373  
ABV78586/C  
ID ABV78586 standard; cDNA; 10 BP.  
XX

AC ABV78586;  
XX  
DT 29-NOV-2002 (first entry)  
XX  
DE Human Th2 cell preferentially expressed gene SAGE tag, SEQ ID NO:297.  
XX  
KW SAGE tag; serial analysis of gene expression; human; Th2 cell;  
KW activated T cell; T lymphocyte; immune response; expression pattern;  
KW preferential expression; immune disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002186482-A.  
XX  
PD 02-JUL-2002.  
XX  
PF 19-DEC-2000; 2000JP-00385816.  
XX  
PR 19-DEC-2000; 2000JP-00385816.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-594261/64.  
XX  
PT Human activated Th1 and Th2 cell expression gene group, useful for the  
PT diagnosis and treatment of Th1 and Th2-related diseases.  
XX  
PS Claim 28; Page 13; 60pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are expressed in activated human Th1  
CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence  
CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif  
CC lying nearest to the polyA region of cDNAs derived from a variety of  
CC genes. These tags serve to uniquely identify each transcript and can thus  
CC be used to analyse the pattern of gene expression in particular cell  
CC types. The invention also relates to proteins encoded by the genes  
CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and  
CC inhibitors of the expression of groups of genes that are expressed in  
CC either or both the two cell types. Groups of genes expressed in Th1  
CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1  
CC and Th2-related disorders. Sequences ABV78561-ABV78610 are SAGE tags  
CC representing 50 genes which are more highly expressed in Th2 cells  
CC compared with Th1 cells  
XX  
SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTGTGG 13  
|||||||  
Db 7 GCTGTGG 1

RESULT 374  
ABV84371/c  
ID ABV84371 standard; cDNA; 10 BP.  
XX  
AC ABV84371;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human MHC class II DR beta 1 SAGE tag #181.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; differential expression; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.

XX 30-JUL-2002.  
PD  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX  
DR WPI; 2002-631294/68.  
XX  
PT Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
PS Claim 10; Page 14; 139pp; Japanese.  
XX  
CC The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84291-ABV84390 are SAGE tags representing the 100 least highly  
CC expressed genes out of those genes which are underexpressed in chronic  
CC hepatitis C liver tissue compared with normal liver tissue  
XX  
SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGT 11  
|||||||  
Db 7 GCGCTGT 1

RESULT 375  
ABV84863/c  
ID ABV84863 standard; cDNA; 10 BP.  
XX  
AC ABV84863;  
XX  
DT 12-DEC-2002 (first entry)  
XX  
DE Human 3,4-catechol oestrogen UDP glucuronosyltransferase SAGE tag #673.  
XX  
KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;  
KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;  
KW expression pattern; ss.  
XX  
OS Homo sapiens.  
XX  
PN JP2002209591-A.  
XX  
PD 30-JUL-2002.  
XX  
PF 19-JAN-2001; 2001JP-00012328.  
XX  
PR 19-JAN-2001; 2001JP-00012328.  
XX  
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-631294/68.  
DR  
XX Human chronic hepatitis C tissue expression exasperating gene group  
PT comprises 100 high-ranking genes.  
XX  
XX Claim 55; Page 29; 139pp; Japanese.  
PS  
XX The invention relates to SAGE (serial analysis of gene expression) tags  
CC representing groups of genes which are differentially expressed in human  
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced  
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.  
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides  
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the  
CC polyA region of cDNAs derived from a variety of genes. These tags serve  
CC to uniquely identify each transcript and can thus be used to analyse the  
CC pattern of gene expression in particular cell types. The invention also  
CC relates to proteins encoded by the genes expressed in chronic hepatitis C  
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of  
CC the expression of groups of genes that are overexpressed in chronic  
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed  
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and  
CC treatment of these diseases. Such genes, inhibitors of their expression  
CC or activity, and antibodies against the gene products may be used in the  
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences  
CC ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly  
CC expressed in chronic hepatitis C liver tissue  
XX  
SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 9 TGTGGCG 15  
Db 7 TGTGGCG 1  
  
RESULT 376  
ABL52041/C  
ID ABL52041 standard; DNA; 10 BP.  
XX  
AC ABL52041;  
XX  
DT 11-JUL-2002 (first entry)  
XX  
DE Human SLC18A2 preferred oligonucleotide primer SEQ ID NO:89.  
XX  
KW Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;  
KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;  
KW single nucleotide polymorphism; antiinflammatory; neuroleptic;  
KW haplotyping; genotyping; respiratory inflammatory disease;  
KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200222652-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 17-SEP-2001; 2001WO-US042217.  
XX  
PR 15-SEP-2000; 2000US-0232895P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Anastasio AE, Han J, Kliem SE, Sausker EA;  
XX  
DR WPI; 2002-393942/42.  
XX  
PT Novel genetic variants of soluble carrier family 18 (vesicular  
PT monoamine), member 2 gene useful for screening drugs to treat diseases

PT e.g. neuropsychiatric disorders involving monoaminergic brain systems.  
XX Claim 19; Page 15; 183pp; English.  
PS  
XX The present invention describes an isolated polynucleotide (I) having a  
CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),  
CC member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a  
CC sequence (SS) of 40023 bp (see ABL51954), and defined by a corresponding  
CC set of polymorphisms whose locations and identities are given in the  
CC specification; or a sequence (S2) complementary to (S1). (I) has  
CC antiinflammatory and neuroleptic activities, and can be used in gene  
CC therapy. Methods from the present invention can be used for haplotyping  
CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known  
CC as the vesicular monoamine transporter (VMAT2). (I) is useful in studying  
CC the expression and function of SLC18A2, and in expressing the SLC18A2  
CC protein for use in screening for candidate drugs to treat diseases  
CC related to SLC18A2 activity and in studying the effect of the variation  
CC on the biological activity of SLC18A2 as well as on the binding affinity  
CC of candidate drugs targeting SLC18A2 for the treatment of respiratory  
CC inflammatory diseases such as neuropsychiatric disorders involving  
CC monoaminergic brain systems. The present sequence represents a preferred  
CC oligonucleotide primer for human SLC18A2, which is given in the present  
CC invention  
XX  
SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CTGTGGC 14  
Db 9 CTGTGGC 3  
  
RESULT 377  
AAS97348/C  
ID AAS97348 standard; DNA; 10 BP.  
XX  
AC AAS97348;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human CRYBB1 gene ASO primer extension PCR primer 3' end #7.  
XX  
KW Human; crystallin beta B1; CRYBB1; chromosome 22q12.1; ophthalmological;  
KW cataract; allele specific oligonucleotide; ASO; ss; haplotype;  
KW genotyping; transgenic animal; PCR primer; primer extension.  
XX  
OS Homo sapiens.  
XX  
PN WO200185998-A1.  
XX  
PD 15-NOV-2001.  
XX  
PF 07-MAY-2001; 2001WO-US014715.  
XX  
PR 05-MAY-2000; 2000US-0202253P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Choi JY, Kazemi A, Kliem SE, Koshy B, Rounds E;  
XX  
DR WPI; 2002-062253/08.  
XX  
PT Novel polymorphic variants of crystallin, beta B1 useful in studying  
PT expression and function of the protein, useful for screening candidate  
PT drugs to treat diseases e.g. cataract.  
XX  
PS Claim 17; Page 13; 94pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising a sequence  
CC which is a polymorphic variant of a reference sequence for crystallin,

CC beta B1 (CRYBB1, located on chromosome 22q12.1) gene or their fragment,  
CC where the polymorphic variant comprises a CRYBB1 isogene defined by a  
CC haplotype from haplotypes 1-16 as given in the specification. Also  
CC included are a transgenic non-human animal transformed or transfected  
CC with the polymorphic variant, a computer system for storing and analysing  
CC polymorphism data for CRYBB1 gene, a genome anthology for the CRYBB1 gene  
CC which comprises the defined CRYBB1 isogenes, methods of determining an  
CC individuals haplotype or genotype as well as methods of determining the  
CC association of a particular haplotype with a disease or trait and a  
CC composition comprising at least one genotyping oligonucleotide  
CC (especially allele-specific oligonucleotides (ASO)) for detecting a  
CC polymorphism in the CRYBB1. The isogenes or haplotypes are useful for  
CC improving the efficiency and reliability of several steps in the  
CC discovery and development of drugs for treating diseases associated with  
CC CRYBB1 activity, e.g. cataract. and can also be used by the  
CC pharmaceutical research scientist to validate CRYBB1 as a candidate  
CC target for, and in design of clinical trials of candidate drugs for,  
CC treating a specific condition drugs or disease predicted to be associated  
CC with CRYBB1 activity. The ASOs are useful as probes and primers, and for  
CC assaying a polymorphism in the target region. The present sequence is the  
CC allele specific 3' end of a PCR primer used in primer extension  
CC experiment to detect polymorphisms in CRYBB1  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CGCTGTG 12  
| | | | |  
DB 10 CGCTGTG 4

RESULT 378  
AAD24500/c  
ID AAD24500 standard; DNA; 10 BP.

XX AAD24500;

DT 07-MAR-2002 (first entry)

XX Retinoid-regulated gene amplifying degenerate PCR primer #2.

DE Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;  
KW cytochrome P450; prostate cancer; drug screening; PCR primer;  
KW retinoid-regulated gene; ss.

XX Unidentified.

XX US6306624-B1.

PN 23-OCT-2001.

PD 25-JUN-1997; 97US-00882164.

PF 21-JUN-1996; 96US-00667546.

PR 01-OCT-1996; 96US-00724466.

PR 23-JUN-1997; 97WO-CA000440.

XX (TOOH ) UNIV QUEENS KINGSTON.

XX Petkovich PM, White JA, Beckett BR, Jones G;

XX WPI; 2002-033254/04.

DR New DNA fragments having promoter activity, useful in retinoid  
XX metabolism, as well as in producing retinoic acid metabolizing cytochrome  
PT P450s that are useful as targets for the treatment of certain cancers.  
XX

PS Disclosure; Col 13; 75pp; English.

XX The present invention relates to retinoid (e.g., retinoic acid (RA),  
CC

CC vitamin A) metabolising proteins and nucleic acid sequences encoding  
CC them. RA metabolising proteins contain a haeme-binding motif which is  
CC characteristic of the group of proteins known as cytochrome P450s. The  
CC sequences of the invention are useful in retinoid metabolism and in  
CC producing retinoic acid metabolising cytochrome P450s. They are  
CC particularly useful as targets for the treatment of certain cancers such  
CC as prostate cancer. The invention also relates to a method of screening  
CC drugs for their effect on activity of RA inducible proteins. The present  
CC DNA sequence is a degenerate PCR primer which is used for amplifying  
CC retinoid regulating genes by differential display of mRNAs  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
| | | | |  
DB 9 TGGCGAA 3

RESULT 379  
ABK30053/c  
ID ABK30053 standard; DNA; 10 BP.

XX ABK30053;

XX 23-APR-2002 (first entry)

DE Vancomycin-resistant enterococci, VanH promoter mutant M11.

XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;  
KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;  
KW vanH promoter; androgen receptor promoter; AR promoter;  
KW human epidermal growth factor receptor 2 promoter; her2 promoter;  
KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;  
KW colon cancer; immunological disorder; prostate cancer; cytostatic;  
KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;  
KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;  
KW gene expression modulator; multiple sclerosis; MS;  
KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;  
KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;  
KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;  
KW mutant; transgenic; ds.

XX Enterococcus sp.

OS WO200194600-A2.

PN 13-DEC-2001.

XX 06-JUN-2001; 2001WO-US018343.

PF 06-JUN-2000; 2000US-0209549P.

PR (GENE-) GENELABS TECHNOLOGIES INC.

XX Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;

XX Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;

XX Lim MY, Bruice TW;

XX WPI; 2002-130595/17.

XX New nucleic acid regulatory sequences, which are able to regulate  
PT expression of a gene operably linked to a promoter, useful for regulating  
PT the expression of transgenes and for treating e.g., cancer and  
PT immunological diseases.  
XX

PS Example 4; Page 50; 95pp; English.

XX The invention describes an isolated nucleic acid regulatory sequence for  
CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci



CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human  
CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase  
CC (Bla) promoter. Transcription regulatory sequences may be used to  
CC regulate expression of the endogenous, autologous or heterologous genes  
CC operably linked to the promoter, and may be incorporated into  
CC heterologous nucleic acid constructs for use in regulated expression of  
CC transgenes. Regulated expression of cyclin D1 can be used in cancer  
CC therapies, such as breast, colon or pancreatic cancers and familial  
CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter  
CC may be used in the treatment of immunological disorders, such as  
CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus  
CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid  
CC arthritis. Regulated expression of genes under the control of the HBV  
CC (hepatitis B)-specific core, pre-S and X promoters can be used in the  
CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,  
CC hepatocellular carcinoma, and in the regulated expression of liver cell-  
CC specific genes. Regulated expression of the vanH gene promoter can be  
CC used in treatment of Enterococcus infection, while regulated expression  
CC of the androgen receptor gene can be used in the treatment of prostate  
CC cancer. This sequence represents a mutated promoter region used in the  
CC invention to determine the regulatory regions involved in gene  
CC expression, described in the method of the invention

XX  
SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGCGCTG 10  
|||  
Db 8 CGCGCTG 2

RESULT 380  
AAS95992/c  
ID AAS95992 standard; DNA; 10 BP.  
XX  
AC AAS95992;  
XX  
DT 26-FEB-2002 (first entry)  
XX  
DE Human CALM1 gene allele-specific oligonucleotide #101.  
XX  
KW Calmodulin 1; CALM1; human; single nucleotide polymorphism; SNP;  
KW haplotyping; SCYA3; Alzheimer's disease; drug screening;  
KW calcium-dependent signal transduction; PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200179218-A2.  
XX  
PD 25-OCT-2001.  
XX  
PF 09-APR-2001; 2001WO-US011509.  
XX  
PR 12-APR-2000; 2000US-0196340P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Bentivegna SC, Chew A, Choi JY, Koshy B, Stephens JC;  
XX  
DR WPI; 2002-049190/06.  
XX  
PT New calmodulin-1 (CALM-1) isogene polymorphic variants, useful in  
PT expressing CALM1 protein for use in screening for candidate drugs to  
PT treat diseases related to CALM1 activity such as Alzheimer's disease.  
XX  
PS Claim 17; Page 14; 82pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising a sequence  
CC selected from a polymorphic variant of calmodulin 1 (CALM1). The  
CC polymorphic variant comprises an CALM1 isogene defined by a haplotype

CC selected from haplotypes 1-21 given in the specification. The  
CC polymorphisms are useful for studying the biological function of CALM1 as  
CC well as in identifying drugs targeting this protein for the treatment of  
CC a disorder related to its abnormal expression or function. The  
CC polymorphic variants may also be used in screening for compounds  
CC targeting CALM1 to treat a specific condition or disease predicted to be  
CC associated with CALM1 activity. Establishing CALM1 haplotype or haplotype  
CC pair of an individual is useful for improving the efficiency and  
CC reliability of several steps in the discovery and development of drugs  
CC for treating diseases associated with SCYA3 activity, e.g. Alzheimer's  
CC disease and diseases involving defects in calcium-dependent signal  
CC transduction. Haplotyping the CALM1 gene in an individual is also useful  
CC in the design of clinical trials of candidate drugs for treating a  
CC specific condition or disease predicted to be associated with CALM1  
CC activity. AAS95892-AAS96018 represent human CALM1 allele- specific  
CC oligonucleotides and PCR primers of the invention

XX  
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
|||||  
Db 10 TGGCGAA 4

RESULT 381  
ADH22188/c  
ID ADH22188 standard; DNA; 10 BP.  
XX  
AC ADH22188;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Primer extension DNA oligo for detecting CHRNG haplotypes SeqID 57.  
XX  
KW human; primer; PCR; ss; cholinergic receptor, nicotinic, gamma; CHRNG;  
KW haplotype; drug discovery; acetylcholine receptor; AChR;  
KW myasthenia gravis; screening assay.  
XX  
OS Homo sapiens.  
XX  
PN WO200222643-A1.  
XX  
PD 21-MAR-2002.  
XX  
PF 17-SEP-2001; 2001WO-US029206.  
XX  
PR 15-SEP-2000; 2000US-0232807P.  
XX  
PA (GENA-) GENAISSANCE PHARM INC.  
XX  
PI Gilson CR, Koshy B, Kliem SE, Sausker EA;  
XX  
DR WPI; 2002-371968/40.  
XX  
PT New genetic variants of cholinergic receptor, nicotinic, gamma  
PT polypeptide, CHRNG gene useful for therapeutic purposes and for  
PT expressing CHRNG protein useful in identifying drugs to treat myasthenia  
PT gravis.  
XX  
PS Claim 18; SEQ ID NO 57; 107pp; English.  
XX  
CC This invention relates to novel genetic markers and variants of the gene  
CC encoding the cholinergic receptor, nicotinic, gamma polypeptide (CHRNG),  
CC located on chromosome 2q33-p34. Specifically, it refers to a set of  
CC haplotypes in the CHRNG gene, which are useful for improving the  
CC efficiency and output of the drug discovery process by the identification  
CC of drugs that can target the CHRNG protein and treat disorders associated  
CC with its abnormal expression or function. The CHRNG protein is the gamma  
CC subunit of the acetylcholine receptor (AChR), and autoantibodies directed

CC against the embryonic form of AChR play an important role in the  
CC pathogenesis of neonatal myasthenia gravis. As such, the present  
CC invention describes a method for identifying an association between a  
CC trait (such as a clinical response to a drug that targets CHRN1) and a  
CC haplotype or haplotype pair of the CHRN1 gene. Furthermore, it is useful  
CC in screening assays, for the development of diagnostic tests and for  
CC therapeutic treatments of myasthenia gravis using gene therapy. This  
CC oligonucleotide sequence is a human primer extension DNA oligo used for  
CC detecting the CHRN1 haplotypes of the invention.

XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGG 13  
Db 10 GCTGTGG 4

RESULT 382  
ACC41737  
ID ACC41737 standard; DNA; 10 BP.  
XX  
AC ACC41737;  
XX  
DT 21-MAY-2003 (first entry)  
XX  
DE Zinc finger protein DNA-binding domain target sequence SEQ ID NO:284.  
XX  
KW Zinc finger domain; zinc finger; zinc finger binding domain; probe;  
KW chimeric nucleic acid; library; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO2003016571-A1.  
XX  
PD 27-FEB-2003.  
XX  
PF 17-AUG-2002; 2002WO-KR001560.  
XX  
PR 17-AUG-2001; 2001US-0313402P.  
PR 22-APR-2002; 2002US-0374355P.  
XX  
PA (TOOL-) TOOLGEN INC.  
XX  
PI Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;  
XX  
DR WPI; 2003-268344/26.  
XX  
PT New library comprising polypeptides having zinc finger domains, useful  
PT for producing chimeric nucleic acids.

XX  
PS Claim 40; Page 106; 234pp; English.  
XX  
CC The present invention describes a library comprising polypeptides. Each  
CC polypeptide comprises a first or second zinc finger domain. The domains  
CC of each polypeptide are identical to a zinc finger domain from a  
CC naturally occurring protein and either do not occur in the same naturally  
CC occurring protein or occur in the same naturally occurring protein in a  
CC different configuration than in the polypeptide. The domains vary among  
CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)  
CC generating an artificial zinc finger polypeptide that specifically binds  
CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc  
CC finger polypeptide that specifically recognises a target DNA site. The  
CC library can be used for producing chimeric nucleic acids. ACC41551 to  
CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid  
CC sequences given in the exemplification of the present invention

XX  
SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCG 7  
Db 3 GGTGCG 9

RESULT 383  
ABT14391/C  
ID ABT14391 standard; DNA; 10 BP.

XX  
AC ABT14391;  
XX  
DT 20-FEB-2003 (first entry)  
XX

DE Nucleic acid PCR amplification method-related RAPD PCR primer #161.  
XX  
KW Nucleic acid amplification; nucleic acid analysis; ss;  
KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

XX Unidentified.

XX WO200281743-A2.

XX 17-OCT-2002.

XX 28-MAR-2002; 2002WO-GB001489.

XX 02-APR-2001; 2001GB-00008182.

XX (HAMI/) HAMILL B.

XX Hamill B;

XX WPI; 2003-075484/07.

XX  
PT Amplification of nucleotide sequences from polynucleotides by chain  
PT extension of oligonucleotide primers, comprises 2 oligonucleotides in  
PT solution, 2 attached to supports and both share complementary sequences.

XX Disclosure; Fig 17; 60pp; English.

XX  
CC The invention comprises a method for the PCR amplification of nucleic  
CC acids. The method involves a set of primers, where two of the primers are  
CC in solution and at least two other primers are attached to a solid  
CC support. The method of the invention can be used for the analysis of a  
CC nucleic acid or a mixture of nucleic acids, including: single-stranded  
CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The  
CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)  
CC PCR primer of the invention

XX Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGG 13  
Db 7 GCTGTGG 1

RESULT 384  
ADA62122  
ID ADA62122 standard; DNA; 10 BP.

XX ADA62122;

XX 20-NOV-2003 (first entry)

XX Zinc finger target sequence DNA #77.

KW ds; target sequence; zinc finger protein;  
KW multi-finger zinc finger protein; improved affinity;  
KW improved specificity; enhanced biological activity.  
XX  
OS Synthetic.  
XX  
PN US2003068675-A1.  
XX  
PD 10-APR-2003.  
XX  
PF 20-NOV-2001; 2001US-00990186.  
XX  
PR 24-MAR-1999; 99US-0126238P.  
PR 24-MAR-1999; 99US-0126239P.  
PR 30-JUL-1999; 99US-0146595P.  
PR 30-JUL-1999; 99US-0146615P.  
PR 23-MAR-2000; 2000US-00535008.  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (LIUQ/) LIU Q.  
XX  
PI Liu Q;  
XX  
DR WPI; 2003-567233/53.  
XX  
CC The invention relates to a method of designing a zinc finger protein. The  
CC method is useful for designing a zinc finger protein. The method provides  
CC multi-finger zinc finger proteins with improved affinity and specificity  
CC for their target sequences, as well as enhanced biological activity. The  
CC present sequence represents a zinc finger protein DNA target sequence.  
XX  
SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 12 GGCGAAG 18  
Db |||||||  
4 GGCGAAG 10  
  
RESULT 385  
ADAC3307  
ID ADA63307 standard; DNA; 10 BP.  
XX  
AC ADA63307;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Zinc finger target sequence DNA #329.  
XX  
KW ds; target sequence; zinc finger protein;  
KW multi-finger zinc finger protein; improved affinity;  
KW improved specificity; enhanced biological activity.  
XX  
OS Synthetic.  
XX  
PN US2003068675-A1.  
XX  
PD 10-APR-2003.  
XX  
PF 20-NOV-2001; 2001US-00990186.  
XX  
PR 24-MAR-1999; 99US-0126238P.  
PR 24-MAR-1999; 99US-0126239P.  
PR 30-JUL-1999; 99US-0146595P.  
PR 30-JUL-1999; 99US-0146615P.

PR 30-JUL-1999; 99US-0146615P.  
PR 23-MAR-2000; 2000US-00535008.  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (LIUQ/) LIU Q.  
XX  
PI Liu Q;  
XX  
DR WPI; 2003-567233/53.  
XX  
PT Designing zinc finger protein that has three zinc fingers from N-terminus  
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target  
PT site, by selecting zinc fingers that bind their respective subsites.  
XX  
PS Disclosure; Page 18; 34pp; English.  
XX  
CC The invention relates to a method of designing a zinc finger protein. The  
CC method is useful for designing a zinc finger protein. The method provides  
CC multi-finger zinc finger proteins with improved affinity and specificity  
CC for their target sequences, as well as enhanced biological activity. The  
CC present sequence represents a zinc finger protein DNA target sequence.  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db |||||||  
4 GCTGTGG 10  
  
RESULT 386  
ADA63696  
ID ADA63696 standard; DNA; 10 BP.  
XX  
AC ADA63696;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Zinc finger target sequence DNA #460.  
XX  
KW ds; target sequence; zinc finger protein;  
KW multi-finger zinc finger protein; improved affinity;  
KW improved specificity; enhanced biological activity.  
XX  
OS Synthetic.  
XX  
PN US2003068675-A1.  
XX  
PD 10-APR-2003.  
XX  
PF 20-NOV-2001; 2001US-00990186.  
XX  
PR 24-MAR-1999; 99US-0126238P.  
PR 24-MAR-1999; 99US-0126239P.  
PR 30-JUL-1999; 99US-0146595P.  
PR 30-JUL-1999; 99US-0146615P.  
PR 23-MAR-2000; 2000US-00535008.  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (LIUQ/) LIU Q.  
XX  
PI Liu Q;  
XX  
DR WPI; 2003-567233/53.  
XX  
PT Designing zinc finger protein that has three zinc fingers from N-terminus  
PT and C-terminus that bind to subsites in 3' to 5' direction, in a target  
PT site, by selecting zinc fingers that bind their respective subsites.  
XX  
PS Disclosure; Page 20; 34pp; English.





KW improved specificity; enhanced biological activity.

XX Synthetic.

OS US2003068675-A1.

PN 10-APR-2003.

XX 20-NOV-2001; 2001US-00990186.

PF 24-MAR-1999; 99US-0126238P.

XX 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX (LIUQ/) LIU Q.

PA Liu Q;

XX WPI; 2003-567233/53.

DR Designing zinc finger protein that has three zinc fingers from N-terminus

PT and C-terminus that bind to subsites in 3' to 5' direction, in a target

PT site, by selecting zinc fingers that bind their respective subsites.

XX Disclosure; Page 20; 34pp; English.

XX The invention relates to a method of designing a zinc finger protein. The

CC method is useful for designing a zinc finger protein. The method provides

CC multi-finger zinc finger proteins with improved affinity and specificity

CC for their target sequences, as well as enhanced biological activity. The

CC present sequence represents a zinc finger protein DNA target sequence.

XX Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7

Db 3 GGTCGCG 9

RESULT 390

ADB81067

ID ADB81067 standard; DNA; 10 BP.

XX ADB81067;

AC 04-DEC-2003 (first entry)

XX LINE retro-position related SART1 oligo, SEQ ID No 27.

DE RNA retro-position; 3' UTR; LINE; APE domain; retro-transposition;

XX endonuclease domain; chromosome; gene therapy; gene transfer; ss.

OS Unidentified.

XX WO2003064644-A1.

PN 07-AUG-2003.

PD 26-NOV-2002; 2002WO-JP012317.

XX 31-JAN-2002; 2002JP-00024226.

PR (DNAV-) Dनावेक रेस इन्क.

XX Fujiwara H, Takahashi H, Hasegawa M;

PI

DR WPI; 2003-627609/59.

XX LINE retro-position by trans-complementation for transferring targeted,

PT specific gene or nucleic acid of e.g. endonuclease domain via

PT substitution to chromosome using virus vector, applicable in gene

PT therapy.

XX Example 5; Fig 3; 96pp; Japanese.

PS The invention relates to a novel RNA retro-position comprising the

CC transcription of an RNA containing a 3' UTR fragment of a LINE in cells;

CC and trans-positioning the ORF protein of such LINE after expressing from

CC other than the RNA. The invention further comprises a similar method in

CC which the transcription of an RNA containing a 3' UTR fragment of an APE

CC domain-carrying type site-specific LINE in cells, and expressing the ORF

CC protein of the LINE in such cells; or transcription of an RNA containing

CC 3' UTR fragment of a LINE in cells, and expressing ORF protein in such

CC cells thereby modifying a retro-transposition target site of a LINE by

CC substituting the endonuclease domain of the LINE by that of another LINE

CC via ORF protein of such LINE. The invention also includes a retro-

CC transposition vector with RNA encoding the 3' UTR fragment of a LINE but

CC not expressing the encoded ORF of the LINE; a vector encoding a protein

CC for substitution of the endonuclease domain of an encoded ORF protein in

CC the site-specific LINE by the endonuclease domain of the encoded ORF

CC protein in another LINE; and a kit for gene transfer through retro-

CC transposition of an RNA. The method is useful for transferring targeted,

CC specific genes or nucleic acids of an endonuclease domain via

CC substitution to a chromosome using a virus vector, which is applicable in

CC gene therapy. The retro-transposition in the host is highly efficient by

CC targeting specifically at LINE, and with little damage to the host due to

CC the gene transfer. This polynucleotide sequence represents an

CC oligonucleotide used in the exemplification of the invention.

XX Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

SQ Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17

Db 1 TGGCGAA 7

RESULT 391

ADE14136/C

ID ADE14136 standard; DNA; 10 BP.

XX ADE14136;

AC 29-JAN-2004 (first entry)

XX Optineurin promoter motif, repeat element or regulatory region #245.

DE Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;

XX SNP; glaucoma; progressive ocular hypertensive disorder;

KW glaucoma related disorder; motif; repeat element; regulatory region.

XX Homo sapiens.

OS US2003190617-A1.

XX 09-OCT-2003.

PN 06-MAR-2002; 2002US-00091281.

XX 06-MAR-2002; 2002US-00091281.

PR (SIEE/) SI E.

XX (RAYM/) RAYMOND V.

PA (MORI/) MORISSETTE J.

XX Raymond V, Morissette J, Si E;

PI

XX WPI; 2003-864168/80.

XX

PT New nucleic acid sequences of the optineurin gene are useful to detect

PT polymorphisms particularly single nucleotide polymorphisms in the

PT optineurin promoter to diagnose, prognose and treat glaucoma and related

PT disorders.

XX

PS Claim 11; SEQ ID NO 247; 159pp; English.

XX

CC The invention relates to an isolated nucleic acid (N1) comprising at

CC least 20 but not more than 1500 consecutive nucleotides of the optineurin

CC promoter appearing as ADE13890. Also included are the optineurin promoter

CC operably linked to a heterologous nucleic acid, a nucleic acid capable of

CC detecting a single nucleotide polymorphism (SNP) in the optineurin

CC promoter, a host cell comprising the promoter operably linked to a

CC heterologous sequence, diagnosing or prognosing glaucoma in a sample

CC obtained from a cell or bodily fluid (comprising detecting a polymorphism

CC in a promoter region of the optineurin gene, associated with a glaucoma

CC phenotype), detecting a SNP sequence variation in a sample containing

CC DNA, detecting the presence of an optineurin promoter sequence variation

CC in a sample containing DNA, determining the presence or increased

CC susceptibility to glaucoma or to a progressive ocular hypertensive

CC disorder resulting in loss of visual field in a patient (or the severity

CC or progression of glaucoma in a patient, comprising providing

CC amplification reaction primers that direct amplification of a selected

CC nucleic acid region containing the variation within the optineurin

CC promoter and amplifying the DNA) and detecting a polymorphism (comprising

CC obtaining a sample containing human genomic DNA, providing a nucleic acid

CC capable of detecting a SNP located within an optineurin promoter, and

CC detecting the polymorphism). The invention is used to diagnose and

CC prognose glaucoma and also to treat glaucoma related disorders. The

CC present sequence is an optineurin promoter motif, repeat element or

CC putative regulatory region.

XX

SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TGGCGAA 17

Db 9 TGGCGAA 3

RESULT 392

ADM22181

ID ADM22181 standard; DNA; 10 BP.

XX

AC ADM22181;

XX

DT 20-MAY-2004 (first entry)

XX

DE Synthetic zinc finger protein target DNA #447.

XX

KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.

XX

OS Unidentified.

XX

PN US2003104526-A1.

XX

PD 05-JUN-2003.

XX

PF 20-NOV-2001; 2001US-00989994.

XX

PR 24-MAR-1999; 99US-0126238P.

PR 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX

PA (LIUQ/) LIU Q.

XX

PI Liu Q;

XX

DR WPI; 2003-843091/78.

XX

PT New zinc finger protein used for recognizing triplet target subsites

PT having nucleotide G in 5'-most position of subsite, that has been

PT optimized with respect to location of subsite within target site.

XX

PS Example 6; SEQ ID NO 1654; 48pp; English.

XX

CC The invention describes a new zinc finger protein that binds to a target

CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,

CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site

CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third

CC (S3) target subsites. The zinc finger proteins can be used for

CC recognising triplet target subsites having the nucleotide G in the 5' -

CC most position of the subsite, that has been optimised with respect to the

CC location of the subsite within the target site. This sequence represents

CC the target polynucleotide of a synthetic zinc finger protein of the

CC invention.

XX

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCGCG 7

Db 3 GGTCGCG 9

RESULT 393

ADM22194

ID ADM22194 standard; DNA; 10 BP.

XX

AC ADM22194;

XX

DT 20-MAY-2004 (first entry)

XX

DE Synthetic zinc finger protein target DNA #460.

XX

KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.

XX

OS Unidentified.

XX

PN US2003104526-A1.

XX

PD 05-JUN-2003.

XX

PF 20-NOV-2001; 2001US-00989994.

XX

PR 24-MAR-1999; 99US-0126238P.

PR 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX

PA (LIUQ/) LIU Q.

XX

PI Liu Q;

XX

DR WPI; 2003-843091/78.

XX

PT New zinc finger protein used for recognizing triplet target subsites

PT having nucleotide G in 5'-most position of subsite, that has been

PT optimized with respect to location of subsite within target site.

XX

PS Example 6; SEQ ID NO 1667; 48pp; English.

XX

PA (LIUQ/) LIU Q.

XX

PI Liu Q;

XX

DR WPI; 2003-843091/78.

XX

PT New zinc finger protein used for recognizing triplet target subsites

PT having nucleotide G in 5'-most position of subsite, that has been

PT optimized with respect to location of subsite within target site.

XX

PS Example 6; SEQ ID NO 1654; 48pp; English.

XX

CC The invention describes a new zinc finger protein that binds to a target

CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,

CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site

CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third

CC (S3) target subsites. The zinc finger proteins can be used for

CC recognising triplet target subsites having the nucleotide G in the 5' -

CC most position of the subsite, that has been optimised with respect to the

CC location of the subsite within the target site. This sequence represents

CC the target polynucleotide of a synthetic zinc finger protein of the

CC invention.

XX

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCGCG 7

Db 3 GGTCGCG 9

RESULT 393

ADM22194

ID ADM22194 standard; DNA; 10 BP.

XX

AC ADM22194;

XX

DT 20-MAY-2004 (first entry)

XX

DE Synthetic zinc finger protein target DNA #460.

XX

KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.

XX

OS Unidentified.

XX

PN US2003104526-A1.

XX

PD 05-JUN-2003.

XX

PF 20-NOV-2001; 2001US-00989994.

XX

PR 24-MAR-1999; 99US-0126238P.

PR 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX

PA (LIUQ/) LIU Q.

XX

PI Liu Q;

XX

DR WPI; 2003-843091/78.

XX

PT New zinc finger protein used for recognizing triplet target subsites

PT having nucleotide G in 5'-most position of subsite, that has been

PT optimized with respect to location of subsite within target site.

XX

PS Example 6; SEQ ID NO 1667; 48pp; English.

XX

CC The invention describes a new zinc finger protein that binds to a target  
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,  
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site  
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third  
CC (S3) target subsites. The zinc finger proteins can be used for  
CC recognising triplet target subsites having the nucleotide G in the 5'-  
CC most position of the subsite, that has been optimised with respect to the  
CC location of the subsite within the target site. This sequence represents  
CC the target polynucleotide of a synthetic zinc finger protein of the  
CC invention.

XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGCG 7  
|||  
Db 3 GGTCGCG 9

RESULT 394  
ADM20326  
ID ADM20326 standard; DNA; 10 BP.

XX  
AC ADM20326;

DT 20-MAY-2004 (first entry)

XX Synthetic zinc finger protein target DNA #77.

DE zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.

XX Unidentified.

OS  
XX US2003104526-A1.

XX  
PD 05-JUN-2003.

XX  
PF 20-NOV-2001; 2001US-00989994.

XX  
PR 24-MAR-1999; 99US-0126238P.

PR 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX  
DR (LIUQ/) LIU Q.

XX  
PI Liu Q;

XX  
XX WPI; 2003-843091/78.

XX New zinc finger protein used for recognizing triplet target subsites

PT having nucleotide G in 5'-most position of subsite, that has been

PT optimized with respect to location of subsite within target site.

XX  
PS Example 6; SEQ ID NO 93; 48pp; English.

XX  
CC The invention describes a new zinc finger protein that binds to a target  
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,  
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site  
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third  
CC (S3) target subsites. The zinc finger proteins can be used for  
CC recognising triplet target subsites having the nucleotide G in the 5'-  
CC most position of the subsite, that has been optimised with respect to the  
CC location of the subsite within the target site. This sequence represents  
CC the target polynucleotide of a synthetic zinc finger protein of the  
CC invention.

XX  
SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCGAAG 18  
|||||  
Db 4 GGCGAAG 10

RESULT 395  
ADM20325  
ID ADM20325 standard; DNA; 10 BP.

XX  
AC ADM20325;

XX  
DT 20-MAY-2004 (first entry)

XX Synthetic zinc finger protein target DNA #76.

XX zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.

XX Unidentified.

XX  
PN US2003104526-A1.

XX  
PD 05-JUN-2003.

XX  
PF 20-NOV-2001; 2001US-00989994.

XX  
PR 24-MAR-1999; 99US-0126238P.

PR 24-MAR-1999; 99US-0126239P.

PR 30-JUL-1999; 99US-0146595P.

PR 30-JUL-1999; 99US-0146615P.

PR 23-MAR-2000; 2000US-00535008.

PR 20-NOV-2000; 2000US-00716637.

XX  
PA (LIUQ/) LIU Q.

XX  
PI Liu Q;

XX  
DR WPI; 2003-843091/78.

XX New zinc finger protein used for recognizing triplet target subsites

PT having nucleotide G in 5'-most position of subsite, that has been

PT optimized with respect to location of subsite within target site.

XX  
PS Example 6; SEQ ID NO 92; 48pp; English.

XX  
CC The invention describes a new zinc finger protein that binds to a target  
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,  
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site  
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third  
CC (S3) target subsites. The zinc finger proteins can be used for  
CC recognising triplet target subsites having the nucleotide G in the 5'-  
CC most position of the subsite, that has been optimised with respect to the  
CC location of the subsite within the target site. This sequence represents  
CC the target polynucleotide of a synthetic zinc finger protein of the  
CC invention.

XX  
SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GGCGAAG 18  
|||||  
Db 4 GGCGAAG 10

RESULT 396  
ADM21511

ID ADM21511 standard; DNA; 10 BP.  
AC ADM21511;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Synthetic zinc finger protein target DNA #329.  
XX  
KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.  
XX  
OS Unidentified.  
XX  
PN US2003104526-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 20-NOV-2001; 2001US-00989994.  
XX  
PR 24-MAR-1999; 99US-0126238P.  
PR 24-MAR-1999; 99US-0126239P.  
PR 30-JUL-1999; 99US-0146595P.  
PR 30-JUL-1999; 99US-0146615P.  
PR 23-MAR-2000; 2000US-00535008.  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (LIUQ/) LIU Q.  
XX  
PI Liu Q;  
XX  
DR WPI; 2003-843091/78.  
XX  
PT New zinc finger protein used for recognizing triplet target subsites  
PT having nucleotide G in 5'-most position of subsite, that has been  
PT optimized with respect to location of subsite within target site.  
XX  
PS Example 6; SEQ ID NO 1278; 48pp; English.  
XX  
CC The invention describes a new zinc finger protein that binds to a target  
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,  
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site  
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third  
CC (S3) target subsites. The zinc finger proteins can be used for  
CC recognising triplet target subsites having the nucleotide G in the 5'-  
CC most position of the subsite, that has been optimised with respect to the  
CC location of the subsite within the target site. This sequence represents  
CC the target polynucleotide of a synthetic zinc finger protein of the  
CC invention.  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 7 GCTGTGG 13  
Db |||||  
4 GCTGTGG 10  
RESULT 397  
ADM22180  
ID ADM22180 standard; DNA; 10 BP.  
XX  
AC ADM22180;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Synthetic zinc finger protein target DNA #446.  
XX  
KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.  
XX  
OS Unidentified.  
XX

PN US2003104526-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 20-NOV-2001; 2001US-00989994.  
XX  
PR 24-MAR-1999; 99US-0126238P.  
PR 24-MAR-1999; 99US-0126239P.  
PR 30-JUL-1999; 99US-0146595P.  
PR 30-JUL-1999; 99US-0146615P.  
PR 23-MAR-2000; 2000US-00535008.  
PR 20-NOV-2000; 2000US-00716637.  
XX  
PA (LIUQ/) LIU Q.  
XX  
PI Liu Q;  
XX  
DR WPI; 2003-843091/78.  
XX  
PT New zinc finger protein used for recognizing triplet target subsites  
PT having nucleotide G in 5'-most position of subsite, that has been  
PT optimized with respect to location of subsite within target site.  
XX  
PS Example 6; SEQ ID NO 1653; 48pp; English.  
XX  
CC The invention describes a new zinc finger protein that binds to a target  
CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,  
CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site  
CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third  
CC (S3) target subsites. The zinc finger proteins can be used for  
CC recognising triplet target subsites having the nucleotide G in the 5'-  
CC most position of the subsite, that has been optimised with respect to the  
CC location of the subsite within the target site. This sequence represents  
CC the target polynucleotide of a synthetic zinc finger protein of the  
CC invention.  
XX  
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTGCGG 7  
Db |||||  
3 GGTGCGG 9  
RESULT 398  
ADH57701/c  
ID ADH57701 standard; DNA; 10 BP.  
XX  
AC ADH57701;  
XX  
DT 25-MAR-2004 (first entry)  
XX  
DE Extendable oligo E190 for DNA sequencing and PCR amplification.  
XX  
KW ss; primer library; extendable oligo; EO; ligation chain reaction; LCR;  
KW rolling circle amplification; strand displacement amplification;  
KW isothermal DNA amplification; biotechnology; agriculture;  
KW medical research; 2,4 diaminopurine nucleotide analogue; PCR; primer.  
OS Synthetic.  
XX  
PN WO2003093500-A1.  
XX  
PD 13-NOV-2003.  
XX  
PF 24-DEC-2002; 2002WO-AU001763.  
XX  
PR 01-MAY-2002; 2002AU-00002045.  
XX  
PA (NUCL-) NUCLEICS PTY LTD.



XX Tillet D, Thomas T;  
PI WPI; 2004-053046/05.  
DR  
XX  
PT Increasing the affinity of an extendable oligonucleotide (EO) for a  
PT target nucleic acid, for providing primers having improved specificity,  
PT comprises hybridization of the EO to a template oligonucleotide (TO) and  
PT extension of the EO.  
XX  
PS Example 9; Page 41; 85pp; English.  
XX  
CC This invention relates to a novel method for the optimisation of primer  
CC libraries. Specifically, it refers to increasing the affinity of short  
CC oligonucleotide primers, also known as extendable oligos (EOs), for their  
CC template sequences. The present invention describes improved methods for  
CC sequencing and the linear and exponential amplification of DNA that can  
CC be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle  
CC amplification, strand displacement amplification and isothermal DNA  
CC amplification. Accordingly, these extendable oligos with improved  
CC specificity and affinity are particularly important in fields ranging  
CC from biotechnology and agriculture to medical research. This  
CC oligonucleotide sequence is an extendable oligonucleotide that includes  
CC an adenine replacement 2,4 diaminopurine nucleotide analogue in the catch  
CC region, and is useful for both DNA sequencing reactions and PCR  
CC amplification in an exemplification of the invention.  
XX  
SQ Sequence 10 BP; 0 A; 5 C; 2 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 GCGAAGG 19  
Db 10 GCGAAGG 4  
  
RESULT 399  
AD113679  
ID AD113679 standard; DNA; 10 BP.  
XX  
AC AD113679;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Extracellular tumour endothelial marker standard tag SEQ ID NO:54.  
XX  
KW tumour endothelial marker; TEM; endothelial cell regulation;  
KW neoangiogenesis inhibition; neoangiogenesis screening;  
KW neoangiogenesis promotion; neoangiogenesis; tumour; wound healing;  
KW cytostatic; vulnerary; human; standard tag; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO2004005883-A2.  
XX  
PD 15-JAN-2004.  
XX  
PF 02-JUL-2003; 2003WO-US016250.  
XX  
PR 02-JUL-2002; 2002US-0393023P.  
PR 01-APR-2003; 2003US-0458964P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
PI St Croix B, Kinzler KW, Vogelstein B;  
XX  
DR WPI; 2004-142995/14.  
XX  
PT Use of tumor endothelial marker proteins for inhibiting neoangiogenesis,  
PT screening for neoangiogenesis, promoting neoangiogenesis, identifying

PT candidate drugs for treating tumors or promoting wound healing.  
XX  
PS Disclosure; SEQ ID NO 54; 113pp; English.  
XX  
CC The present invention describes the use of tumour endothelial marker  
CC (TEM) proteins for identifying a ligand involved in endothelial cell  
CC regulation, inhibiting neoangiogenesis, screening for neoangiogenesis,  
CC promoting neoangiogenesis, identifying candidate drugs for treating  
CC tumours or promoting wound healing or identifying endothelial cells. Also  
CC described: (1) identification of a ligand involved in endothelial cell  
CC regulation; (2) inhibiting neoangiogenesis; (3) promoting neoangiogenesis  
CC in a patient; (4) screening for neoangiogenesis in a patient; (5)  
CC identify candidate drugs for treating tumours or promoting wound healing;  
CC and (6) identifying endothelial cells. TEM proteins have cytostatic and  
CC vulnerary activities. The TEM proteins are useful for identifying a  
CC ligand involved in endothelial cell regulation, inhibiting  
CC neoangiogenesis, screening for neoangiogenesis, promoting  
CC neoangiogenesis, identifying candidate drugs for treating tumours or  
CC promoting wound healing or identifying endothelial cells. The present  
CC sequence represents an extracellular tumour endothelial marker standard  
CC tag oligonucleotide, which is used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db 1 GCTGTGG 7  
  
RESULT 400  
ADL70389/c  
ID ADL70389 standard; DNA; 10 BP.  
XX  
AC ADL70389;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Enhancer sequence for nucleic acid detection by tail cleavage assay.  
XX  
KW Nucleic acid detection; Tail cleavage assay; ss.  
XX  
OS Synthetic.  
XX  
PN WO2004018626-A2.  
XX  
PD 04-MAR-2004.  
XX  
PF 20-AUG-2003; 2003WO-US026133.  
XX  
PR 21-AUG-2002; 2002US-0405642P.  
XX  
PA (EPOC-) EPOCH BIOSCIENCES INC.  
XX  
PI Kutyaivin IV, Milesi D, Hoekstra M;  
XX  
DR WPI; 2004-248069/23.  
XX  
PT Detecting target nucleic acid in sample, comprises contacting sample with  
PT apurinic/aprimidinic site probe and endonuclease, incubating mixture to  
PT cleave phosphodiester bond and detecting reporter group.  
XX  
PS Example 3; Page 34; 61pp; English.  
XX  
CC The present invention provides a novel method for detection and/or  
CC genotyping of nucleic acids that utilises the specificity of an abasic  
CC (apurinic/aprimidinic) (AP) endonuclease. An AP site probe is used that  
CC comprises an oligonucleotide which hybridises to a target nucleic acid  
CC and a functional tail composed of a detectable reporter group and an AP

CC endonuclease cleavage site. The functional tail is attached through a  
CC phosphodiester bond of a phosphate group to the 3' terminal nucleotide of  
CC the oligonucleotide, and the reporter group is not detected when the  
CC functional tail is attached to the oligonucleotide. Methods of detecting  
CC a target nucleic acid involve contacting the sample with an AP site probe  
CC and an AP endonuclease, incubating under conditions that allow the AP  
CC endonuclease to cleave the phosphodiester bond, and detecting the  
CC reporter group on the cleaved functional tail. The method is exquisitely  
CC sensitive to the detection of single base pair mismatches between the  
CC probe and target because the AP endonuclease preferentially cleaves the  
CC phosphodiester bond when the oligonucleotide is hybridised with a fully  
CC complementary nucleic acid sequence. The present sequence is that of an  
CC enhancer sequence, which was used in an example from the invention  
CC illustrating the substrate specificity of Escherichia coli endonuclease  
CC IV. The enhancer hybridises to the 5' end of a target nucleic acid  
CC ADL70387 and is used to support the tail cleavage reaction.

SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCG 15  
Db 8 TGTGGCG 2

RESULT 401  
ADN36844/C  
ID ADN36844 standard; RNA; 10 BP.

XX AC ADN36844;

XX DT 15-JUL-2004 (first entry)

DE West Nile virus detection-related oligonucleotide probe SeqID166.

XX hybridisation assay probe; nucleic acid detection;  
KW target-complementary sequence; flavivirus; West Nile virus; WNV;  
KW RNA virus; infection; meningitis; encephalitis;  
KW high throughput screening; probe; ss.

OS West Nile virus.

XX FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"

XX PN WO2004036190-A2.

XX PD 29-APR-2004.

XX PF 10-OCT-2003; 2003WO-US033639.

XX PR 16-OCT-2002; 2002US-0418891P.

XX PR 25-NOV-2002; 2002US-0429006P.

XX PR 24-FEB-2003; 2003US-0449810P.

XX PA (GENP-) GEN-PROBE INC.

XX PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;

XX DR WPI; 2004-389590/36.

XX New hybridization assay probe comprising target-complementary sequence of  
PT bases, useful in detecting flavivirus, e.g. West Nile virus.  
XX Claim 43; SEQ ID NO 166; 135pp; English.  
PS This invention relates to a novel hybridisation assay probe, for

CC detecting a nucleic acid, which is a probe sequence that comprises a  
CC target-complementary sequence of bases, and optionally one or more base  
CC sequences that are not complementary to the nucleic acid that is to be  
CC detected. The hybridisation assay probes and the kits are useful in  
CC detecting and amplifying a target nucleic acid sequence, for example  
CC flavivirus like West Nile virus, that may be present in a biological  
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects  
CC birds and culex mosquitoes, with humans and horses serving as incidental  
CC hosts. Infection of humans can lead to meningitis or encephalitis. The  
CC invention may allow for accurate and efficient high throughput screening.  
CC The present sequence is that of an oligonucleotide probe which is related  
CC to the invention.

SQ Sequence 10 BP; 0 A; 4 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGAAGG 19  
Db 10 GCGAAGG 4

RESULT 402  
ADR16068  
ID ADR16068 standard; DNA; 10 BP.

XX AC ADR16068;

XX DT 04-NOV-2004 (first entry)

DE Loquat crown-gall disease resistance gene-specific PCR primer #1.

XX loquat; crown-gall disease resistance gene; marker;

KW crown-gall disease resistant seedling; PCR; primer; ss.

XX Eriobotrya japonica.

XX PN JP2004229571-A.

XX PD 19-AUG-2004.

XX PF 30-JAN-2003; 2003JP-00022874.

XX PR 30-JAN-2003; 2003JP-00022874.

XX PA (NAGA-) NAGASAKI KEN PREFECTURE.

XX DR WPI; 2004-586543/57.

XX Novel loquat crown-gall disease resistant gene, useful as a marker for  
PT identifying loquat plant resistant to crown-gall disease.

XX PS Claim 3; SEQ ID NO 3; 9pp; Japanese.

XX The invention comprises two DNA sequences of a loquat crown-gall disease  
CC resistance gene, the invention also comprises PCR primers that are  
CC specific to this gene. The loquat crown-gall disease resistance gene DNA  
CC sequences of the invention are useful as a marker for identifying loquat  
CC crown-gall disease resistant seedlings. The present DNA sequence  
CC represents a PCR primer that is specific for the loquat crown-gall  
CC disease resistance gene of the invention.

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 GCGAAGG 19  
Db 2 GCGAAGG 8

RESULT 403  
AD27959/c  
ID ADR27959 standard; DNA; 10 BP.  
XX  
AC ADR27959;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Murine VE-statin exon 7 3' oligonucleotide.  
XX  
KW Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;  
VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;  
KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; mouse;  
KW ds.  
XX  
OS Mus musculus.  
XX  
PN FR2851249-A1.  
XX  
PD 20-AUG-2004.  
XX  
PF 17-FEB-2003; 2003FR-00001875.  
XX  
PR 17-FEB-2003; 2003FR-00001875.  
XX  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
XX  
PI Soncin F, Mattot V;  
XX  
DR WPI; 2004-618122/60.  
XX  
XX  
PT Using VE-statins to inhibit recruitment of perivascular smooth muscle  
PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,  
PT related nucleic acids and antibodies.  
XX  
PS Example 3; Page 11; 63pp; French.  
XX  
CC The present invention relates to a method for preparing a composition for  
CC inhibiting recruitment of perivascular cells of smooth muscle type using  
CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,  
CC soluble factors secreted by endothelial cells of the blood vessels, block  
CC recruitment of perivascular smooth muscle cells (but do not affect their  
CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide  
CC fragments, nucleic acids encoding them and vectors containing this  
CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis  
CC and restenosis, including in gene therapy. The VE-statin nucleic acids  
CC can also be used to produce transgenic animals (for studying the VE-  
CC statin proteins and genes); the VE-statins are used to screen for  
CC specific (ant)agonists, and antibodies specific for VE-statins can be  
CC used to determine expression profiles, particularly for diagnosis of  
CC diseases associated with VE-statins. The present sequence was used to  
CC illustrate the structure of the murine VE-statin gene.  
XX  
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 7 GCTGTGG 13  
Db |||||  
8 GCTGTGG 2  
  
RESULT 404  
ADU18248/c  
ID ADU18248 standard; DNA; 10 BP.  
XX  
AC ADU18248;  
XX  
DT 13-JAN-2005 (first entry)

XX  
DE Hypoxia-related tumorigenesis-related SAGE tag #39.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004092198-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 09-APR-2004; 2004WO-US011087.  
XX  
PR 09-APR-2003; 2003US-0461712P.  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
PI Nacht M;  
XX  
DR WPI; 2004-758333/74.  
XX  
XX  
PT Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX  
PS Disclosure; Page 57; 100pp; English.  
XX  
CC The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 8 CTGTGGC 14  
Db |||||  
10 CTGTGGC 4  
  
RESULT 405  
ADU19824  
ID ADU19824 standard; DNA; 10 BP.  
XX  
AC ADU19824;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Hypoxia-related tumorigenesis-related SAGE tag #1615.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.  
XX  
PN WO2004092198-A2.  
XX  
PD 28-OCT-2004.  
XX  
PF 09-APR-2004; 2004WO-US011087.  
XX  
PR 09-APR-2003; 2003US-0461712P.

XX (GENZ ) GENZYME CORP.  
XX Nacht M;  
XX WPI; 2004-758333/74.  
XX Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX  
PS Disclosure; Page 88; 100pp; English.  
XX  
XX The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX  
XX Sequence 10 BP; 0 A; 1 C; 6 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 TGTGGCG 15  
Db | | | | |  
1 TGTGGCG 7  
RESULT 406  
ADU18636/c  
ID ADU18636 standard; DNA; 10 BP.  
XX  
AC ADU18636;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Hypoxia-related tumorigenesis-related SAGE tag #427.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.  
XX  
XX WO2004092198-A2.  
PN  
XX  
AC ADU18636;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Hypoxia-related tumorigenesis-related SAGE tag #427.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.  
XX  
XX WO2004092198-A2.  
PN  
XX  
PD 28-OCT-2004.  
XX  
XX 09-APR-2004; 2004WO-US011087.  
PF  
XX  
XX 09-APR-2003; 2003US-0461712P.  
PR  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
XX Nacht M;  
XX WPI; 2004-758333/74.  
DR  
XX Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX  
PS Disclosure; Page 64; 100pp; English.  
XX  
XX The invention comprises a method of screening for candidate agents

CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 8 CTGTGGC 14  
Db | | | | |  
9 CTGTGGC 3  
RESULT 407  
ADU18717/c  
ID ADU18717 standard; DNA; 10 BP.  
XX  
AC ADU18717;  
XX  
DT 13-JAN-2005 (first entry)  
XX  
DE Hypoxia-related tumorigenesis-related SAGE tag #508.  
XX  
KW screening; hypoxia-related tumorigenesis;  
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.  
XX  
OS Unidentified.  
XX  
XX WO2004092198-A2.  
PN  
XX  
PD 28-OCT-2004.  
XX  
XX 09-APR-2004; 2004WO-US011087.  
PF  
XX  
XX 09-APR-2003; 2003US-0461712P.  
PR  
XX  
PA (GENZ ) GENZYME CORP.  
XX  
XX Nacht M;  
XX WPI; 2004-758333/74.  
DR  
XX Identifying agents that alter biological activity of a polypeptide  
PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis  
PT comprises contacting an agent with a target cell and monitoring activity  
PT of expressed product.  
XX  
XX Disclosure; Page 65; 100pp; English.  
XX  
XX The invention comprises a method of screening for candidate agents  
CC capable of altering the biological activity of a protein encoded by a  
CC nucleotide involved in hypoxia-related tumorigenesis. The method of the  
CC invention involves: contacting a test agent with a target cell expressing  
CC the nucleotide, and monitoring the activity of the expressed protein  
CC product; if the test agent modifies the activity of the expressed protein  
CC then this is a candidate agent. The method of the invention is useful for  
CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing  
CC or treating tumours. The present DNA sequence represents a SAGE tag that  
CC was used in the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 8 CTGTGGC 14  
Db 7 CTGTGGC 1

RESULT 408  
ADU66846/c  
ID ADU66846 standard; DNA; 10 BP.  
XX  
AC ADU66846;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE zP450RAI gene isolating PCR primer, SEQ:25.  
XX  
KW Retinoic acid-inducible retinoid metabolising protein; cytochrome P450;  
KW CYP26; cancer; actinic keratosis; tumour; basal cell carcinoma; RA; acne;  
KW psoriasis; cytostatic; keratolytic; antiseborrheic; dermatological;  
KW antipsoriatic; PCR; primer; ss; zP450RAI.  
XX  
OS Danio rerio.  
XX  
PN US2004235057-A1.  
XX  
PD 25-NOV-2004.  
XX  
PF 28-MAY-2004; 2004US-00855595.  
XX  
PR 21-JUN-1996; 96US-00667546.  
PR 01-OCT-1996; 96US-00724466.  
PR 23-JUN-1997; 97WO-CA000440.  
PR 25-JUN-1997; 97US-00882164.  
PR 25-SEP-2000; 2000US-00668482.  
XX  
PA (TOOH ) UNIV QUEENS KINGSTON.  
XX  
PI Petkovich PM, White JA, Beckett BR, Jones G;  
XX  
DR WPI; 2004-832945/82.  
XX  
PT Novel antibody specifically binding to protein that oxidizes retinoid,  
PT useful for inhibiting retinoic acid hydroxylation in human.  
XX  
PS Disclosure; SEQ ID NO 25; 78pp; English.  
XX  
CC The invention relates to retinoic acid (RA)-inducible retinoid  
CC metabolising proteins found in human (hp450RAI), mouse (mp450RAI) and  
CC zebrafish (zp450RAI) and to nucleic acid molecules encoding such  
CC proteins. P450RAI is a novel member of cytochrome P450 family and is also  
CC referred to as CYP26. The invention is useful for determining protein  
CC which oxidises retinoid. It is also useful for inhibiting RA  
CC hydroxylation in an organism such as human who is need of treatment  
CC against a disease chosen from cancer, actinic keratosis, secondary tumour  
CC of the head and/or neck, basal cell carcinoma, skin cancer, acne or  
CC psoriasis. The present sequence is a PCR primer used to isolate zp450RAI  
CC gene using differential display procedure.  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
Db 9 TGGCGAA 3

RESULT 409  
ADV90786/c  
ID ADV90786 standard; DNA; 10 BP.  
XX

AC ADV90786;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Degenerate primer, SEQ ID 25.  
XX  
KW Drug screening; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN US2004259074-A1.  
XX  
PD 23-DEC-2004.  
XX  
PF 28-MAY-2004; 2004US-00855532.  
XX  
PR 21-JUN-1996; 96US-00667546.  
PR 01-OCT-1996; 96US-00724466.  
PR 23-JUN-1997; 97WO-CA000440.  
PR 25-JUN-1997; 97US-00882164.  
PR 25-SEP-2000; 2000US-00668482.  
XX  
PA (TOOH ) UNIV QUEENS KINGSTON.  
XX  
PI Petkovich PM, White JA, Beckett BR, Jones G;  
XX  
DR WPI; 2005-078941/09.  
XX  
PT Screening drugs for their effect on activity of retinoid metabolizing  
PT protein, by exposing cell transfected with nucleic acid molecule encoding  
PT protein and expressing protein, to drug, determining effect of drug on  
PT activity of protein.  
XX  
PS Disclosure; SEQ ID NO 25; 78pp; English.  
XX  
CC The present invention relates to novel retinoic acid-inducible, retinoid-  
CC metabolizing proteins (ADV90763, ADV90765 and ADV90793) and their coding  
CC sequences (ADV90764, ADV90766 and ADV90792). The retinoid-metabolizing  
CC proteins contain a heme-binding motif characteristic of the cytochrome  
CC P450 proteins. The P450RAI family has been designated CYP26. The retinoid  
CC -metabolizing proteins are useful for screening (M1) drugs for their  
CC effect on the activity of the retinoid-metabolizing proteins. (M1)  
CC involves exposing cells transfected with a retinoid-metabolizing protein  
CC coding sequence to a drug, where the transfected cell expresses the  
CC protein; and determining the effect of the drug on the activity of the  
CC protein, where the protein oxidizes a retinoid or hydroxylates a retinoid  
CC at the C4-position of the beta-ionone ring. The drugs screened by (M1),  
CC are useful for inhibiting retinoic acid metabolism, preferably retinoic  
CC acid hydroxylation in an organism for treating diseases such as cancer,  
CC actinic keratosis, oral leukoplakia, secondary tumor of head and/or neck,  
CC basal cell carcinoma, skin cancer, premalignancy associated actinic  
CC keratosis, acne, psoriasis, ichthyosis, eczema, etc. The present primer  
CC was used during differential mRNA display.  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGCGAA 17  
Db 9 TGGCGAA 3

RESULT 410  
ADY62603/c  
ID ADY62603 standard; DNA; 10 BP.  
XX  
AC ADY62603;  
XX  
DT 19-MAY-2005 (first entry)  
XX

DE Zebrafish P450RAI cDNA differential display oligo #14.  
KW DNA purification; retinoic acid; microsome; metabolism; primer; ss.  
XX  
OS Danio rerio.  
XX  
PN US6861238-B1.  
XX  
PD 01-MAR-2005.  
XX  
PF 25-SEP-2000; 2000US-00668482.  
XX  
PR 21-JUN-1996; 96US-00667546.  
PR 01-OCT-1996; 96US-00724466.  
PR 23-JUN-1997; 97WO-CA000440.  
PR 25-JUN-1997; 97US-00882164.  
XX  
PA (TOOH ) UNIV QUEENS KINGSTON.  
XX  
PI Petkovich PM, White JA, Beckett BR, Jones G;  
XX  
DR WPI; 2005-201182/21.  
XX  
XX Microsomal preparation of a cell transfected with a nucleic acid molecule  
PT encoding a protein that oxidizes/hydroxylates all-trans retinoic acid at  
PT the C4-position of beta-ionone ring, useful for metabolizing retinoic  
PT acid in a cell.  
XX  
PS Disclosure; SEQ ID NO 25; 65pp; English.  
XX  
CC The invention relates to a microsomal preparation of a cell that has been  
CC transfected with a nucleic acid molecule encoding a protein, or of its  
CC descendant cell, where the protein oxidizes or hydroxylates all-trans  
CC retinoic acid at the C4-position of the beta -ionone ring, the nucleic  
CC acid molecule comprising a nucleotide sequence that hybridizes under high  
CC stringency conditions, where high stringency conditions include a wash  
CC step of about 0.2xSCC at 65 deg. C, to a polynucleotide having a fully  
CC defined 1850 base pairs sequence given in the specification, the  
CC microsomal preparation comprising the protein. The microsomal preparation  
CC is useful for metabolizing retinoic acid in an organism or cell. This  
CC sequence corresponds to an oligonucleotide used for differential display  
CC analysis of the zebrafish P450RAI gene which encodes the P450RAI protein  
CC involved in retinoic acid metabolism.  
XX  
SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 TGGCGAA 17  
Db ||||| 3  
9 TGGCGAA 3  
  
RESULT 411  
ADY95141  
ID ADY95141 standard; DNA; 10 BP.  
XX  
AC ADY95141;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Oligonucleotide related to photo dynamic therapy, ODN2-fw.  
XX  
KW ss; photo dynamic therapy; DNA damage.  
OS Synthetic.  
XX  
PN W02005030329-A1.  
XX  
PD 07-APR-2005.  
XX

PF 29-MAR-2004; 2004WO-JP004472.  
XX  
PR 29-SEP-2003; 2003JP-00338082.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
XX  
PI Majima T, Kawai K;  
XX  
DR WPI; 2005-305912/31.  
XX  
PT Biomolecule damaging method involves irradiating photosensitized  
PT substance with optical beams of different wavelength, so as to induce  
PT multiple excitations of photosensitized substance.  
XX  
PS Example 2; SEQ ID NO 3; 49pp; Japanese.  
XX  
CC The invention relates to a method whereby photosensitized substance is  
CC irradiated with optical beams of different wavelength, so as to induce  
CC multiple excitations of photosensitized substance. Also included is a  
CC biomolecule damaging apparatus. The method is used for damaging  
CC biomolecules, by photosensitized one-electron oxidation reaction in photo  
CC dynamic therapy. The methods enables damaging of the biomolecules  
CC effectively and quickly, while reducing the strain on patients and the  
CC workload of doctors. The present sequence is an oligonucleotide used in  
CC the exemplification of the invention.  
XX  
SQ Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;  
  
Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 TCGCGCT 9  
Db ||||| 3  
TCGCGCT 9  
  
RESULT 412  
ADY95142/c  
ID ADY95142 standard; DNA; 10 BP.  
XX  
AC ADY95142;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Oligonucleotide related to photo dynamic therapy, ODN2-rev.  
XX  
KW ss; photo dynamic therapy; DNA damage.  
XX  
OS Synthetic.  
XX  
PN W02005030329-A1.  
XX  
PD 07-APR-2005.  
XX  
PF 29-MAR-2004; 2004WO-JP004472.  
XX  
PR 29-SEP-2003; 2003JP-00338082.  
XX  
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
XX  
PI Majima T, Kawai K;  
XX  
DR WPI; 2005-305912/31.  
XX  
PT Biomolecule damaging method involves irradiating photosensitized  
PT substance with optical beams of different wavelength, so as to induce  
PT multiple excitations of photosensitized substance.  
XX  
PS Example 2; SEQ ID NO 4; 49pp; Japanese.  
XX  
CC The invention relates to a method whereby photosensitized substance is  
CC irradiated with optical beams of different wavelength, so as to induce

multiple excitations of photosensitized substance. Also included is a biomolecule damaging apparatus. The method is used for damaging biomolecules, by photosensitized one-electron oxidation reaction in photo dynamic therapy. The methods enables damaging of the biomolecules effectively and quickly, while reducing the strain on patients and the workload of doctors. The present sequence is an oligonucleotide used in the exemplification of the invention.

```

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	3	TCGCGCT	9
Db	8	TCGCGCT	2

RESULT 413  
ADY95147  
ID ADY95147 standard; DNA; 10 BP.  
XX  
AC ADY95147;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Oligonucleotide related to photo dynamic therapy, ODN3-fw.

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Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 3 TCGCGCT 9  
|||

Db 3 TCGCGCT 9

RESULT 414  
ADY95148/c  
ID ADY95148 standard; DNA; 10 BP.  
XX  
AC ADY95148;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Oligonucleotide related to photo dynamic therapy, ODN3-fw.

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3	TCGCGCT	9
p <sub>b</sub>	8	TCGCGCT	2

Search completed: May 9, 2006, 15:49:46  
Job time : 1 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 15:51:35 ; Search time 0.001 seconds  
(without alignments)  
66.234 Million cell updates/sec

Title: US-09-904-968A-19-COPY  
Perfect score: 19  
Sequence: 1 ggtcgcgtgtggcgaagg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 154 seqs, 1743 residues

Total number of hits satisfying chosen parameters: 308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 154 summaries

Database : pubmaindb19:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	19	1	US-09-904-968A-19
2	11	57.9	13	1	US-10-257-017B-116243
3	11	57.9	13	1	US-10-257-017B-116244
4	10.4	54.7	14	1	US-09-847-601B-115
5	10	52.6	12	1	US-10-994-626-27
6	10	52.6	12	1	US-11-078-601-46
7	10	52.6	13	1	US-10-257-017B-20773
8	10	52.6	13	1	US-10-257-017B-20774
9	9.8	51.6	13	1	US-10-257-017B-23021
10	9.8	51.6	13	1	US-10-257-017B-23022
11	9.8	51.6	13	1	US-10-257-017B-88973
12	9.8	51.6	13	1	US-10-257-017B-88974
13	9.8	51.6	13	1	US-10-257-017B-88989
14	9.8	51.6	13	1	US-10-257-017B-88990
15	9.8	51.6	13	1	US-10-257-017B-117103
16	9.8	51.6	13	1	US-10-257-017B-117104
17	9.8	51.6	14	1	US-10-291-230-33
18	9.8	51.6	14	1	US-10-291-249-33
19	9.4	49.5	12	1	US-10-257-017B-284862
20	9.4	49.5	12	1	US-10-257-017B-290687
21	9.4	49.5	12	1	US-10-257-017B-350230
22	9.4	49.5	13	1	US-10-257-017B-53147
23	9.4	49.5	13	1	US-10-257-017B-53148
24	9.4	49.5	13	1	US-10-257-017B-63161
25	9.4	49.5	13	1	US-10-257-017B-63162
26	9.4	49.5	13	1	US-10-257-017B-77009
27	9.4	49.5	13	1	US-10-257-017B-77010
28	9.4	49.5	13	1	US-10-257-017B-86991
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36	9.4	49.5	13	1	US-10-257-017B-116241	Sequence 116241,
37	9.4	49.5	13	1	US-10-257-017B-116242	Sequence 116242,
38	9.4	49.5	13	1	US-10-257-017B-219517	Sequence 219517,
39	9.4	49.5	13	1	US-10-257-017B-219518	Sequence 219518,
40	9.4	49.5	13	1	US-10-257-017B-219519	Sequence 219519,
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43	9.4	49.5	13	1	US-10-257-017B-232664	Sequence 232664,
44	9.4	49.5	13	1	US-10-257-017B-265117	Sequence 265117,
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48	9	47.4	10	1	US-08-825-486-18	Sequence 18, Appl
49	9	47.4	10	1	US-08-870-434-18	Sequence 18, Appl
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56	8.8	46.3	12	1	US-10-257-017B-359284	Sequence 359284,
57	8.4	44.2	10	1	US-10-033-145-250	Sequence 250, App
58	8.4	44.2	10	1	US-10-033-145-273	Sequence 273, App
59	8.4	44.2	10	1	US-10-330-627-903	Sequence 903, App
60	8.4	44.2	10	1	US-10-487-934-173	Sequence 173, App
61	8.4	44.2	11	1	US-10-314-322-305	Sequence 305, App
62	8.4	44.2	11	1	US-10-450-797-16	Sequence 16, Appl
63	8.4	44.2	11	1	US-10-450-797-923	Sequence 923, App
64	8.4	44.2	12	1	US-09-949-041A-50	Sequence 50, Appl
65	8.4	44.2	12	1	US-10-257-017B-271986	Sequence 271986,
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76	8.4	44.2	12	1	US-10-257-017B-317080	Sequence 317080,
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80	8.4	44.2	12	1	US-10-257-017B-329721	Sequence 329721,
81	8.4	44.2	12	1	US-10-257-017B-350774	Sequence 350774,
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83	8.4	44.2	12	1	US-10-912-032-28	Sequence 28, Appl
84	8	42.1	10	1	US-10-033-145-1534	Sequence 1534, Ap
85	8	42.1	10	1	US-10-330-627-718	Sequence 718, App
86	8	42.1	10	1	US-10-257-021-108	Sequence 108, App
87	8	42.1	10	1	US-10-293-222-326	Sequence 326, App
88	8	42.1	10	1	US-10-487-934-119	Sequence 119, App
89	8	42.1	10	1	US-10-487-934-266	Sequence 266, App
90	7.8	41.1	11	1	US-10-037-677-8	Sequence 8, Appli
91	7.8	41.1	11	1	US-10-215-647-10	Sequence 10, Appl
92	7.8	41.1	11	1	US-10-719-571-10	Sequence 10, Appl
93	7.8	41.1	11	1	US-10-450-797-851	Sequence 851, App
94	7.8	41.1	11	1	US-10-450-797-985	Sequence 985, App
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96	7.8	41.1	11	1	US-10-754-408-8	Sequence 8, Appli
97	7.4	38.9	10	1	US-09-775-743A-12	Sequence 9, Appli
98	7.4	38.9	10	1	US-09-848-537A-9	Sequence 1209, Ap
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102	7.4	38.9	10	1	US-10-033-145-2103	Sequence 279, App
103	7.4	38.9	10	1	US-10-330-627-279	Sequence 280, App
104	7.4	38.9	10	1	US-10-330-627-280	Sequence 447, App
105	7.4	38.9	10	1	US-10-330-627-447	Sequence 586, App
106	7.4	38.9	10	1	US-10-330-627-586	



C 107 7.4 38.9 10 1 US-10-330-627-734 Sequence 734, App  
108 7.4 38.9 10 1 US-10-330-627-1025 Sequence 1025, Ap  
109 7.4 38.9 10 1 US-10-330-627-1064 Sequence 1064, Ap  
C 110 7.4 38.9 10 1 US-10-197-019-109 Sequence 109, App  
C 111 7.4 38.9 10 1 US-10-293-222-205 Sequence 205, App  
C 112 7.4 38.9 10 1 US-10-723-940-92 Sequence 92, Appl  
113 7.4 38.9 10 1 US-10-487-934-14 Sequence 14, Appl  
C 114 7.4 38.9 10 1 US-10-487-934-123 Sequence 123, App  
115 7.4 38.9 10 1 US-10-487-934-184 Sequence 184, App  
C 116 7.4 38.9 10 1 US-10-784-589-12 Sequence 12, Appl  
C 117 7.4 38.9 10 1 US-10-987-549-29 Sequence 29, Appl  
C 118 7.4 38.9 10 1 US-10-987-549-30 Sequence 30, Appl  
C 119 7.4 38.9 10 1 US-11-035-899-259 Sequence 259, App  
C 120 7.4 38.9 10 1 US-11-035-899-260 Sequence 260, App  
121 7 36.8 10 1 US-09-867-262-5 Sequence 5, Appli  
122 7 36.8 10 1 US-09-885-551A-6 Sequence 6, Appli  
123 7 36.8 10 1 US-09-990-186-92 Sequence 92, Appl  
124 7 36.8 10 1 US-09-990-186-93 Sequence 93, Appl  
125 7 36.8 10 1 US-09-990-186-1278 Sequence 1278, Ap  
126 7 36.8 10 1 US-09-990-186-1653 Sequence 1653, Ap  
127 7 36.8 10 1 US-09-990-186-1654 Sequence 1654, Ap  
128 7 36.8 10 1 US-09-990-186-1667 Sequence 1667, Ap  
129 7 36.8 10 1 US-09-989-994-92 Sequence 92, Appl  
130 7 36.8 10 1 US-09-989-994-93 Sequence 93, Appl  
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136 7 36.8 10 1 US-10-033-145-299 Sequence 299, App  
C 137 7 36.8 10 1 US-10-033-145-527 Sequence 527, App  
C 138 7 36.8 10 1 US-10-033-145-1855 Sequence 1855, Ap  
139 7 36.8 10 1 US-10-033-145-2019 Sequence 2019, Ap  
140 7 36.8 10 1 US-10-108-077-6 Sequence 6, Appli  
C 141 7 36.8 10 1 US-10-142-111-23 Sequence 23, Appl  
142 7 36.8 10 1 US-10-223-765-284 Sequence 284, App  
143 7 36.8 10 1 US-10-330-627-524 Sequence 524, App  
C 144 7 36.8 10 1 US-10-091-281-247 Sequence 247, App  
145 7 36.8 10 1 US-10-422-523-28 Sequence 28, Appl  
146 7 36.8 10 1 US-10-029-221C-5 Sequence 5, Appli  
C 147 7 36.8 10 1 US-10-816-079-27 Sequence 27, Appl  
C 148 7 36.8 10 1 US-10-855-595-25 Sequence 25, Appl  
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C 150 7 36.8 10 1 US-10-855-532-25 Sequence 25, Appl  
C 151 7 36.8 10 1 US-10-688-489-166 Sequence 166, App  
152 7 36.8 10 1 US-10-398-271-14 Sequence 14, Appl  
C 153 7 36.8 10 1 US-10-987-549-31 Sequence 31, Appl  
C 154 7 36.8 10 1 US-10-987-549-32 Sequence 32, Appl

ALIGNMENTS

RESULT 1  
US-09-904-968A-19  
; Sequence 19, Application US/09904968A  
; Publication No. US2003008288A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: GERMINO, Gregory  
; APPLICANT: WATNICK, Terry  
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong  
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE  
; FILE REFERENCE: JHU1680-2  
; CURRENT APPLICATION NUMBER: US/09/904,968A  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/283,691  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/218,261  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19

; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer 1F1  
US-09-904-968A-19  
Query Match 100.0%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGTCGCGCTGTGGCGAAGG 19  
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Db 1 GGTCGCGCTGTGGCGAAGG 19  
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US-10-257-017B-116243  
; Sequence 116243, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 116243  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111  
US-10-257-017B-116243  
Query Match 57.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 2 TGTGGCGAAGG 12  
RESULT 3  
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; Sequence 116244, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 116244  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111  
US-10-257-017B-116244

Query Match 57.9%; Score 11; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19  
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Db 12 TGTGGCGAAGG 2

RESULT 4  
US-09-847-601B-115  
; Sequence 115, Application US/09847601B  
; Publication No. US20050096282A1  
; GENERAL INFORMATION:  
; APPLICANT: LEWIN, ALFRED S.  
; APPLICANT: SHAW, LYNN C.  
; APPLICANT: GRANT, MARIA B.  
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES  
; FILE REFERENCE: 4300.014100  
; CURRENT APPLICATION NUMBER: US/09/847,601B  
; CURRENT FILING DATE: 2001-05-01  
; PRIOR APPLICATION NUMBER: 09/063,667  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/046,147  
; PRIOR FILING DATE: 1997-05-09  
; PRIOR APPLICATION NUMBER: 60/044,492  
; PRIOR FILING DATE: 1997-04-21  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 115  
; LENGTH: 14  
; TYPE: RNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE  
US-09-847-601B-115

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Best Local Similarity 75.0%; Pred. No. 19;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGTGGCGAAGG 19  
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Db 1 CUGUGGAGAAGG 12

RESULT 5  
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; Sequence 27, Application US/10994626  
; Publication No. US20050112677A1  
; GENERAL INFORMATION:  
; APPLICANT: Samsung Electronics Co. Ltd.  
; TITLE OF INVENTION: A substrate having an oxide layer, method for detecting a target  
; TITLE OF INVENTION: substance using the same and optical sensor containing the same  
; FILE REFERENCE: PN051212  
; CURRENT APPLICATION NUMBER: US/10/994,626  
; CURRENT FILING DATE: 2004-11-22  
; NUMBER OF SEQ ID NOS: 79  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 27  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: probe oligonucleotide  
US-10-994-626-27

Query Match 52.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 10 TGTGGCGAAG 1  
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RESULT 6  
US-11-078-601-46/c  
; Sequence 46, Application US/11078601  
; Publication No. US20050202492A1  
; GENERAL INFORMATION:  
; APPLICANT: Samsung Electronics Co. Ltd.  
; TITLE OF INVENTION: A microarray having probe polynucleotide spots binding to a same  
; TITLE OF INVENTION: target polynucleotide fragment maximally apart therebetween and  
; TITLE OF INVENTION: method of producing the same  
; FILE REFERENCE: PN052961  
; CURRENT APPLICATION NUMBER: US/11/078,601  
; CURRENT FILING DATE: 2005-03-11  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 46  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: probe polynucleotide  
US-11-078-601-46

Query Match 52.6%; Score 10; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | | | |  
Db 10 TGTGGCGAAG 1

RESULT 7  
US-10-257-017B-20773  
; Sequence 20773, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 20773  
; LENGTH: 13  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004222  
US-10-257-017B-20773

Query Match 52.6%; Score 10; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
| | | | | | | | | |  
Db 1 TGTGGCGAAG 10

RESULT 8  
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; Sequence 20774, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:

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; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 20774
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004222
US-10-257-017B-20774

Query Match          52.6%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 13 TGTGGCGAAG 4

RESULT 9
US-10-257-017B-23021
; Sequence 23021, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 23021
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004520
US-10-257-017B-23021

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGG 13
Db 1 GGTCGCGTTGTGG 13

RESULT 10
US-10-257-017B-23022/c
; Sequence 23022, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
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; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 23022
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0004520
US-10-257-017B-23022

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGG 13
Db 13 GGTCGCGTTGTGG 1

RESULT 11
US-10-257-017B-88973
; Sequence 88973, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88973
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88973

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCG 15
Db 1 TCGCGTTGTTCG 13

RESULT 12
US-10-257-017B-88974/c
; Sequence 88974, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88974
; LENGTH: 13
; TYPE: DNA
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88974

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGGCG 15
    ||||| ||| |||
Db 13 TCGCGTGTGTGCG 1

RESULT 13
US-10-257-017B-88989
; Sequence 88989, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88989
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88989

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGGCG 15
    ||||| ||| |||
Db 13 TCGCGCGGTGCG 13

RESULT 14
US-10-257-017B-88990/c
; Sequence 88990, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 88990
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0022356
US-10-257-017B-88990

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGGCG 15
    ||||| ||| |||
Db 13 TCGCGCGGTGCG 13

RESULT 15
US-10-257-017B-117103
; Sequence 117103, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117103
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029306
US-10-257-017B-117103

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGAAGG 19
    ||||| |||||
Db 1 GTTGTGTGAAGG 13

RESULT 16
US-10-257-017B-117104/c
; Sequence 117104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117104
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029306
US-10-257-017B-117104

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGAAGG 19
    ||||| |||||
Db 13 GTTGTGTGAAGG 1
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Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TCGCGCTGTGGCG 15
    ||||| ||| |||
Db 13 TCGCGCGGTGCG 1

RESULT 15
US-10-257-017B-117103
; Sequence 117103, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117103
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029306
US-10-257-017B-117103

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGAAGG 19
    ||||| |||||
Db 1 GTTGTGTGAAGG 13

RESULT 16
US-10-257-017B-117104/c
; Sequence 117104, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 117104
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029306
US-10-257-017B-117104

Query Match          51.6%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGAAGG 19
    ||||| |||||
Db 13 GTTGTGTGAAGG 1
```



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RESULT 17
US-10-291-230-33
; Sequence 33, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.A
; CURRENT APPLICATION NUMBER: US/10/291,230
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-230-33
Query Match      51.6%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  GTCGGCGCTGTGGC 14
      || ||||| |||
Db      2  GTGGCGCTGGGGC 14

RESULT 18
US-10-291-249-33
; Sequence 33, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678.US.B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-249-33
Query Match      51.6%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 25;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
RESULT 19
US-10-257-017B-284862/c
; Sequence 284862, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 284862
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0012030
US-10-257-017B-284862
Query Match      49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5  GCGCTGTGGCG 15
      ||||| |||||
Db      11 GCGCGGTGGCG 1

RESULT 20
US-10-257-017B-290687/c
; Sequence 290687, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290687
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014474
US-10-257-017B-290687
Query Match      49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9  TGTGGCGAAGG 19
      ||||| |||||
Db      12 TGTGGGAAGG 2

RESULT 21
US-10-257-017B-350230/c
; Sequence 350230, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
```

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; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350230
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008276
US-10-257-017B-350230

Query Match          49.5%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      9 TGTGGCGAAGG 19
      ||||| |||||
Db      12 TGTGGGAAGG 2

RESULT 22
US-10-257-017B-53147
; Sequence 53147, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 53147
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014679
US-10-257-017B-53147

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      9 TGTGGCGAAGG 19
      ||||| |||||
Db      2 TGTGGGAAGG 12

RESULT 23
US-10-257-017B-53148/c
; Sequence 53148, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
```

```
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 53148
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0014679
US-10-257-017B-53148
```

```
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
```

```
QY      9 TGTGGCGAAGG 19
      ||||| |||||
Db      12 TGTGGGAAGG 2
```

```
RESULT 24
US-10-257-017B-63161
; Sequence 63161, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63161
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016688
US-10-257-017B-63161
```

```
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 0;
```

```
QY      9 TGTGGCGAAGG 19
      ||||| |||||
Db      2 TTTGGCGAAGG 12
```

```
RESULT 25
US-10-257-017B-63162/c
; Sequence 63162, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 63162
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
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```

; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016688
US-10-257-017B-63162

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TTTGGCGAAGG 2

RESULT 26
US-10-257-017B-77009
; Sequence 77009, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 77009
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019655
US-10-257-017B-77009

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
Db 2 GTCGCGTTGTG 12

RESULT 27
US-10-257-017B-77010/c
; Sequence 77010, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 77010
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019655
US-10-257-017B-77010

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
Db 2 GTCGCGTTGTG 12

RESULT 28
US-10-257-017B-86991
; Sequence 86991, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86991
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021858
US-10-257-017B-86991

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 3 TGTGGGGAAGG 13

RESULT 29
US-10-257-017B-86992/c
; Sequence 86992, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86992
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021858
US-10-257-017B-86992

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 11 TGTGGGGAAGG 1

RESULT 30
```

```

; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0016688
US-10-257-017B-63162

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TTTGGCGAAGG 2

RESULT 26
US-10-257-017B-77009
; Sequence 77009, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 77009
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019655
US-10-257-017B-77009

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
Db 2 GTCGCGTTGTG 12

RESULT 27
US-10-257-017B-77010/c
; Sequence 77010, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 77010
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0019655
US-10-257-017B-77010

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
Db 2 GTCGCGTTGTG 12

RESULT 28
US-10-257-017B-86991
; Sequence 86991, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86991
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021858
US-10-257-017B-86991

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 3 TGTGGGGAAGG 13

RESULT 29
US-10-257-017B-86992/c
; Sequence 86992, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 86992
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0021858
US-10-257-017B-86992

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 11 TGTGGGGAAGG 1

RESULT 30
```

```

US-10-257-017B-103959
; Sequence 103959, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single r
; TITLE OF INVENTION: methyloations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,01
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103959
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for c
US-10-257-017B-103959

```

```

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 GGTCGCGCTGT 11  
db 1 GGTCGCGCTGT 11

**RESULT 31**

```

US-10-257-017B-103960/c
; Sequence 103960, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,01
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 103960
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for
US-10-257-017B-103960

```

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 29;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GGT	CGC	TGT	11
Db	13	GGT <th>CGC</th> <th>TGT</th> <th>3</th>	CGC	TGT	3

**RESULT 32**

US-10-257-017B-104971  
; Sequence 104971, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 29;  
Matches 10; Conservative 0; Mismatches 1; Indels

Qy 9 TGTGGCGAAGG 19  
|||  
Db 1 TGTGGAGAAAG 11

RESULT 33

```

US-10-257-017B-104972/c
; Sequence 104972, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nu
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 104972
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for de
US-10-257-017B-104972

```

Query Match 49.5%; Score 9.4; DB 1; Length 13;  
Best Local Similarity 90.9%; Pred. No. 29;  
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TGTGGCGAAGG 19  
|||  
Db 13 TGTGGAGAAGG 3

## RESULT 34

```

US-10-257-017B-116159
; Sequence 116159, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,01
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07

```



```

; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116159
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029108
US-10-257-017B-116159

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
   ||||| |||
Db 2 TGTGGCGGAGG 12

RESULT 35
US-10-257-017B-116160/c
; Sequence 116160, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116160
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029108
US-10-257-017B-116160

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
   ||||| |||
Db 12 TGTGGCGGAGG 2

RESULT 36
US-10-257-017B-116241
; Sequence 116241, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116241
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111
US-10-257-017B-116241
```

```

US-10-257-017B-116241

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
   ||||| |||
Db 2 TGTGGTGAAGG 12

RESULT 37
US-10-257-017B-116242/c
; Sequence 116242, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 116242
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0029111
US-10-257-017B-116242

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
   ||||| |||
Db 12 TGTGGTGAAGG 2

RESULT 38
US-10-257-017B-219517
; Sequence 219517, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219517
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0053391
US-10-257-017B-219517

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
```

```
Db          2 TGTGGGGAAGG 12
||||| |||||
RESULT 39
US-10-257-017B-219518/c
; Sequence 219518, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219518
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00533391
US-10-257-017B-219518
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TGTGGCGAAGG 19
||||| |||||
Db          12 TGTGGGGAAGG 2

RESULT 40
US-10-257-017B-219519
; Sequence 219519, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219519
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00533391
US-10-257-017B-219519
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TGTGGCGAAGG 19
||||| |||||
Db          2 TGTGGGGAAGG 12

RESULT 41
US-10-257-017B-219520/c
; Sequence 219520, Application US/10257017B
```

```
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 219520
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC00533391
US-10-257-017B-219520
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TGTGGCGAAGG 19
||||| |||||
Db          12 TGTGGGGAAGG 2

RESULT 42
US-10-257-017B-232663
; Sequence 232663, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 232663
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056734
US-10-257-017B-232663
Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          9 TGTGGCGAAGG 19
|| ||||| ||
Db          2 TGGGGCGAAGG 12

RESULT 43
US-10-257-017B-232664/c
; Sequence 232664, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 232664
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0056734
US-10-257-017B-232664

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGGGGCGAAGG 2

RESULT 44
US-10-257-017B-265117
; Sequence 265117, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 265117
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0064243
US-10-257-017B-265117

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 2 TGTGACGAAGG 12

RESULT 45
US-10-257-017B-265118/c
; Sequence 265118, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 265118
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0064243
US-10-257-017B-265118
```

```
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0064243
US-10-257-017B-265118

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAGG 19
Db 12 TGTGACGAAGG 2

RESULT 46
US-10-994-626-16
; Sequence 16, Application US/10994626
; Publication No. US20050112677A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A substrate having an oxide layer, method for detecting a target
; FILE REFERENCE: PN051212
; CURRENT APPLICATION NUMBER: US/10/994,626
; CURRENT FILING DATE: 2004-11-22
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 16
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe oligonucleotide
US-10-994-626-16

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGG 13
Db 3 TCCCGCTGTGG 13

RESULT 47
US-11-078-601-42
; Sequence 42, Application US/11078601
; Publication No. US20050202492A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A microarray having probe polynucleotide spots binding to a same
; FILE REFERENCE: PN052961
; CURRENT APPLICATION NUMBER: US/11/078,601
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 42
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe polynucleotide
US-11-078-601-42

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGG 13
Db 3 TCCCGCTGTGG 13

RESULT 48
US-11-078-601-42
; Sequence 42, Application US/11078601
; Publication No. US20050202492A1
; GENERAL INFORMATION:
; APPLICANT: Samsung Electronics Co. Ltd.
; TITLE OF INVENTION: A microarray having probe polynucleotide spots binding to a same
; FILE REFERENCE: PN052961
; CURRENT APPLICATION NUMBER: US/11/078,601
; CURRENT FILING DATE: 2005-03-11
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 42
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: probe polynucleotide
US-11-078-601-42

Query Match          49.5%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 29;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGG 13
```

Db 3 TCCGCGTGTGG 13  
|| |||||  
RESULT 48  
US-08-825-486-18/c  
; Sequence 18, Application US/08825486  
; Publication No. US20020016303A1  
; GENERAL INFORMATION:  
; APPLICANT: Falb, Dean  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: THE TREATMENT AND DIAGNOSIS OF  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/825,486  
; FILING DATE: 28-MAR-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/799,910  
; FILING DATE: 13-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-077-999  
; TELEPHONE: (212)7909090  
; TELEFAX: (212)8699741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other  
US-08-825-486-18  
Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 GTGGCGAAG 18  
|||  
Db 10 GTGGCGAAG 2  
|||  
RESULT 49  
US-08-870-434-18/c  
; Sequence 18, Application US/08870434  
; Publication No. US20020034736A1  
; GENERAL INFORMATION:  
; APPLICANT: Falb, Dean  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY

; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/870,434  
; FILING DATE: 06-JUN-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/799,910  
; FILING DATE: 13-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-084  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-870-434-18  
Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 GTGGCGAAG 18  
|||  
Db 10 GTGGCGAAG 2  
|||  
RESULT 50  
US-09-372-044-18/c  
; Sequence 18, Application US/09372044A  
; Patent No. US20020102603A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean FALB et al.  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Treatment and Diagnosis of Cardiovascular Disease  
; FILE REFERENCE: 7853-152  
; CURRENT APPLICATION NUMBER: US/09/372,044A  
; CURRENT FILING DATE: 1999-08-11  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-372-044-18  
Query Match 47.4%; Score 9; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 10 GTGGCGAAG 18  
|||  
Db 10 GTGGCGAAG 2  
|||  
RESULT 51  
US-09-560-150-18/c  
; Sequence 18, Application US/09560150  
; Publication No. US20030073076A1  
; GENERAL INFORMATION:



; APPLICANT: FALB, Dean A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; FILE REFERENCE: 7853-126
; CURRENT APPLICATION NUMBER: US/09/560,150
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 08/126,640
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/870,434
; PRIOR FILING DATE: 1997-02-13
; PRIOR APPLICATION NUMBER: 08/799,910
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 60/011,787
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-560-150-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
| | | | |
Db 10 GTGGCGAAG 2

RESULT 52
US-10-067-741-18/c
; Sequence 18, Application US/10067741
; Publication No. US20030097668A1
; GENERAL INFORMATION:
; APPLICANT: Dean A. Falb
; APPLICANT: Katherine Galvin
; APPLICANT: Michael Donovan
; APPLICANT: Dennis Huszar
; APPLICANT: Michael A. Gimbrone, Jr.
; TITLE OF INVENTION: Compositions and Methods for the Treatment and
; TITLE OF INVENTION: Diagnosis of
; TITLE OF INVENTION: Cardiovascular Disease
; FILE REFERENCE: 7853-140-999
; CURRENT APPLICATION NUMBER: US/10/067,741
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/288,292
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 08/870,434
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 08/799,910
; PRIOR FILING DATE: 1997-02-13
; PRIOR APPLICATION NUMBER: 60/011,787
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/485,573
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/386,844
; PRIOR FILING DATE: 1995-02-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-741-18

Query Match 47.4%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 18
| | | | |
Db 10 GTGGCGAAG 2

RESULT 53
US-10-257-017B-303992/c
; Sequence 303992, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 303992
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0020735
US-10-257-017B-303992

Query Match 47.4%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TGTGGCGAA 17
| | | | |
Db 10 TGTGGCGAA 2

RESULT 54
US-10-257-017B-289187
; Sequence 289187, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 289187
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0013829
US-10-257-017B-289187

Query Match 46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCTGTGGCGA 16
| | | | |
Db 1 GGGTTGTGGCGA 12

RESULT 55
US-10-257-017B-324838/c

```
; Sequence 324838, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 324838
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0032252
US-10-257-017B-324838

Query Match          46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY      7 GCTGTGGCGAAG 18
Db      12 GATGTGGCGGAG 1

RESULT 56
US-10-257-017B-359284/c
; Sequence 359284, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 359284
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0008283
US-10-257-017B-359284

Query Match          46.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY      4 CGCGCTGTGGCG 15
Db      12 CGCGTTGTGGAG 1

RESULT 57
US-10-033-145-250/c
; Sequence 250, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
```

```
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 250
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-250

Query Match          44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTCGCGCTG 10
Db      10 GGGCGCGCTG 1

RESULT 58
US-10-033-145-273
; Sequence 273, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-273

Query Match          44.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 CGCTGTGGCG 15
Db      1 CGCTGTGGGG 10

RESULT 59
US-10-330-627-903/c
; Sequence 903, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
```

US-10-330-627-903

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 42;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCGGCTG 10  
Db 10 GGGCGGCGTG 1

RESULT 60

US-10-487-934-173

; Sequence 173, Application US/10487934  
; Publication No. US20040265824A1  
; GENERAL INFORMATION:  
; APPLICANT: Buckhaults, Phillip  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES  
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS  
; FILE REFERENCE: 001107.00429  
; CURRENT APPLICATION NUMBER: US/10/487,934  
; CURRENT FILING DATE: 2004-03-03  
; PRIOR APPLICATION NUMBER: 60/317,494  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/383,805  
; PRIOR FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 173  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-487-934-173

Query Match 44.2%; Score 8.4; DB 1; Length 10;  
Best Local Similarity 90.0%; Pred. No. 42;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CGTGTGTGGC 15  
Db 1 CGTGTGTGGG 10

RESULT 61

US-10-314-322-305

; Sequence 305, Application US/10314322  
; Publication No. US20030229911A1  
; GENERAL INFORMATION:  
; APPLICANT: Heber-Katz, Ellen  
; TITLE OF INVENTION: Compositions and Methods for Wound  
; TITLE OF INVENTION: Healing  
; FILE REFERENCE: 000486.00016  
; CURRENT APPLICATION NUMBER: US/10/314,322  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/074,737  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/097,937  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: US 60/102,051  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: US 09/249,155  
; PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 305  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Mus musculus

US-10-314-322-305

Query Match 44.2%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCTGTGGCGA 16  
Db 1 GCTGTGGCCA 10

RESULT 62

US-10-450-797-16

; Sequence 16, Application US/10450797  
; Publication No. US20040142335A1  
; GENERAL INFORMATION:  
; APPLICANT: Petersohn, Dirk  
; APPLICANT: Conradt, Marcus  
; APPLICANT: Hofmann, Kay  
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO  
; FILE REFERENCE: HENK-0041  
; CURRENT APPLICATION NUMBER: US/10/450,797  
; CURRENT FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: PCT/EP01/15178  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: DE 101 00 121.5  
; PRIOR FILING DATE: 2001-01-03  
; NUMBER OF SEQ ID NOS: 1435  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-450-797-16

Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTGGCGAAGG 19  
Db 1 GTGGCGAATG 10

RESULT 63

US-10-450-797-923/c

; Sequence 923, Application US/10450797  
; Publication No. US20040142335A1  
; GENERAL INFORMATION:  
; APPLICANT: Petersohn, Dirk  
; APPLICANT: Conradt, Marcus  
; APPLICANT: Hofmann, Kay  
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO  
; FILE REFERENCE: HENK-0041  
; CURRENT APPLICATION NUMBER: US/10/450,797  
; CURRENT FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: PCT/EP01/15178  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR APPLICATION NUMBER: DE 101 00 121.5  
; PRIOR FILING DATE: 2001-01-03  
; NUMBER OF SEQ ID NOS: 1435  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 923  
; LENGTH: 11  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-10-450-797-923

Query Match 44.2%; Score 8.4; DB 1; Length 11;  
Best Local Similarity 90.0%; Pred. No. 43;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 GTGGCGAAGG 19  
Db 11 GTGGAGAGG 2

RESULT 64  
US-09-949-041A-50/c  
; Sequence 50, Application US/09949041A  
; Publication No. US20030104387A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Meng  
; APPLICANT: Woo, Hok  
; TITLE OF INVENTION: Mutation Detection of RNA Polymerase Beta Subunit Gene Having Rif  
; TITLE OF INVENTION: Resistance  
; FILE REFERENCE: fp4637  
; CURRENT APPLICATION NUMBER: US/09/949,041A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 50  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-09-949-041A-50

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 45;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGGC 14  
| | | | | | | |  
Db 11 GCGCTGGGGC 2

RESULT 65  
US-10-257-017B-271986  
; Sequence 271986, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 271986  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0002677  
US-10-257-017B-271986

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 45;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19  
| | | | | | | |  
Db 2 GAGGCGAAGG 11

RESULT 66  
US-10-257-017B-273770  
; Sequence 273770, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 273770  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0003303  
US-10-257-017B-273770

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 45;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
| | | | | | | |  
Db 2 TGTGGTGAAG 11

RESULT 67  
US-10-257-017B-290024/c  
; Sequence 290024, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 382046  
; SEQ ID NO 290024  
; LENGTH: 12  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014187  
US-10-257-017B-290024

Query Match 44.2%; Score 8.4; DB 1; Length 12;  
Best Local Similarity 90.0%; Pred. No. 45;  
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18  
| | | | | | | |  
Db 12 TGTGGCGAGG 3

RESULT 68  
US-10-257-017B-290182  
; Sequence 290182, Application US/10257017B  
; Publication No. US20040241651A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexander Olek  
; APPLICANT: Christian Piepenbrock  
; APPLICANT: Kurt Berlin  
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin  
; TITLE OF INVENTION: methylations  
; FILE REFERENCE: E01/1193/WO  
; CURRENT APPLICATION NUMBER: US/10/257,017B  
; CURRENT FILING DATE: 2002-10-07  
; PRIOR APPLICATION NUMBER: DE 10019173.8  
; PRIOR FILING DATE: 2000-04-07



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; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290182
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014238
US-10-257-017B-290182

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGCGCTGTGG 13
    ||||| |||||
Db 2 CGCGCGGTGG 11

RESULT 69
US-10-257-017B-290343/c
; Sequence 290343, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290343
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014318
US-10-257-017B-290343

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
    ||||| |||||
Db 12 TGTGGGGAAG 3

RESULT 70
US-10-257-017B-290346/c
; Sequence 290346, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 290346
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014318
US-10-257-017B-290346
```

```

US-10-257-017B-290346

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
    ||||| |||||
Db 12 TGTGGGGAAG 3

RESULT 71
US-10-257-017B-295960
; Sequence 295960, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295960
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016826
US-10-257-017B-295960

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 19
    ||||| |||||
Db 1 GTGGCGTAGG 10

RESULT 72
US-10-257-017B-295962
; Sequence 295962, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295962
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016826
US-10-257-017B-295962

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 19
    ||||| |||||
Db 1 GTGGCGTAGG 10

RESULT 73
US-10-257-017B-295962
; Sequence 295962, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 295962
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0016826
US-10-257-017B-295962

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAG 19
    ||||| |||||
Db 1 GTGGCGTAGG 10
```

```
Db          ||||| |||
            1 GTGGCGTAGG 10

RESULT 73
US-10-257-017B-306594/c
; Sequence 306594, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 306594
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0022080
US-10-257-017B-306594

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
      ||||| |||||
Db      10 GTGGAGAAGG 1

RESULT 74
US-10-257-017B-312013
; Sequence 312013, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 312013
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024800
US-10-257-017B-312013

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 TCGCGCTGTG 12
      ||||| |||||
Db      3 TCGCGTTGTG 12

RESULT 75
US-10-257-017B-312889
; Sequence 312889, Application US/10257017B
```

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; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 312889
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonukleotid-Primer
US-10-257-017B-312889

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAGG 19
      ||||| |||||
Db      3 GTAGCGAAGG 12

RESULT 76
US-10-257-017B-317080
; Sequence 317080, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 317080
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0027806
US-10-257-017B-317080

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCTGTGGCGA 16
      ||||| |||||
Db      3 GGTGTGGCGA 12

RESULT 77
US-10-257-017B-323594
; Sequence 323594, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 323594
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031477
US-10-257-017B-323594

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
Db 1 GTGGGGAAGG 10

RESULT 78
US-10-257-017B-325659
; Sequence 325659, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 325659
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0032649
US-10-257-017B-325659

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 3 TGTGGCGAGG 12

RESULT 79
US-10-257-017B-326801
; Sequence 326801, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 326801
```

```
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0033283
US-10-257-017B-326801

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 GTGGCGAAGG 19
Db 1 GTGGGGAAGG 10

RESULT 80
US-10-257-017B-329721/c
; Sequence 329721, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 329721
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0035109
US-10-257-017B-329721

Query Match          44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TGTGGCGAAG 18
Db 11 TGTGGAGAAG 2

RESULT 81
US-10-257-017B-350774
; Sequence 350774, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 350774
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0046869
US-10-257-017B-350774
```

```
Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TGTGGCGAAG 18
      ||| |||||
Db      2 TGTTCGAAG 11

RESULT 82
US-10-257-017B-364089/c
; Sequence 364089, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 364089
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0006574
US-10-257-017B-364089

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAG 19
      ||| |||||
Db      10 GTGGTGAAG 1

RESULT 83
US-10-912-032-28/c
; Sequence 28, Application US/10912032
; Publication No. US20050089893A1
; GENERAL INFORMATION:
; APPLICANT: Lopez, Martin J.
; APPLICANT: Eritja, Ramon
; APPLICANT: Munzer, Martin
; TITLE OF INVENTION: Methods and Compositions for In Vitro and In Vivo Use of Parallel
; TITLE OF INVENTION: Stranded Hairpins and Triplex Structures as Nucleic Acid Ligands
; FILE REFERENCE: 040358
; CURRENT APPLICATION NUMBER: US/10/912,032
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/493,092
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: hairpin component
US-10-912-032-28

Query Match      44.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 45;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 GTGGCGAAG 19
      | |||||
```

```
Db      12 GAGGCGAAG 3

RESULT 84
US-10-033-145-1534
; Sequence 1534, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1534
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1534

Query Match      42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGAAG 18
      |||||
Db      3 TGGCGAAG 10

RESULT 85
US-10-330-627-718
; Sequence 718, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 718
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-718

Query Match      42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCTGTG 12
      |||||
Db      3 GCGCTGTG 10

RESULT 86
US-10-257-021-108
; Sequence 108, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Patrice J.
; APPLICANT: Sherman-Baust, Cheryl A.
; APPLICANT: Pizer, Ellen S.
```



```
; APPLICANT: Hough, Colleen D.
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
; FILE REFERENCE: 14014.0369U2
; CURRENT APPLICATION NUMBER: US/10/257,021
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10947
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,336
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-021-108
```

```
Query Match          42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 TCGCGCTG 10
          |||||||
Db       2 TCGCGCTG 9
```

```
RESULT 87
US-10-293-222-326
; Sequence 326, Application US/10293222
; Publication No. US2004003932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 326
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-326
```

```
Query Match          42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GCGCTGTG 12
          |||||||
Db       3 GCGCTGTG 10
```

```
RESULT 88
US-10-487-934-119
; Sequence 119, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
```

```
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-119
```

```
Query Match          42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CTGTGGCG 15
          |||||||
Db       2 CTGTGGCG 9
```

```
RESULT 89
US-10-487-934-266
; Sequence 266, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 266
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-266
```

```
Query Match          42.1%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GCGCTGTG 12
          |||||||
Db       3 GCGCTGTG 10
```

```
RESULT 90
US-10-037-677-8
; Sequence 8, Application US/10037677
; Publication No. US20020173003A1
; GENERAL INFORMATION:
; APPLICANT: Schellenberger, Volker
; APPLICANT: Liu, Amy D.
; APPLICANT: Selifonova, Olga V.
; TITLE OF INVENTION: Directed Evolution of Microorganisms
; FILE REFERENCE: GC560
; CURRENT APPLICATION NUMBER: US/10/037,677
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/314,847
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 11
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pos102 mutD mutated gene
US-10-037-677-8

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
   || |||||
Db 1 GTGCCGCTGTG 11

RESULT 91
US-10-215-647-10
; Sequence 10, Application US/10215647
; Publication No. US20030129170A1
; GENERAL INFORMATION:
; APPLICANT: IACOVITTI, LORRAINE
; APPLICANT: KESSLER, MARK A.
; TITLE OF INVENTION: HUMAN TYROSINE HYDROXYLASE PROMOTER AND USES THEREOF
; TITLE OF INVENTION: RELATED APPLICATIONS
; FILE REFERENCE: 003252-52860
; CURRENT APPLICATION NUMBER: US/10/215,647
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/942,325
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/228,931
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-215-647-10

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GCGCTGTGGCG 15
   ||| |||||
Db 1 GCGTGTGGCG 11

RESULT 92
US-10-719-571-10
; Sequence 10, Application US/10719571
; Publication No. US20040086972A1
; GENERAL INFORMATION:
; APPLICANT: Schellenberger, Volker
; APPLICANT: Liu, Amy D.
; APPLICANT: Selifonova, Olga V.
; TITLE OF INVENTION: Directed Evolution of Microorganisms
; FILE REFERENCE: GC560-D1
; CURRENT APPLICATION NUMBER: US/10/719,571
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 09/314,847
; PRIOR FILING DATE: 1999-05-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pos102 mutD mutated gene
US-10-719-571-10

Query Match          41.1%; Score 7.8; DB 1; Length 11;
```

```

Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTG 12
   || |||||
Db 1 GTGCCGCTGTG 11

RESULT 93
US-10-450-797-851/c
; Sequence 851, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 851
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-851

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGCGCTGTGGC 14
   ||||| |||
Db 11 CTCGCTGGGC 1

RESULT 94
US-10-450-797-985/c
; Sequence 985, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 985
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-985

Query Match          41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTGTGGCGGAAG 18
   ||| |||||
Db 11 CTGGGCGCTAAG 1
```

```
RESULT 95
US-10-450-797-1022
; Sequence 1022, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1022
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-797-1022
```

```
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 8 CTGTGGCGGAG 18
    |||||
Db 1 CTGGGGGGAAG 11
```

```
RESULT 96
US-10-754-408-8
; Sequence 8, Application US/10754408
; Publication No. US20040203035A1
; GENERAL INFORMATION:
; APPLICANT: Mast, Andrea L.
; APPLICANT: Dorn, Erin
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Accola, Molly
; APPLICANT: Wigdal, Susan S.
; TITLE OF INVENTION: Connexin Allele Detection Assays
; FILE REFERENCE: FORS-08724
; CURRENT APPLICATION NUMBER: US/10/754,408
; CURRENT FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-754-408-8
```

```
Query Match 41.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 57;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 4 CGCGCTGTGGC 14
    |||||
Db 1 CGGCCCGAGGC 11
```

```
RESULT 97
US-09-775-743A-12/c
; Sequence 12, Application US/09775743A
; Patent No. US20020058619A1
; GENERAL INFORMATION:
; APPLICANT: Supratek Pharma, Inc.
```

```
; TITLE OF INVENTION: Vascular Endothelial Growth/Factor Receptor
; FILE REFERENCE: 082181-36154
; CURRENT APPLICATION NUMBER: US/09/775,743A
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/180,568
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chemical
; OTHER INFORMATION: synthesis
US-09-775-743A-12
```

```
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GGTCGCGCT 9
    |||||
Db 10 GGTGGCGCT 2
```

```
RESULT 98
US-09-848-537A-9/c
; Sequence 9, Application US/09848537A
; Patent No. US20020137684A1
; GENERAL INFORMATION:
; APPLICANT: Tchistiakova, Liudmila
; APPLICANT: Li, Shengmin
; APPLICANT: Pietrzynski, Grzegorz
; APPLICANT: Alakhov, Valery
; TITLE OF INVENTION: Ligand For Enhancing Oral And CNS Delivery of
; FILE REFERENCE: 082181-36910
; CURRENT APPLICATION NUMBER: US/09/848,537A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
US-09-848-537A-9
```

```
Query Match 38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GGTCGCGCT 9
    |||||
Db 10 GGTGGCGCT 2
```

```
RESULT 99
US-10-033-145-1209/c
; Sequence 1209, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GAO201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
```

; NUMBER OF SEQ ID NOS: 2137  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1209  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-033-145-1209

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
| | | | |  
Db 10 TGGAGAAGG 2

RESULT 100

US-10-033-145-1502/c  
; Sequence 1502, Application US/10033145  
; Publication No. US2002015151A1  
; GENERAL INFORMATION:  
; APPLICANT: GENZYME CORPORATION  
; APPLICANT: ROBERTS, BRUCE  
; APPLICANT: SHANKARA, SRINIVAS  
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
; FILE REFERENCE: GA0201C  
; CURRENT APPLICATION NUMBER: US/10/033,145  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: PCT/US99/13800  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 2137  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1502  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-033-145-1502

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15  
| | | | |  
Db 10 GCTGTGGG 2

RESULT 101

US-10-033-145-1908  
; Sequence 1908, Application US/10033145  
; Publication No. US2002015151A1  
; GENERAL INFORMATION:  
; APPLICANT: GENZYME CORPORATION  
; APPLICANT: ROBERTS, BRUCE  
; APPLICANT: SHANKARA, SRINIVAS  
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
; FILE REFERENCE: GA0201C  
; CURRENT APPLICATION NUMBER: US/10/033,145  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: PCT/US99/13800  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 2137  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1908  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-033-145-1908

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15  
| | | | |  
Db 2 GCTGTGGG 10

RESULT 102

US-10-033-145-2103  
; Sequence 2103, Application US/10033145  
; Publication No. US2002015151A1  
; GENERAL INFORMATION:  
; APPLICANT: GENZYME CORPORATION  
; APPLICANT: ROBERTS, BRUCE  
; APPLICANT: SHANKARA, SRINIVAS  
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES  
; FILE REFERENCE: GA0201C  
; CURRENT APPLICATION NUMBER: US/10/033,145  
; CURRENT FILING DATE: 2001-11-05  
; PRIOR APPLICATION NUMBER: PCT/US99/13800  
; PRIOR FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 2137  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2103  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-033-145-2103

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13  
| | | | |  
Db 2 GGGCTGTGG 10

RESULT 103

US-10-330-627-279  
; Sequence 279, Application US/10330627  
; Publication No. US20030175771A1  
; GENERAL INFORMATION:  
; APPLICANT: Velculescu, Victor E.  
; APPLICANT: Kinzler, Kenneth W  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: Human Transcriptomes  
; FILE REFERENCE: 001107.00319  
; CURRENT APPLICATION NUMBER: US/10/330,627  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 09/448,480  
; PRIOR FILING DATE: 1999-11-24  
; NUMBER OF SEQ ID NOS: 1564  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 279  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-330-627-279

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13  
| | | | |  
Db 2 GGGCTGTGG 10

RESULT 104

US-10-330-627-280  
; Sequence 280, Application US/10330627  
; Publication No. US20030175771A1  
; GENERAL INFORMATION:



```
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-280

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GCGCTGTGG 13
| |||||
Db 2 GGGCTGTGG 10

RESULT 105
US-10-330-627-447/c
; Sequence 447, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-447

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
|||||
Db 9 CGCTGGGGC 1

RESULT 106
US-10-330-627-586/c
; Sequence 586, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 447
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-447

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
|||||
Db 9 CGCTGGGGC 1

RESULT 107
US-10-330-627-734/c
; Sequence 734, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 734
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-734

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
|||||
Db 10 CGCAGTGGC 2

RESULT 108
US-10-330-627-1025
; Sequence 1025, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1025

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
```

```
; SEQ ID NO 586
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-586

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CGCTGTGGC 14
|||||
Db 10 CGCAGTGGC 2

RESULT 107
US-10-330-627-734/c
; Sequence 734, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 734
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-734

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19
|||||
Db 10 TGGAGAAGG 2

RESULT 108
US-10-330-627-1025
; Sequence 1025, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1025
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1025

Query Match      38.9%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCTGTGGCG 15
```

Db 1 GCTGTTGG 9  
||||| |||

RESULT 109  
US-10-330-627-1064  
; Sequence 1064, Application US/10330627  
; Publication No. US20030175771A1  
; GENERAL INFORMATION:  
; APPLICANT: Velculescu, Victor E.  
; APPLICANT: Kinzler, Kenneth W  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: Human Transcriptomes  
; FILE REFERENCE: 001107.00319  
; CURRENT APPLICATION NUMBER: US/10/330,627  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 09/448,480  
; PRIOR FILING DATE: 1999-11-24  
; NUMBER OF SEQ ID NOS: 1564  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1064  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-330-627-1064

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 TGGCGAAGG 19  
||| |||||  
Db 2 TGGTGAAGG 10

RESULT 110  
US-10-197-019-109/c  
; Sequence 109, Application US/10197019  
; Publication No. US20030207284A1  
; GENERAL INFORMATION:  
; APPLICANT: Chew, Anne  
; APPLICANT: Denton, R. Rex  
; APPLICANT: Gilson, Christopher Raleigh  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Parks, Katie E.  
; TITLE OF INVENTION: HAPLOTYPES OF THE UCP2 GENE  
; FILE REFERENCE: MWH-0042US  
; CURRENT APPLICATION NUMBER: US/10/197,019  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: PCT/US01/02485  
; PRIOR FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 109  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-197-019-109

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCGCGCTG 10  
|| |||||  
Db 9 GTAGCGCTG 1

RESULT 111  
US-10-293-222-205/c  
; Sequence 205, Application US/10293222  
; Publication No. US20040033932A1  
; GENERAL INFORMATION:

; APPLICANT: Versteeg, Rogier  
; APPLICANT: Caron, Hubertus N.  
; TITLE OF INVENTION: MYC targets  
; FILE REFERENCE: 2183-5580US  
; CURRENT APPLICATION NUMBER: US/10/293,222  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: PCT/NL01/00361  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: EP 00201698.8  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: EP 00202284.6  
; PRIOR FILING DATE: 2000-06-29  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 205  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-293-222-205

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCGCGCT 9  
||| |||||  
Db 10 GGTCGCGCT 2

RESULT 112  
US-10-723-940-92/c  
; Sequence 92, Application US/10723940  
; Publication No. US20040185468A1  
; GENERAL INFORMATION:  
; APPLICANT: Leonard, Sherry  
; APPLICANT: Freeman, Robert  
; TITLE OF INVENTION: Promoter Variants in the Alpha-7 Nicotinic Acetylcholine Receptor  
; TITLE OF INVENTION: Gene  
; FILE REFERENCE: VARD-07989  
; CURRENT APPLICATION NUMBER: US/10/723,940  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 08/956,518  
; PRIOR FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 92  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-723-940-92

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGTGGCGA 16  
||| |||||  
Db 10 CTGTGGAGA 2

RESULT 113  
US-10-487-934-14  
; Sequence 14, Application US/10487934  
; Publication No. US20040265824A1  
; GENERAL INFORMATION:  
; APPLICANT: Buckhaults, Phillip  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES  
; FILE REFERENCE: 001107.00429

; CURRENT APPLICATION NUMBER: US/10/487,934  
; CURRENT FILING DATE: 2004-03-03  
; PRIOR APPLICATION NUMBER: 60/317,494  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/383,805  
; PRIOR FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-487-934-14

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
|||||  
Db 2 TGGCAAAGG 10

RESULT 114  
US-10-487-934-123/c  
; Sequence 123, Application US/10487934  
; Publication No. US20040265824A1  
; GENERAL INFORMATION:  
; APPLICANT: Buckhaults, Phillip  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES  
; FILE REFERENCE: 001107.00429  
; CURRENT APPLICATION NUMBER: US/10/487,934  
; CURRENT FILING DATE: 2004-03-03  
; PRIOR APPLICATION NUMBER: 60/317,494  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/383,805  
; PRIOR FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 123  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-487-934-123

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
|||||  
Db 9 GGTCGGGCT 1

RESULT 115  
US-10-487-934-184  
; Sequence 184, Application US/10487934  
; Publication No. US20040265824A1  
; GENERAL INFORMATION:  
; APPLICANT: Buckhaults, Phillip  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: SECRETED AND CELL SURFACE GENES  
; FILE REFERENCE: 001107.00429  
; CURRENT APPLICATION NUMBER: US/10/487,934  
; CURRENT FILING DATE: 2004-03-03  
; PRIOR APPLICATION NUMBER: 60/317,494  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/383,805

; PRIOR FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 184  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-487-934-184

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGCGAAGG 19  
|||||  
Db 2 TGGCAAAGG 10

RESULT 116  
US-10-784-589-12/c  
; Sequence 12, Application US/10784589  
; Publication No. US20040266694A1  
; GENERAL INFORMATION:  
; APPLICANT: Supratek Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: 082181-36154  
; CURRENT APPLICATION NUMBER: US/10/784,589  
; CURRENT FILING DATE: 2004-02-23  
; PRIOR APPLICATION NUMBER: US/09/775,743  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/180,568  
; PRIOR FILING DATE: 2000-02-04  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-10-784-589-12

Query Match 38.9%; Score 7.4; DB 1; Length 10;  
Best Local Similarity 88.9%; Pred. No. 66;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGCGCT 9  
|||||  
Db 10 GGTCGGGCT 2

RESULT 117  
US-10-987-549-29/c  
; Sequence 29, Application US/10987549  
; Publication No. US20050191656A1  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, R.  
; APPLICANT: Drmanac, S.  
; APPLICANT: Kita, D.  
; APPLICANT: Cooke, C.  
; APPLICANT: Xu, C.  
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES  
; FILE REFERENCE: 30311/35918  
; CURRENT APPLICATION NUMBER: US/10/987,549  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: US/09/479,608  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: US 60/115,284  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 10





```

; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 260:
US-11-035-899-260
    Query Match      38.9%; Score 7.4; DB 1; Length 10;
    Best Local Similarity 88.9%; Pred. No. 66;
    Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY      10 GTGGCGAAG 18
Db      9 GTGGCTAAG 1

RESULT 121
US-09-867-262-5
; Sequence 5, Application US/09867262
; Patent No. US20020119457A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DEVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-867-262-5
    Query Match      36.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 78;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
Db      1 CGCGCTG 7

RESULT 122
US-09-990-186-92
; Sequence 92, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-92
    Query Match      36.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 78;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGCGAAG 18
Db      4 GGCGAAG 10

RESULT 124
```

```

Db      1 CGCGCTG 7

RESULT 122
US-09-885-551A-6
; Sequence 6, Application US/09885551A
; Patent No. US20020146762A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsothe
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; TITLE OF INVENTION: DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/09/885,551A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-09-885-551A-6
    Query Match      36.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 78;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
Db      1 CGCGCTG 7

RESULT 123
US-09-990-186-92
; Sequence 92, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-92
    Query Match      36.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 78;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGCGAAG 18
Db      4 GGCGAAG 10

RESULT 124
```

```
US-09-990-186-93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-93
Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GGCGAAG 18
      |||||
Db       4 GGCGAAG 10

RESULT 125
US-09-990-186-1278
; Sequence 1278, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1278
Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
      |||||
Db       4 GCTGTGG 10

RESULT 126
US-09-990-186-1653
; Sequence 1653, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1653
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1653
Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
      |||||
Db       3 GGTCGCG 9

RESULT 127
US-09-990-186-1654
; Sequence 1654, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1654
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1654
Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
      |||||
Db       3 GGTCGCG 9

RESULT 128
US-09-990-186-1667
; Sequence 1667, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1667
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1667
Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTCGCG 7
      |||||
Db       3 GGTCGCG 9
```

```
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCG 7
Db 3 GGTCGCG 9

RESULT 129
US-09-989-994-92
; Sequence 92, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-92

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGCGAAG 18
Db 4 GGCGAAG 10

RESULT 130
US-09-989-994-93
; Sequence 93, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-93

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GGCGAAG 18
Db 4 GGCGAAG 10

RESULT 131
US-09-989-994-1278
; Sequence 1278, Application US/09989994
```

```
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1278
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1278

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTGTGG 13
Db 4 GCTGTGG 10

RESULT 132
US-09-989-994-1653
; Sequence 1653, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1653
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1653

Query Match 36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCGCG 7
Db 3 GGTCGCG 9

RESULT 133
US-09-989-994-1654
; Sequence 1654, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1654
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1654

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGTCGCG 7
Db      3 GGTCGCG 9

RESULT 134
US-09-989-994-1667
; Sequence 1667, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1667
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1667

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGTCGCG 7
Db      3 GGTCGCG 9

RESULT 135
US-10-087-426-6
; Sequence 6, Application US/10087426
; Publication No. US20020142394A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
```

```
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-087-426-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CGCGCTG 10
Db      1 CGCGCTG 7

RESULT 136
US-10-033-145-299
; Sequence 299, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 299
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-299

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CGCTGTG 12
Db      1 CGCTGTG 7

RESULT 137
US-10-033-145-527/c
; Sequence 527, Application US/10033145
; Publication No. US20020151515A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 527
```



```

;   LENGTH: 10
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-145-527

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
      |||||
Db      9 CTGTGGC 3

RESULT 138
US-10-033-145-1855/c
; Sequence 1855, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1855
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1855

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
      |||||
Db      9 GCTGTGG 3

RESULT 139
US-10-033-145-2019
; Sequence 2019, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2019
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2019

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
      |||||
```

```

Db      1 GCTGTGG 7

RESULT 140
US-10-108-077-6
; Sequence 6, Application US/10108077
; Publication No. US20030036116A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTIO
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/108,077
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-108-077-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
      |||||
Db      1 CGCGCTG 7

RESULT 141
US-10-142-111-23/c
; Sequence 23, Application US/10142111
; Publication No. US20030101485A1
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/142,111
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-142-111-23

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GCTGTGG 13
      |||||
Db      7 GCTGTGG 1

RESULT 142
```

```
US-10-223-765-284
; Sequence 284, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-284

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTGCGC 7
      |||||
Db      3 GGTGCGC 9

RESULT 143
US-10-330-627-524
; Sequence 524, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 524
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-524

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
      |||||
Db      4 CTGTGGC 10

RESULT 144
US-10-091-281-247/c
; Sequence 247, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
```

```
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 247
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative CREB/HLF.01 motif
US-10-091-281-247

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGAA 17
      |||||
Db      9 TGGCGAA 3

RESULT 145
US-10-422-523-28
; Sequence 28, Application US/10422523
; Publication No. US20040002103A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; TITLE OF INVENTION: SYNTHETIC LIGATION REASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIV-1460-15A US
; CURRENT APPLICATION NUMBER: US/10/422,523
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 09/332,835
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-422-523-28

Query Match      36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
      |||||
Db      1 CGCGCTG 7

RESULT 146
US-10-029-221C-5
; Sequence 5, Application US/10029221C
; Publication No. US20040152077A1
; GENERAL INFORMATION:
; APPLICANT: SHORT, JAY M.
; APPLICANT: DJAVAKHISHVILI, TSOTNE D.
; APPLICANT: FREY, GERHARD J.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
; FILE REFERENCE: DIV-1460-21
; CURRENT APPLICATION NUMBER: US/10/029,221C
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/008,311
; PRIOR FILING DATE: 1995-12-07
```

```
; PRIOR APPLICATION NUMBER: 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: restriction enzyme recognition site
US-10-029-221C-5

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CGCGCTG 10
        |||||||
Db      1 CGCGCTG 7

RESULT 147
US-10-816-079-27/c
; Sequence 27, Application US/10816079
; Publication No. US20040166527A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Beaudry, Gary A
; APPLICANT: Madden, Stephen L
; APPLICANT: Bertelsen, Arthur H
; TITLE OF INVENTION: Composition and Methods for the Identification of Lung Tumor
; FILE REFERENCE: GA0129C2
; CURRENT APPLICATION NUMBER: US/10/816,079
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: 09/663,516
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/080,037
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SAGE tag
US-10-816-079-27

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGTGGC 14
        |||||||
Db      9 CTGTGGC 3

RESULT 148
US-10-855-595-25/c
; Sequence 25, Application US/10855595
; Publication No. US20040235057A1
; GENERAL INFORMATION:
; APPLICANT: Petkovich, P. Martin, White, Jay A.,
; Beckett, Barbara R., Jones, Glenville
; TITLE OF INVENTION: Retinoid Metabolizing Protein
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Blake, Cassels & Graydon
; STREET: Box 25, Commerce Court West
; CITY: Toronto
; STATE: Ontario
```

```
; COUNTRY: Canada
; ZIP: M5L 1A9
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
; COMPUTER: COMPAQ, IBM PC compatible
; OPERATING SYSTEM: MS-DOS 5.1
; SOFTWARE: WORD PERFECT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/855,595
; FILING DATE: 28-May-2004
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,482
; FILING DATE: 25-Sep-2000
; APPLICATION NUMBER: 08/882,164
; FILING DATE: June 25, 1997
; APPLICATION NUMBER: 08/667,546
; FILING DATE: June 21, 1996
; APPLICATION NUMBER: 08/724,466
; FILING DATE: October 1, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunt, John C.
; REGISTRATION NUMBER: 36,424
; REFERENCE/DOCKET NUMBER: 50767/00010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 863-4344
; TELEFAX: (416) 863-2653
; INFORMATION FOR SEQ ID NO: 25
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25
US-10-855-595-25

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 TGGCGAA 17
        |||||||
Db      9 TGGCGAA 3

RESULT 149
US-10-631-544-6
; Sequence 6, Application US/10631544
; Publication No. US20040248143A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DJAVAKHISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN DIRECTED EVOLUTI
; FILE REFERENCE: DIVER1460-14
; CURRENT APPLICATION NUMBER: US/10/631,544
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/535,754
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/522,289
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: BspG I restriction site
US-10-631-544-6

Query Match          36.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 78;
```

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 CGCGCTG 10  
| | | | |  
Db 1 CGCGCTG 7

RESULT 150

US-10-855-532-25/c  
; Sequence 25, Application US/10855532  
; Publication No. US20040259074A1  
; GENERAL INFORMATION:  
; APPLICANT: Petkovich, P. Martin, White, Jay A.,  
; Beckett, Barbara R., Jones, Glenville  
; TITLE OF INVENTION: Retinoid Metabolizing Protein  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Blake, Cassels & Graydon  
; STREET: Box 25, Commerce Court West  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5L 1A9  
; MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
; COMPUTER: COMPAQ, IBM PC compatible  
; OPERATING SYSTEM: MS-DOS 5.1  
; SOFTWARE: WORD PERFECT  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/855,532  
; FILING DATE: 28-May-2004  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/668,482  
; FILING DATE: 25-Sep-2000  
; APPLICATION NUMBER: 08/882,164  
; FILING DATE: June 25, 1997  
; APPLICATION NUMBER: 08/667,546  
; FILING DATE: June 21, 1996  
; APPLICATION NUMBER: 08/724,466  
; FILING DATE: October 1, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunt, John C.  
; REGISTRATION NUMBER: 36,424  
; REFERENCE/DOCKET NUMBER: 50767/00010  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 863-4344  
; TELEFAX: (416) 863-2653  
; INFORMATION FOR SEQ ID NO: 25  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 25

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 TGGCGAA 17  
| | | | |  
Db 9 TGGCGAA 3

RESULT 151

US-10-688-489-166/c  
; Sequence 166, Application US/10688489  
; Publication No. US20040259108A1  
; GENERAL INFORMATION:  
; APPLICANT: Linnen, Jeffrey M.  
; APPLICANT: Pollner, Reinhold B.  
; APPLICANT: Wu, Wen

; APPLICANT: Dennis, Geoffrey G.  
; APPLICANT: Darby, Paul M.  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: West Nile Virus  
; FILE REFERENCE: GP140-04.UT  
; CURRENT APPLICATION NUMBER: US/10/688,489  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: 60/418,891  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: 60/429,006  
; PRIOR FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: 60/449,810  
; PRIOR FILING DATE: 2003-02-24  
; NUMBER OF SEQ ID NOS: 196  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 166  
; LENGTH: 10  
; TYPE: RNA  
; ORGANISM: West Nile Virus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(10)  
; OTHER INFORMATION: 2'-Ome nucleotide analogs  
US-10-688-489-166

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 GCGAAGG 19  
| | | | |  
Db 10 GCGAAGG 4

RESULT 152

US-10-398-271-14  
; Sequence 14, Application US/10398271  
; Publication No. US20050124010A1  
; GENERAL INFORMATION:  
; APPLICANT: Short, Jay M.  
; APPLICANT: Fu, Pengcheng  
; APPLICANT: Latterich, Martin  
; APPLICANT: Wei, Jing  
; APPLICANT: Levin, Michael  
; TITLE OF INVENTION: WHOLE CELL ENGINEERING BY MUTAGENIZING A  
; TITLE OF INVENTION: SUBSTANTIAL PORTION OF A STARTING GENOME, COMBINING  
; TITLE OF INVENTION: MUTATIONS, AND OPTIONALLY REPEATING  
; FILE REFERENCE: 09010-060US1  
; CURRENT APPLICATION NUMBER: US/10/398,271  
; CURRENT FILING DATE: 2004-03-26  
; PRIOR APPLICATION NUMBER: PCT/US01/31004  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/US01/19367  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/279,702  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 09/677,584  
; PRIOR FILING DATE: 2000-09-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polynucleotide sequence of a restriction site  
US-10-398-271-14

Query Match 36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 CGCGCTG 10



Db                   |||||||  
                  1 CGCGCTG 7

RESULT 153

US-10-987-549-31/c  
; Sequence 31, Application US/10987549  
; Publication No. US20050191656A1  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, R.  
; APPLICANT: Drmanac, S.  
; APPLICANT: Kita, D.  
; APPLICANT: Cooke, C.  
; APPLICANT: Xu, C.  
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES  
; FILE REFERENCE: 30311/35918  
; CURRENT APPLICATION NUMBER: US/10/987,549  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: US/09/479,608  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: US 60/115,284  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hypothetical sequence  
US-10-987-549-31

Query Match                   36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity   100.0%; Pred. No. 78;  
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY                   8 CTGTGGC 14  
                  |||||||  
Db                   8 CTGTGGC 2

RESULT 154

US-10-987-549-32/c  
; Sequence 32, Application US/10987549  
; Publication No. US20050191656A1  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, R.  
; APPLICANT: Drmanac, S.  
; APPLICANT: Kita, D.  
; APPLICANT: Cooke, C.  
; APPLICANT: Xu, C.  
; TITLE OF INVENTION: ENHANCED SEQUENCING BY HYBRIDIZATION USING POOLS OF PROBES  
; FILE REFERENCE: 30311/35918  
; CURRENT APPLICATION NUMBER: US/10/987,549  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: US/09/479,608  
; PRIOR FILING DATE: 2000-01-06  
; PRIOR APPLICATION NUMBER: US 60/115,284  
; PRIOR FILING DATE: 1999-01-06  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 32  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hypothetical sequence  
US-10-987-549-32

Query Match                   36.8%; Score 7; DB 1; Length 10;  
Best Local Similarity   100.0%; Pred. No. 78;  
Matches   7; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY                   8 CTGTGGC 14  
                  |||||||  
Db                   7 CTGTGGC 1

Search completed: May 9, 2006, 15:51:35  
Job time : 0.001 secs